



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 148934

TO: Patricia Duffy  
Location: REM-3B05&3C18  
Art Unit: 1645  
Friday, April 08, 2005

Case Serial Number: 10/063563

From: Paul Schulwitz  
Location: Biotech-Chem Library  
REM-1A65  
Phone: 571-272-2527

paul.schulwitz@uspto.gov

### Search Notes

AA

rik

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STIC-Biotech/ChemLib

149934

From: Duffy, Patricia  
Sent: Tuesday, April 05, 2005 12:51 PM  
To: STIC-Biotech/ChemLib  
Subject: SPDI 10/063,563

In re: 10/063,563

Please search SEQ ID NO:56 and oligomers thereof.  
Please include a commercial and interference search.  
Standard SPDI printout.

CRFB

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 4/8 \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.1.6  
OM protein - protein search, using sw model  
Run on: April 7, 2005, 04:43:49 ; Search time 172 Seconds  
(without alignments)  
173.143 Million cell updates/sec

Title: US-10-063-563-56  
Perfect score: 77  
Sequence: 1 MGPKVQLKRMFPETRIATI.....LSFIPFARDVKKCFVAVCLA 77  
Scoring table: Oligo

Searched: Gapop 60.0 , Capext 60.0  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Database : A\_Geneseq\_16dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV66715	standard; protein; 77 AA.				
DE	Membrane-bound protein PRO1027.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 3;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 2						
ID	AAU29130	standard; protein; 77 AA.				
DE	Human PRO polypeptide sequence #107.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 3;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 3						
ID	AA87553	standard; protein; 77 AA.				
DE	Human PRO1027.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 4;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 4						
ID	AA65238	standard; protein; 77 AA.				
DE	Human PRO1027 (UNQ512) protein sequence SEQ ID NO:283.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 4;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 5						
ID	ABG95878	standard; protein; 77 AA.				
DE	Human secreted/transmembrane protein PRO1027.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 4;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 6						
ID	ABU58506	standard; protein; 77 AA.				
DE	Human PRO polypeptide #107.					
PN	US2003027272-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 5;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 7						
ID	ABU8054	standard; protein; 77 AA.				
DE	Novel human secreted and transmembrane protein PRO1027.					
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 8						
ID	ABU84369	standard; protein; 77 AA.				
DE	Human secreted/transmembrane protein (PRO) #107.					
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 9						
ID	ABR66243	standard; protein; 77 AA.				
DE	Human secreted polypeptide PRO1027, SEQ ID NO:214.					
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 10						
ID	ABR65633	standard; protein; 77 AA.				
DE	Human secreted polypeptide PRO1027, SEQ ID NO:214.					
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 11						
ID	ABU99573	standard; protein; 77 AA.				
DE	Human secreted/transmembrane protein (PRO) #107.					
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 12						
ID	ABU58053	standard; protein; 77 AA.				
DE	Human PRO polypeptide #85.					
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 13						
ID	ABU59131	standard; protein; 77 AA.				
DE	Novel human secreted or transmembrane protein PRO1027.					
PN	US200213252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 14						
ID	ABU82643	standard; protein; 77 AA.				
DE	Human secreted/transmembrane protein PRO1027.					
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 15						
ID	ABU82812	standard; protein; 77 AA.				
DE	Human PRO polypeptide #107.					
PN	US2003032113-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				
RESULT 16						
ID	ABU89933	standard; protein; 77 AA.				
DE	Novel human secreted and transmembrane protein PRO1027.					
PN	US2003036147-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 77;	DB 6;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;				

RESULT 17  
ID ABR68182 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 18  
ID ABU60562 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, #115.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 19  
ID ABU96235 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 20  
ID ABU92666 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 21  
ID ABO08743 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 22  
ID ABO02795 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 23  
ID ABR74949 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 24  
ID ABR94711 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 25  
ID ABU13944 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 26  
ID ABU85684 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 27  
ID ABU98844 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 28  
ID ABU98059 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 29  
ID ABU91765 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 30  
ID ABU89458 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 31  
ID ABU86299 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 32  
ID ABU67512 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036182-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 33  
ID ABU80540 standard; protein; 77 AA.  
DE Human PRO protein #107.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 34  
ID ABU72529 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 35  
ID ABU90903 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 36  
ID ABO33962 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003009013-A1.  
PD 09-JAN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 37  
ID ABR99458 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 38  
ID ABR98848 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 39  
ID ABO16371 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 40  
ID ABR92271 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 41  
ID ABO18912 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 42  
ID ABR78333 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 43  
ID ABR71979 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 44  
ID ABR5069 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 45  
ID ABO00208 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 46  
ID ABO11540 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036124-A1.  
PD 20-FEB-2003.

Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 47  
ID ABO2185 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 48  
ID ABR8759 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 49  
ID ABR3454 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 50  
ID ABO6255 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 51  
ID ABR59291 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 52  
ID ABO9353 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 53  
ID ABO19217 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 54  
ID ABO11235 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 55  
ID ABR66853 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 56  
ID ABO16066 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 57  
ID ABO13772 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 58  
ID ABU71533 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
PA (GETH ) GENENTECH INC.  
RESULT 59  
ID ABU65675 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, SEQ ID 214.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 60  
ID ABO07523 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 61  
ID ABO03710 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 62  
ID ABR67158 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 63  
ID ABO15761 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
PA (GETH ) GENENTECH INC.  
RESULT 64  
ID ABU56042 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, PRO1027.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 65  
ID ABU72314 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
PA (GETH ) GENENTECH INC.  
RESULT 66  
ID ABU65370 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 67  
ID ABU95315 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 68  
ID ABU71218 standard; protein; 77 AA.  
DE Human PRO1027 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 69  
ID ABO07828 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 70  
ID ABR70069 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 71  
ID ABR69402 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 72  
ID ABO01543 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 73  
ID ABU81345 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 74  
ID ABR60142 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 75  
ID ABU90987 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 76  
ID ABR67877 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 77  
ID ABR65265 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 78  
ID ABR68487 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 79  
ID ABR71899 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 80  
ID ABUS9278 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, #115.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 81  
ID ABUS5379 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 82  
ID ABUS9069 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 83  
ID ABUS3149 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 84  
ID ABUS5005 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 85  
ID ABUS0553 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 86  
ID ABUS4064 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 87  
ID ABUS3715 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 88  
ID ABO25975 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 89  
ID ABR64960 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 90  
ID ABO27308 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO1027.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 91  
ID ABR68792 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 92  
ID ABO06608 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 93  
ID ABR99153 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 94  
ID ABUS7037 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 95  
ID ABUS5989 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 96  
ID ABUS2276 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 97  
ID ABUS7287 standard; protein; 77 AA.

DE Human PRO polypeptide #107.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 98  
ID ABU81759 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 99  
ID ABO8133 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 100  
ID ABU92503 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 101  
ID ABU81844 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 102  
ID ABU6608 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 103  
ID ABU81173 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 104  
ID ABR59837 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 105  
ID ABU94025 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 106  
ID ABU99878 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 107  
ID ABR66548 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.

PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 108  
ID ABR90966 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 109  
ID ABO53288 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 110  
ID ABUS8984 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, #115.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 111  
ID ABU94393 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 112  
ID ABU79275 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 113  
ID ABUS8604 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 114  
ID ABUS8909 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 115  
ID ABUS94698 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 116  
ID ABO04625 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 117  
ID ABR70374 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.

PN US2003032139-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 118  
 ID ABO92362 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003022187-A1.  
 PD 30-JAN-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 119  
 ID ABO98539 standard; protein; 77 AA.  
 DE Human PRO polypeptide #107.  
 PN US2003022301-A1.  
 PD 30-JAN-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 120  
 ID ABR65938 standard; protein; 77 AA.  
 DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
 PN US2003036165-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 121  
 ID ABR64655 standard; protein; 77 AA.  
 DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
 PN US2003027262-A1.  
 PD 06-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 122  
 ID ARU59427 standard; protein; 77 AA.  
 DE Novel human secreted or transmembrane protein PRO1107.  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 123  
 ID ARU79580 standard; protein; 77 AA.  
 DE Human PRO polypeptide #107.  
 PN US2003032110-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 124  
 ID ABU92971 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein (PRO) #107.  
 PN US2003036142-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 125  
 ID ABU95930 standard; protein; 77 AA.  
 DE Human PRO polypeptide #107.  
 PN US2003036145-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 126  
 ID ABU91150 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003036154-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 127  
 ID ASU90243 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003036153-A1.  
 PD 20-FEB-2003.

Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 128  
 ID ABO09658 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein (PRO) #107.  
 PN US2003044931-A1.  
 PD 06-MAR-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 129  
 ID ABO10930 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein (PRO) #107.  
 PN US2003036150-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 130  
 ID ABR70984 standard; protein; 77 AA.  
 DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
 PN US2003040069-A1.  
 PD 27-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 131  
 ID ABU98290 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2002183493-A1.  
 PD 05-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 132  
 ID ABU87592 standard; protein; 77 AA.  
 DE Human PRO polypeptide #107.  
 PN US2003022293-A1.  
 PD 30-JAN-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 133  
 ID ABU91460 standard; protein; 77 AA.  
 DE Human PRO polypeptide #107.  
 PN US2003032128-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 134  
 ID ASU89295 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003036634-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 135  
 ID ABU84674 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein (PRO) #107.  
 PN US2003032116-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 136  
 ID ABR69764 standard; protein; 77 AA.  
 DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
 PN US2003032122-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 137  
 ID ABU80141 standard; protein; 77 AA.  
 DE Human PRO protein #107.  
 PN US2003036139-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 77; DB 6; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;

Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 138  
ID ABU2502 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 139  
ID ABU92193 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 140  
ID ABU93410 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 141  
ID ABO09963 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 142  
ID ABO09048 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 143  
ID ABU96466 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 144  
ID ABU10899 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 145  
ID ABU10616 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein #107.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 146  
ID ABU81651 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 147  
ID ABU72136 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003023042-A1.

PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 148  
ID ABU95625 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 149  
ID ABU96834 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 150  
ID ABR70679 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 151  
ID ABO05030 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 152  
ID ABO08438 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 153  
ID ABU88590 standard; protein; 77 AA.  
DE Human secreted and transmembrane polypeptide PRO1027.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 154  
ID ABO34104 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 155  
ID ABO05645 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 156  
ID ABR74034 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 157  
ID ABR95626 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.

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PD US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 158
ID ABR0923 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 159
ID ABR1228 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 160
ID ABM00924 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049789-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 161
ID ABR8526 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 162
ID ABM77347 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 163
ID ABO28831 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 164
ID ABO31576 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 165
ID ABM07993 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 166
ID ABO40473 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068682-A1.

PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 167
ID ABO35898 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 168
ID ABO44037 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 169
ID ADA77966 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 170
ID ABM24832 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 171
ID ABO03100 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 172
ID ABR90356 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 173
ID ABM17270 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 174
ID ABR95016 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 175
ID ABR95321 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 176
ID ABO40473 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068682-A1.

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ID ADB17113 standard; protein; 77 AA.  
DE Human transmembrane PRO polypeptide (SeqID 56).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 177  
ID ABO21559 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 178  
ID ABR97823 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 179  
ID ABR87611 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 180  
ID ABM77652 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 181  
ID ABM27892 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 182  
ID ABM06163 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 183  
ID ABM03669 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 184  
ID ABM35120 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 185  
ID ABM26357 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.

PN US200304549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 186  
ID ABO48139 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 187  
ID ABR92881 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 188  
ID ABO24642 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 189  
ID ADA37794 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 190  
ID ABM11653 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 191  
ID ABM02754 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 192  
ID ABM16050 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 193  
ID ABO27611 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 194  
ID ABM29102 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068721-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 195  
ID ABO07078 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 196  
ID ABO21172 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 197  
ID ABO09518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 198  
ID ABO41388 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 199  
ID ABO36203 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 200  
ID ABO43732 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 201  
ID ABO76432 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 202  
ID ABO76128 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 203  
ID ABO25747 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;

Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 204  
ID ABO26052 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 205  
ID ABO21480 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 206  
ID ABO3405 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 207  
ID ABO02490 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 208  
ID ABO44266 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO 1027.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 209  
ID ABO90661 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 210  
ID ABO73729 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 211  
ID ABO16981 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 212  
ID ABO94406 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 213  
ID ABO75913 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;

Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 214  
ID ABR71289 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 215  
ID ABR93186 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 216  
ID ABR93491 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 217  
ID ADA10267 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, PRO1027.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 218  
ID ABR87916 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 219  
ID ABO27916 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 220  
ID ABO30051 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003084461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 221  
ID ABO33260 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 222  
ID ABM04948 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 223  
ID ABO23727 standard; protein; 77 AA.

ID ABM08908 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 224  
ID ABO36508 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 225  
ID ABO35593 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 226  
ID ABO39558 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 227  
ID ABM10433 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 228  
ID ABM11958 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 229  
ID ABO52104 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 230  
ID ABO52409 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 231  
ID ADA19918 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 232  
ID ABO23727 standard; protein; 77 AA.

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DE Human secreted/transmembrane protein (PRO) #107.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 233
ID ADB17301 standard; protein; 77 AA.
DE Human transmembrane PRO polypeptide (SeqID 56).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 234
ID ADA17811 standard; protein; 77 AA.
DE Human PRO1027 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 235
ID ABR97213 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 236
ID ABR87001 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 237
ID ABM11043 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 238
ID ABM28187 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 239
ID ABO32186 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 240
ID ABM15313 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 241
ID ABM06468 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068709-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 242
ID ABM04279 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 243
ID ABM22392 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 244
ID ABM07688 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 245
ID ABO40778 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 246
ID ABM35425 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 247
ID ABM33188 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 248
ID ABO52714 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 249
ID ABO50274 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
RESULT 250
ID ABU99268 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 77; DB 6; Length 77;
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RESULT 251  
ID ABO4320 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 252  
ID ABO5950 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 253  
ID ABM18490 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 254  
ID ADA27919 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 255  
ID ABR97518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 256  
ID ABR80618 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 257  
ID ABM01229 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 258  
ID ABR88831 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 259  
ID ABM13483 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003084457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 260  
ID ABM20867 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068711-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 261  
ID ABO41998 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 262  
ID ABO42608 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 263  
ID ABM10128 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 264  
ID ABO38643 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 265  
ID ABM32883 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 266  
ID ABM22697 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 267  
ID ABM74908 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 268  
ID ADA9758 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 269  
ID ABR96298 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 270  
ID ABM02449 standard; protein; 77 AA.

DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 271  
ID ABR86391 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 272  
ID ABR86696 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 273  
ID ABR16660 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 274  
ID ABR29712 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 275  
ID ABO29136 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 276  
ID ABR23917 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 277  
ID ABR23307 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 278  
ID ABR22087 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 279  
ID ABO37728 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 280  
ID ABR28492 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 281  
ID ABR28797 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 282  
ID ABR66441 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 283  
ID ABR75823 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 284  
ID ABR34103 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 285  
ID ABR34408 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 286  
ID ABO20339 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 287  
ID ABO21254 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 288  
ID ABO22169 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 289  
ID ADA20090 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 290  
ID ABO34194 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO 1027.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 291  
ID ABR96603 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 292  
ID ADA94499 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 293  
ID ABR85781 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 294  
ID ABR99763 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 295  
ID ABM00314 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 296  
ID ABM00619 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 297  
ID ABO29746 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003088700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 298  
ID ABM23612 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068736-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 299  
ID ABM29407 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 300  
ID ABO38338 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 301  
ID ABO45638 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 302  
ID ABM20562 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 303  
ID ADA81485 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 304  
ID ABO16676 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 305  
ID ABO18302 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 306  
ID ABO22729 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 307  
ID ABO23034 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 308  
ID ABR2576 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 309  
ID ABR81533 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 310  
ID ABM77957 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 311  
ID ABR89746 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 312  
ID ABM26662 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 313  
ID ABM13788 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 314  
ID ABO28526 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 315  
ID ABO30356 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 316  
ID ABM07383 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 317  
ID ABM03974 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 318  
ID ABO37118 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 319  
ID ABO41693 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 320  
ID ABO35288 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 321  
ID ABM25137 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 322  
ID ABO47529 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 323  
ID ABO47834 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 324  
ID ABO48444 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 325  
ID ABO51494 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 326  
ID ABO51799 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 327  
ID ABO50579 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 328  
ID ABR79703 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 329  
ID ABM16965 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 330  
ID ABO17997 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 331  
ID ABO20949 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 332  
ID ABR96908 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 333  
ID ADA38724 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 334  
ID ABM12263 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 335  
ID ABM16355 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 336  
ID ABM24222 standard; protein; 77 AA.

DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 337  
ID ABM14703 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 338  
ID ABM04584 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 339  
ID ABM06773 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 340  
ID ABM09213 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 341  
ID ABO39253 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 342  
ID ABM75518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 343  
ID ABM25442 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 344  
ID ABM19952 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 345  
ID ABO46858 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 346  
ID ABO47163 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 347  
ID ADA83283 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 348  
ID ABR71594 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 349  
ID ABR72204 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 350  
ID ABR98543 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 351  
ID ABO06913 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 352  
ID ABR84866 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 353  
ID ABR73424 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 354  
ID ABR76518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 355  
ID ABR73119 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027270-A1.  
PD 06-FEB-2003.

Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 356  
ID ABM18185 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 357  
ID ABO20644 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003052126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 358  
ID ABO25387 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 359  
ID ABO25692 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 360  
ID ABR94101 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 361  
ID ADA92845 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 362  
ID ABR80008 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 363  
ID ABM11348 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 364  
ID ABO32955 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 365  
ID ABO30661 standard; protein; 77 AA.

DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 366  
ID ABO30966 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003084468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 367  
ID ABM27272 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 368  
ID ABM30017 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 369  
ID ABM05553 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 370  
ID ABM15618 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 371  
ID ABM08603 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 372  
ID ABO42303 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 373  
ID ABO38033 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 374  
ID ABO45943 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.

PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 375  
ID ABM66746 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 376  
ID ADB20326 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 377  
ID ABM19647 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 378  
ID ABO49359 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 379  
ID ABO49664 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 380  
ID ADA78578 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 381  
ID ABR88221 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 382  
ID ADA00387 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO 1027.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 383  
ID ABM26967 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068739-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 384  
ID ABO03364 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 385  
ID ABO39863 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 386  
ID ABO49969 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 387  
ID ABO50884 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 388  
ID ABO05340 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 389  
ID ABR74644 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 390  
ID ABR77123 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 391  
ID ABR17880 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 392  
ID ABR95931 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 393  
ID ABO21864 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.

PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 394  
ID ABO20034 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 395  
ID ABO24337 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 396  
ID ABR86086 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 397  
ID ABR10738 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 398  
ID ABR76737 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 399  
ID ABR89441 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 400  
ID ABR12568 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 401  
ID ABR05858 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 402  
ID ABO34983 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 403  
ID ABO03059 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 404  
ID ABO19037 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 405  
ID ABO19342 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 406  
ID ABO46553 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 407  
ID ABO49054 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 408  
ID ABR69097 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 409  
ID ABR89136 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 410  
ID ABR72509 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 411  
ID ABR74339 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 412  
ID ABO18607 standard; protein; 77 AA.

DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 413  
ID ABR80313 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 414  
ID ABO1534 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 415  
ID ABO2144 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 416  
ID ABR87306 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 417  
ID ABO12873 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 418  
ID ABO30627 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 419  
ID ABO24527 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 420  
ID ABO29441 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 421  
ID ABO31271 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068710-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 422  
ID ABM14398 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 423  
ID ABM09823 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 424  
ID ABO38948 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 425  
ID ABM34713 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 426  
ID ABO51189 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 427  
ID ABO4015 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 428  
ID ABO10485 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 429  
ID ABO53190 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 430  
ID ABR77728 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 431  
ID ABR78938 standard; protein; 77 AA.

DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 432  
ID ABO24032 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 433  
ID ABR93796 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 434  
ID ABM01839 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 435  
ID ABM78262 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 436  
ID ABR90051 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 437  
ID ADA22406 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO1027.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 438  
ID ABM27577 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 439  
ID ABM13178 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 440  
ID ABO31881 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003088731-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 441  
ID ABM14093 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 442  
ID ABM08298 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 443  
ID ABO40168 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 444  
ID ABM74603 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 445  
ID ABM33798 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 446  
ID ABM20257 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 447  
ID ABO48749 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 448  
ID ABO22560 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 449  
ID ABR72814 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US200306122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 450  
ID ABO15456 standard; protein; 77 AA.

DE Human secreted/transmembrane protein (PRO) #107.  
PN US200306121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 451  
ID ABR85171 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 452  
ID ABO15151 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 453  
ID ABO17286 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 454  
ID ABM17575 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 455  
ID ADA06572 standard; protein; 77 AA.  
DE Human secreted/transmembrane PRO polypeptide #85.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 456  
ID ADA39265 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 457  
ID ABR85476 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 458  
ID ABM77042 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 459  
ID ABO28221 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 460

ID ABM23002 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 461  
ID ABM30322 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 462  
ID ABM21782 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 463  
ID ABM21477 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 464  
ID ABM15008 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 465  
ID ABO41083 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 466  
ID ABO36813 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 467  
ID ABO37423 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 468  
ID ABM75213 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 469  
ID ABM33493 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 470  
ID ABO46248 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 471  
ID ADA82649 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 472  
ID ADB85629 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 473  
ID ADB96291 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 474  
ID ABM31847 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 475  
ID ABM31237 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 476  
ID ADB85957 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 477  
ID ABM32152 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 478  
ID ABM32457 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068713-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 479  
 ID ADB68308 standard; protein; 77 AA.  
 DE Human PRO1027 protein.  
 PN US2003065161-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 480  
 ID ADB68115 standard; protein; 77 AA.  
 DE Human PRO1027 protein.  
 PN US2003060600-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 481  
 ID ABM31542 standard; protein; 77 AA.  
 DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
 PN US2003088761-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 482  
 ID ABM30932 standard; protein; 77 AA.  
 DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
 PN US2003068771-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 483  
 ID ADB90932 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003083473-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 484  
 ID ADC57763 standard; protein; 77 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003027754-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 485  
 ID ADC55127 standard; protein; 77 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003045463-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 486  
 ID ADC1194 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein PRO1027.  
 PN US2003049681-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 487  
 ID ADC07012 standard; protein; 77 AA.  
 DE Human PRO1027 protein.  
 PN US2003060602-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 488

ID ADC56416 standard; protein; 77 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003064375-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 489  
 ID ADC17191 standard; protein; 77 AA.  
 DE Mammalian PRO polypeptide (SeqID 56).  
 PN US2003065143-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 490  
 ID ADC07471 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein PRO1027.  
 PN US2003068647-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 491  
 ID ADC11461 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein PRO1027.  
 PN US2003069403-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 492  
 ID ADC14889 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003073208-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 493  
 ID ADC52384 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003138882-A1.  
 PD 24-JUL-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 494  
 ID ADC14583 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003082546-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 495  
 ID ADD08115 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003068623-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 496  
 ID ADC81940 standard; protein; 77 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003083461-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 497  
 ID ADD07582 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2002193299-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 7; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;

RESULT 498  
ID ADC82473 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 499  
ID ADD05687 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 500  
ID ADD08653 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 501  
ID ADD06902 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 502  
ID ADC83149 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 503  
ID ADD5256 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 504  
ID ADD36060 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 505  
ID ADD56214 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 506  
ID ADD54652 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 507  
ID ADE26806 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 508  
ID ADE26273 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 509  
ID ADF67210 standard; protein; 77 AA.  
DE Human PRO1027 amino acid sequence SEQ ID NO:283.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 510  
ID ADG01061 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 511  
ID ADG08614 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 512  
ID ADG02682 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 513  
ID ADG01389 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 514  
ID ADF9564 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 515  
ID ADF95235 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 516  
ID ADG12379 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 517  
ID ADH24088 standard; protein; 77 AA.

DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 518  
ID ADH34114 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 519  
ID ADH29947 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 520  
ID ADH23918 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 521  
ID ADH09039 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 522  
ID ADH95322 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 523  
ID ADH24598 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 524  
ID ADH37454 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 525  
ID ADH02043 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 526  
ID ADH37624 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.

PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 527  
ID ADG85662 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 528  
ID ADH24258 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 529  
ID ADH38552 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 530  
ID ADG83673 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 531  
ID ADH28481 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 532  
ID ADH27597 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 533  
ID ADH37794 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 534  
ID ADH37971 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 535  
ID ADH57391 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180920-A1.

Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 545				
ID AD103596 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181656-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 546				
ID AD111953 standard; protein; 77 AA.				
DE Human PRO polypeptide #28.				
FN US2003181686-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 547				
ID ADH90027 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181697-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 548				
ID ADH99956 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003049682-A1.				
PD 13-MAR-2003.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 549				
ID ADH98428 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181707-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 550				
ID AD111103 standard; protein; 77 AA.				
DE Human PRO polypeptide #28.				
FN US2003181682-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 551				
ID AD111613 standard; protein; 77 AA.				
DE Human PRO polypeptide #28.				
FN US2003181684-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 552				
ID AD111613 standard; protein; 77 AA.				
DE Human PRO polypeptide #28.				
FN US2003181684-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 553				
ID ADH98258 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181709-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 554				
ID ADH98598 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181708-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 555				
ID ADH98598 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181708-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 556				
ID ADH98598 standard; protein; 77 AA.				
DE Novel human secreted and transmembrane protein PRO1027.				
FN US2003181708-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 77;	DB 7;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 4.4e-75;		
RESULT 557				
ID ADH98598 standard; protein; 77 AA.				

RESULT 554  
ID ADH9088 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 555  
ID ADI05076 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 556  
ID ADI03426 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 557  
ID ADI04821 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 558  
ID ADH9275 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 559  
ID ADI19619 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 560  
ID ADH90367 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 561  
ID ADI03086 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 562  
ID ADH77935 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 563  
ID ADH97918 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 564  
ID ADI01303 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003190659-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 565  
ID ADI01998 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 566  
ID ADI03256 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 567  
ID ADI11443 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 568  
ID ADI02345 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 569  
ID ADI11783 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 570  
ID ADI05420 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 571  
ID ADH79492 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 572  
ID ADI19449 standard; protein; 77 AA.

DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181675-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 573  
ID ADI0250 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 574  
ID ADH79662 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 575  
ID ADI01488 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 576  
ID ADI01658 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 577  
ID ADI01828 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 578  
ID ADH79832 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 579  
ID ADI04650 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 580  
ID ADI02786 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 581  
ID ADH78105 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.

PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 582  
ID ADI25744 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 583  
ID ADI25914 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 584  
ID ADK65426 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 585  
ID ADH98768 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 586  
ID ADH80009 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 587  
ID ADL32820 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 588  
ID ADM30354 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 589  
ID ADL93740 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 590  
ID ADC52194 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003130483-A1.

PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 591  
ID ADE74351 standard; protein; 77 AA.  
DE Novel human secreted/transmembrane protein (PRO) #107.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 592  
ID ADE74963 standard; protein; 77 AA.  
DE Novel human secreted/transmembrane protein (PRO) #107.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 593  
ID ADF35409 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 594  
ID ADG11659 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 595  
ID ADF96176 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 596  
ID ADG04447 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 597  
ID ADG00607 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 598  
ID ADH06626 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 599  
ID ADH06456 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 600  
ID ADH26144 standard; protein; 77 AA.

ID ADG68877 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 601  
ID ADH2767 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 602  
ID ADH25108 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 603  
ID ADH33740 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 604  
ID ADG82863 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 605  
ID ADH02383 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 606  
ID ADH07990 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 607  
ID ADG69387 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 608  
ID ADH39208 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 609  
ID ADH26144 standard; protein; 77 AA.

DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 610  
ID ADG83948 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 611  
ID ADH19529 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 612  
ID ADG85492 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 613  
ID ADH06286 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 614  
ID ADH30116 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 615  
ID ADH24428 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 616  
ID ADH33113 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 617  
ID ADG69557 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 618  
ID ADH07820 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 619  
ID ADG85832 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 620  
ID ADH33378 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 621  
ID ADH33570 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 622  
ID ADH33910 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 623  
ID ADH01120 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 624  
ID ADG69727 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 625  
ID ADH21022 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 626  
ID ADH02213 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 627  
ID ADG69217 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180847-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 628  
 ID ADH86002 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180862-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 629  
 ID ADH24938 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180909-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 630  
 ID ADH39555 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180915-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 631  
 ID ADH20062 standard; protein; 77 AA.  
 DE Human secreted/transmembrane protein PRO1027.  
 PN US2003219856-A1.  
 PD 27-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 632  
 ID ADH02553 standard; protein; 77 AA.  
 DE Human PRO polypeptide #28.  
 PN US2003180840-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 633  
 ID ADG69047 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180849-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 634  
 ID ADH07650 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180850-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 635  
 ID ADG86172 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180863-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 636  
 ID ADH24768 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180908-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 637  
 ID ADH25816 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180911-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 638  
 ID ADH38382 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180922-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 639  
 ID ADH57221 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003181642-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 640  
 ID ADH52208 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180921-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 641  
 ID ADH49575 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003180857-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 642  
 ID ADH90537 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003181700-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 643  
 ID ADI11273 standard; protein; 77 AA.  
 DE Human PRO polypeptide #28.  
 PN US2003181683-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 644  
 ID ADH98938 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003190698-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 645  
 ID ADI02168 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003190659-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
 RESULT 646  
 ID ADI02168 standard; protein; 77 AA.  
 DE Novel human secreted and transmembrane protein PRO1027.  
 PN US2003190659-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 77; DB 8; Length 77;

Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 646  
ID ADH90707 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 647  
ID ADJ54852 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 648  
ID ADJ98582 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181797-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 649  
ID ADJ98752 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 650  
ID ADH78911 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 651  
ID ADJ99145 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 652  
ID ADJ99315 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 653  
ID ADJ98933 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 654  
ID ADH79081 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 655  
ID ADK00941 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 656  
ID ADK14462 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 657  
ID ADJ64623 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 658  
ID ADM31519 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 659  
ID ADM36566 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 660  
ID ADM40371 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 661  
ID ADM80911 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 662  
ID ADN37979 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 77; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 4.4e-75;  
RESULT 663  
ID AAB12126 standard; protein; 160 AA.  
DE Hydrophobic domain protein isolated from HT-1080 cells.  
PN WO200029448-A2.  
PD 25-MAY-2000.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 100.0%; Score 77; DB 3; Length 160;  
Best Local Similarity 100.0%; Pred. No. 8.8e-75;

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RESULT 664
ID ABB11987 standard; peptide; 170 AA.
DE Human secreted protein homologue, SEQ ID NO:2357.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 77; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.3e-75;
RESULT 665
ID AAY35997 standard; protein; 160 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 382.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST ) GENSET.
Query Match 89.6%; Score 69; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.8e-66;
RESULT 666
ID ADP19305 standard; protein; 160 AA.
DE Human secreted polypeptide #156.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST ) GENSET SA.
Query Match 89.6%; Score 69; DB 8; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.8e-66;
RESULT 667
ID ABP75976 standard; protein; 77 AA.
DE Human GENSET protein SEQ ID 183.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST ) GENSET.
Query Match 49.4%; Score 38; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.8e-33;
RESULT 668
ID ABP76142 standard; protein; 77 AA.
DE Human GENSET protein SEQ ID 468.
PN WO200283898-A1.
PD 24-OCT-2002.
PA (GEST ) GENSET.
Query Match 49.4%; Score 38; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.8e-33;
RESULT 669
ID ABB89647 standard; protein; 124 AA.
DE Human polypeptide SEQ ID NO 2023.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.4%; Score 8; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3;
RESULT 670
ID AAM39275 standard; protein; 159 AA.
DE Human polypeptide SEQ ID NO 2420.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 8; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.9;
RESULT 671
ID AAG89299 standard; protein; 159 AA.
DE Human secreted protein, SEQ ID NO: 419.
PN WO200142451-A2.
PD 14-JUN-2001.
PA (GEST ) GENSET.
Query Match 10.4%; Score 8; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.9;
RESULT 672
ID ADP55700 standard; protein; 159 AA.
DE Human PRO protein sequence SEQ ID NO:1676.
PN WO200403956-A2.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.4%; Score 8; DB 8; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.9;
RESULT 673
ID ADF76452 standard; protein; 178 AA.
DE Novel human secreted and transmembrane protein SeqID 126.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.4%; Score 8; DB 7; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.2;
RESULT 674
ID ADRI4033 standard; protein; 178 AA.
DE Human NF-kappaB pathway-associated protein SeqID34.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 10.4%; Score 8; DB 8; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.2;
RESULT 675
ID AAY31835 standard; protein; 179 AA.
DE Human foetal kidney secreted protein pk266_4.
PN WO9947555-A1.
PD 23-SEP-1999.
PA (GEMY ) GENETICS INST INC.
Query Match 10.4%; Score 8; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 3.2;
RESULT 676
ID AAM41061 standard; protein; 203 AA.
DE Human polypeptide SEQ ID NO 5992.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 8; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.6;
RESULT 677
ID ABU45593 standard; protein; 412 AA.
DE Protein encoded by Prokaryotic essential gene #31120.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.4%; Score 8; DB 6; Length 412;
Best Local Similarity 100.0%; Pred. No. 7.1;
RESULT 678
ID ABU32397 standard; protein; 436 AA.
DE Protein encoded by Prokaryotic essential gene #17924.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.4%; Score 8; DB 6; Length 436;
Best Local Similarity 100.0%; Pred. No. 7.4;
RESULT 679
ID ABU48248 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #33775.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.4%; Score 8; DB 6; Length 438;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 680
ID ABU15404 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #931.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 10.4%; Score 8; DB 6; Length 438;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 681
ID ABO63574 standard; protein; 441 AA.
DE Klebsiella pneumoniae polypeptide seqid 10091.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 10.4%; Score 8; DB 7; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.5;
RESULT 682
ID ABG29718 standard; protein; 72 AA.

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DE Novel human diagnostic protein #29709.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.1%; Score 7; DB 4; Length 72;  
Best Local Similarity 100.0%; Pred. No. 16;  
RESULT 683  
ID AAU44109 standard; protein; 96 AA.  
DE Propionibacterium acnes immunogenic protein #5005.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.1%; Score 7; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 22;  
RESULT 684  
ID ABM40628 standard; protein; 96 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #5304.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 9.1%; Score 7; DB 6; Length 96;  
Best Local Similarity 100.0%; Pred. No. 22;  
RESULT 685  
ID ABG24335 standard; protein; 146 AA.  
DE Novel human diagnostic protein #24326.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.1%; Score 7; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 32;  
RESULT 686  
ID ABB71351 standard; protein; 163 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40845.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 9.1%; Score 7; DB 4; Length 163;  
Best Local Similarity 100.0%; Pred. No. 35;  
RESULT 687  
ID ABB53448 standard; protein; 183 AA.  
DE Lactococcus lactis protein ybeH.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 9.1%; Score 7; DB 5; Length 183;  
Best Local Similarity 100.0%; Pred. No. 40;  
RESULT 688  
ID ABB55201 standard; protein; 197 AA.  
DE Lactococcus lactis protein yfca.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 9.1%; Score 7; DB 5; Length 197;  
Best Local Similarity 100.0%; Pred. No. 42;  
RESULT 689  
ID ABO64144 standard; protein; 199 AA.  
DE Klebsiella pneumoniae polypeptide seqid 10661.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.1%; Score 7; DB 7; Length 199;  
Best Local Similarity 100.0%; Pred. No. 43;  
RESULT 690  
ID ABB90704 standard; protein; 212 AA.  
DE Chlamydia pneumoniae cp6723 protein, SEQ ID NO:357.  
PN WO200202606-A2.  
PD 10-JAN-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 9.1%; Score 7; DB 5; Length 212;  
Best Local Similarity 100.0%; Pred. No. 45;  
RESULT 691  
ID AAY35043 standard; protein; 220 AA.  
DE Chlamydia pneumoniae transmembrane protein sequence.  
PN WO9927105-A2.  
PD 03-JUN-1999.  
PA (GEST-) GENSET.  
Query Match 9.1%; Score 7; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 47;  
RESULT 692  
ID ABP28531 standard; protein; 247 AA.  
DE Streptococcus polypeptide SEQ ID NO 6238.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 9.1%; Score 7; DB 5; Length 247;  
Best Local Similarity 100.0%; Pred. No. 52;  
RESULT 693  
ID ABU43092 standard; protein; 304 AA.  
DE Protein encoded by Prokaryotic essential gene #28619.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 9.1%; Score 7; DB 6; Length 304;  
Best Local Similarity 100.0%; Pred. No. 64;  
RESULT 694  
ID AAG71882 standard; protein; 314 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1563.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA-) YEDA RES & DEV CO LTD.  
Query Match 9.1%; Score 7; DB 4; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 695  
ID AAU24647 standard; protein; 314 AA.  
DE Human olfactory receptor AOLFRI43.  
PN WO200168805-A2.  
PD 20-SEP-2001.  
PA (SENO-) SENOMYX INC.  
Query Match 9.1%; Score 7; DB 4; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 696  
ID ABJ03989 standard; protein; 314 AA.  
DE Human G-protein coupled receptor SEQ ID NO: 44.  
PN WO200255558-A2.  
PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.1%; Score 7; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 697  
ID ABP95687 standard; protein; 314 AA.  
DE Human GPCR polypeptide SEQ ID NO 184.  
PN WO200216548-A2.  
PD 28-FEB-2002.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 9.1%; Score 7; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 698  
ID AAU95721 standard; protein; 314 AA.  
DE Human olfactory and pheromone G protein-coupled receptor #208.  
PN WO200224726-A2.  
PD 28-MAR-2002.  
PA (CHEN-) CHEMCOM SA.  
Query Match 9.1%; Score 7; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 699  
ID AAU85267 standard; protein; 314 AA.  
DE G-coupled olfactory receptor #128.  
PN WO200198526-A2.  
PD 27-DEC-2001.  
PA (SENO-) SENOMYX INC.  
Query Match 9.1%; Score 7; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 700  
ID ADH30852 standard; protein; 314 AA.

DE Human G-protein coupled receptor (GPCR) polypeptide #22.  
PN US2003232332-A1.  
PD 18-DEC-2003.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (LILL/) LI L.  
PA (BALL/) BALLINGER R A.  
PA (CASW/) CASMAN S J.  
PA (SPYT/) SPYTEK K A.  
PA (COLM/) COLMAN S D.  
PA (VERN/) VERNET C A M.  
PA (SHEN/) SHENOY S G.  
PA (GUSE/) GUSEV V Y.  
PA (MALY/) MALYANKAR U M.  
PA (EDIN/) EDINGER S R.  
PA (GERL/) GERLACH V.  
PA (SMIT/) SMITHSON G.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MACD/) MACDOUGALL J R.  
PA (GUNT/) GUNTHER E.  
PA (PEYM/) PEYMAN J A.  
PA (ELLE/) ELLERMAN K.  
PA (MILL/) MILLET I.  
PA (TCHE/) TCHERNEV V T.  
PA (ANDE/) ANDERSON D W.  
PA (WOLE/) WOLENC A R.  
Query Match 9.1%; Score 7; DB 8; Length 314;  
Best Local Similarity 100.0%; Pred. No. 66;  
RESULT 701  
ID ABG26995 standard; protein; 347 AA.  
DE Novel human diagnostic protein #26986.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.1%; Score 7; DB 4; Length 347;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 702  
ID ABG24341 standard; protein; 359 AA.  
DE Novel human diagnostic protein #24332.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.1%; Score 7; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 75;  
RESULT 703  
ID ABG29719 standard; protein; 368 AA.  
DE Novel human diagnostic protein #29710.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.1%; Score 7; DB 4; Length 368;  
Best Local Similarity 100.0%; Pred. No. 76;  
RESULT 704  
ID ADG86524 standard; protein; 373 AA.  
DE Human endogenous orphan GPCR hARE-2 mutant G285K.  
PN US2003229216-A1.  
PD 11-DEC-2003.  
PA (CHEN/) CHEN R.  
PA (LIAW/) LIAW C W.  
PA (LOWI/) LOWITZ K.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
Query Match 9.1%; Score 7; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 77;  
RESULT 705  
ID ADQ75135 standard; protein; 373 AA.  
DE Human G protein-coupled receptor ARE-2, Gly285Lys mutant.  
PN US2004137509-A1.  
PD 15-JUL-2004.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 9.1%; Score 7; DB 8; Length 373;

Best Local Similarity 100.0%; Pred. No. 77;  
RESULT 706  
ID ABB58557 standard; protein; 441 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2463.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.1%; Score 7; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 90;  
RESULT 707  
ID ADN17847 standard; protein; 448 AA.  
DE Bacterial polypeptide #500.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.1%; Score 7; DB 8; Length 448;  
Best Local Similarity 100.0%; Pred. No. 92;  
RESULT 708  
ID ADS42790 standard; protein; 449 AA.  
DE Bacterial polypeptide #21220.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.1%; Score 7; DB 8; Length 449;  
Best Local Similarity 100.0%; Pred. No. 92;  
RESULT 709  
ID ABW70211 standard; protein; 459 AA.  
DE Photorhabdus luminescens protein sequence #3308.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 9.1%; Score 7; DB 6; Length 459;  
Best Local Similarity 100.0%; Pred. No. 94;  
RESULT 710  
ID ABP74127 standard; protein; 552 AA.  
DE Human TRICH SEQ ID NO 32.  
PN WO200246415-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.1%; Score 7; DB 5; Length 552;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 711  
ID ABB47595 standard; protein; 672 AA.  
DE Listeria monocytogenes protein #299.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 9.1%; Score 7; DB 5; Length 672;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 712  
ID ADS20997 standard; protein; 891 AA.  
DE Bacterial polypeptide #10030.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.1%; Score 7; DB 8; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 713  
ID ADS23514 standard; protein; 1053 AA.  
DE Bacterial polypeptide #12547.

PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 9.1%; Score 7; DB 8; Length 1053;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 714  
ID ABB41551 standard; protein; 1215 AA.  
DE Protein encoded by Prokaryotic essential gene #27078.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 9.1%; Score 7; DB 6; Length 1215;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 715  
ID ADM33093 standard; peptide; 6 AA.  
DE Human immunodeficiency virus 1 cell entry inhibitor peptide #121.  
PN WO2004024173-A2.  
PD 25-MAR-2004.  
PA (CREA-) CREABILIS THERAPEUTICS SRL.  
Query Match 7.8%; Score 6; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 716  
ID AAB90019 standard; peptide; 15 AA.  
DE HIV gp120 protein binding peptide #1112.  
PN WO200116182-A2.  
PD 08-MAR-2001.  
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 7.8%; Score 6; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 45;  
RESULT 717  
ID AAB90036 standard; peptide; 15 AA.  
DE HIV gp120 protein binding peptide #1129.  
PN WO200116182-A2.  
PD 08-MAR-2001.  
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 7.8%; Score 6; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 45;  
RESULT 718  
ID ABR44049 standard; peptide; 16 AA.  
DE Mutant LhAOC4-17 fragment.  
PN WO2003035882-A2.  
PD 01-MAY-2003.  
PA (SYGN-) SYNGENTA LTD.  
Query Match 7.8%; Score 6; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 48;  
RESULT 719  
ID ADS33743 standard; peptide; 22 AA.  
DE cMET-HGF binding peptide #396.  
PN WO2004078778-A2.  
PD 16-SEP-2004.  
PA (DYAX-) DYAX CORP.  
PA (BRAC-) BRACCO INT BV.  
Query Match 7.8%; Score 6; DB 8; Length 22;  
Best Local Similarity 100.0%; Pred. No. 65;  
RESULT 720  
ID AAB51941 standard; protein; 26 AA.  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:73.  
PN WO2000058334-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 76;  
RESULT 721  
ID AAM89067 standard; protein; 38 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:16660.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
RESULT 722  
ID AAU22331 standard; protein; 56 AA.  
DE Human cardiovascular system antigen polypeptide SEQ ID NO 1105.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
RESULT 723  
ID ADE46299 standard; protein; 56 AA.  
DE Human cardiovascular system related polypeptide #480.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 7; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
RESULT 724  
ID ADJ07717 standard; protein; 56 AA.  
DE Human cardiovascular system associated polypeptide SeqID1105.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 8; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
RESULT 725  
ID AAO09696 standard; protein; 58 AA.  
DE Human polypeptide SEQ ID NO 23588.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
RESULT 726  
ID AAB38599 standard; protein; 62 AA.  
DE Human secreted protein sequence encoded by gene 17 SEQ ID NO:136.  
PN WO200056882-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 3; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 727  
ID AAM20362 standard; protein; 62 AA.  
DE Peptide #6796 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 728  
ID ABB40953 standard; peptide; 62 AA.  
DE Peptide #8459 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 729  
ID AAM34727 standard; protein; 62 AA.  
DE Peptide #8764 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 730  
ID ABB25065 standard; protein; 62 AA.  
DE Protein #7064 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

RESULT 731  
ID AAM74616 standard; protein; 62 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34922.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 732  
ID AAU41414 standard; protein; 62 AA.  
DE Propionibacterium acnes immunogenic protein #2310.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 733  
ID AAM61815 standard; protein; 62 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33920.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 734  
ID ABG56400 standard; peptide; 62 AA.  
DE Human liver peptide, SEQ ID No 35048.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 735  
ID ABG44443 standard; peptide; 62 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34108.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 5; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 736  
ID ABM37933 standard; protein; 62 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #2609.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 6; DB 6; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
RESULT 737  
ID AAB85512 standard; protein; 66 AA.  
DE Human protein kinase SGK162.  
PN WO200155356-A2.  
PD 02-AUG-2001.  
PA (SUGE-) SUGEN INC.  
Query Match 7.8%; Score 6; DB 4; Length 66;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
RESULT 738  
ID AAO10410 standard; protein; 69 AA.  
DE Human polypeptide SEQ ID NO 24302.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
RESULT 739  
ID AAG58965 standard; protein; 71 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76221.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 71;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
RESULT 740  
ID AAU31963 standard; protein; 76 AA.

DE Novel human secreted protein #2454.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 741  
ID AAG58964 standard; protein; 77 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76220.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 742  
ID ADQ91844 standard; protein; 77 AA.  
DE Amino acid sequence of the IDA protein.  
PN WO2004057004-A2.  
PD 08-JUL-2004.  
PA (BUTE/) BUTENKO M.  
PA (AALE/) AALEN R.  
Query Match 7.8%; Score 6; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 743  
ID ABR38910 standard; protein; 78 AA.  
DE pBAL ORF 41 # SEQ ID 6.  
PN WO2003016536-A2.  
PD 27-FEB-2003.  
PA (UYDE-) UNIV DENMARK TECH DTU.  
Query Match 7.8%; Score 6; DB 6; Length 78;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 744  
ID ABU55738 standard; protein; 82 AA.  
DE Tomato growth regulating protein, LeGREP4.  
PN WO2002083901-A2.  
PD 24-OCT-2002.  
PA (CROP-) CROPDDESIGN NV.  
PA (SAUT/) SAUTER M.  
Query Match 7.8%; Score 6; DB 6; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
RESULT 745  
ID ABB12217 standard; peptide; 83 AA.  
DE Human adapter protein homologue, SEQ ID NO: 2587.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 83;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 746  
ID ABU55718 standard; protein; 83 AA.  
DE Rape partial growth regulating protein, BnGREP1.  
PN WO2002083901-A2.  
PD 24-OCT-2002.  
PA (CROP-) CROPDDESIGN NV.  
PA (SAUT/) SAUTER M.  
Query Match 7.8%; Score 6; DB 6; Length 83;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 747  
ID ABB17001 standard; protein; 86 AA.  
DE Human nervous system related polypeptide SEQ ID NO 5658.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 748  
ID ABB17956 standard; protein; 86 AA.  
DE Human nervous system related polypeptide SEQ ID NO 6613.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
RESULT 749

DE AAM16451 standard; protein; 89 AA.  
DE Peptide #2895 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.8%; Score 6; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 750  
ID ABP08561 standard; protein; 90 AA.  
DE Human ORFX protein sequence SEQ ID NO:13104.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 6; DB 5; Length 90;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 751  
ID AAM84021 standard; protein; 92 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:11614.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 92;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
RESULT 752  
ID ADM19869 standard; protein; 94 AA.  
DE Protein encoded by novel human channel/transporter gene #187.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 94;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
RESULT 753  
ID ABB11577 standard; peptide; 95 AA.  
DE Human secreted protein homologue, SEQ ID NO:1947.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 754  
ID AAU21547 standard; protein; 95 AA.  
DE Human novel foetal antigen, SEQ ID NO 1791.  
PN WO200155312-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 755  
ID AAM96161 standard; protein; 96 AA.  
DE Human reproductive system related antigen SEQ ID NO: 4819.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 756  
ID AAU22855 standard; protein; 96 AA.  
DE Human prostate cancer antigen, Seq ID NO 374.  
PN WO200155316-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 757  
ID ADJ09428 standard; protein; 96 AA.  
DE Human prostate cancer associated polypeptide SeqID374.  
PN US2003054373-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 7; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
ID ADR95657 standard; protein; 96 AA.

DE Novel S. pneumoniae protein sequence, SEQ ID 4292.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPUTICS CORP.  
Query Match 7.8%; Score 6; DB 8; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 759  
ID ABB79227 standard; protein; 98 AA.  
DE Human prostate specific protein sequence SEQ ID NO:176.  
PN WO200236808-A2.  
PD 10-MAY-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 7.8%; Score 6; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 760  
ID AAU60442 standard; protein; 100 AA.  
DE Propionibacterium acnes immunogenic protein #21338.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 6; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 761  
ID ABM56961 standard; protein; 100 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #21637.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 6; DB 6; Length 100;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 762  
ID ABP11255 standard; protein; 106 AA.  
DE Human ORFX protein sequence SEQ ID NO:22492.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 6; DB 5; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 763  
ID AAO27176 standard; protein; 107 AA.  
DE S7 protein -11\_17.  
PN CN1381478-A.  
PD 27-NOV-2002.  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
Query Match 7.8%; Score 6; DB 6; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 764  
ID AAG58963 standard; protein; 109 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 76219.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 765  
ID ADC95743 standard; protein; 112 AA.  
DE E. faecium protein sequence SEQ ID 5370.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 766  
ID AAM52544 standard; protein; 118 AA.  
DE Human NF-E2-associated factor 13.  
PN WO200175024-A2.  
PD 11-OCT-2001.  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
Query Match 7.8%; Score 6; DB 5; Length 118;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
RESULT 767  
ID AAY95028 standard; protein; 120 AA.  
DE Human clone vp7\_1 ORF2, SEQ ID NO:128.  
PN WO200011015-A1.

PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 7.8%; Score 6; DB 3; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
RESULT 768  
ID ABO61313 standard; protein; 120 AA.  
DE Klebsiella pneumoniae polypeptide seqid 7830.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
RESULT 769  
ID ABO65064 standard; protein; 123 AA.  
DE Klebsiella pneumoniae polypeptide seqid 11581.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 123;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 770  
ID RAY42642 standard; protein; 124 AA.  
DE B. subtilis response regulator protein SpoOF.  
PN WO9949046-A1.  
PD 30-SEP-1999.  
PA (BIOG-) BIOGEMMA UK LTD.  
Query Match 7.8%; Score 6; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 771  
ID AAO29554 standard; protein; 124 AA.  
DE Human Pc0370 protein.  
PN WO2003040331-A2.  
PD 15-MAY-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 7.8%; Score 6; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 772  
ID ABR58286 standard; protein; 124 AA.  
DE BC00149 protein #SEQ ID 18.  
PN WO2003029421-A2.  
PD 10-APR-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 7.8%; Score 6; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 773  
ID ABB11372 standard; peptide; 126 AA.  
DE Human breast cancer related protein BCRB2 homologue, SEQ ID NO:1742.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 126;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 774  
ID ADS12020 standard; protein; 126 AA.  
DE Human therapeutic contig protein - SEQ ID 2257.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 7.8%; Score 6; DB 8; Length 126;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 775  
ID ADS11864 standard; protein; 126 AA.  
DE Human therapeutic contig protein - SEQ ID 2101.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 7.8%; Score 6; DB 8; Length 126;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 776  
ID ADS11863 standard; protein; 126 AA.  
DE Human therapeutic contig protein - SEQ ID 2100.  
PN WO2004080148-A2.  
PD 23-SEP-2004.

PA (NUVE-) NUVELO INC.  
Query Match 7.8%; Score 6; DB 8; Length 126;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
RESULT 777  
ID ADC97370 standard; protein; 128 AA.  
DE E. faecium protein sequence SEQ ID 6997.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 778  
ID ADF04401 standard; protein; 128 AA.  
DE Bacterial polypeptide #514.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 128;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 779  
ID AAB85730 standard; protein; 130 AA.  
DE Enzyme involved in carotenoid biosynthetic pathway.  
PN JP2001149077-A.  
PD 05-JUN-2001.  
PA (MITU) MITSUBISHI CHEM CORP.  
Query Match 7.8%; Score 6; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 780  
ID AAG90438 standard; protein; 130 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4192.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match 7.8%; Score 6; DB 4; Length 130;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 781  
ID AAR45156 standard; protein; 133 AA.  
DE Botrocetin alpha subunit.  
PN EP574621-A1.  
PD 22-DEC-1993.  
PA (UYFU-) UNIV FUJITA HEALTH.  
PA (GENZ) GENZYME CORP.  
Query Match 7.8%; Score 6; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 782  
ID AAM41921 standard; protein; 135 AA.  
DE Human polypeptide SEQ ID NO 6852.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 135;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 783  
ID ADE10004 standard; protein; 135 AA.  
DE Novel protein-related contig polypeptide sequence #592.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 135;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 784  
ID ADA55086 standard; protein; 136 AA.  
DE Human protein, SEQ ID 2654.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.8%; Score 6; DB 6; Length 136;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
RESULT 785  
ID ABU26249 standard; protein; 142 AA.  
DE Protein encoded by Prokaryotic essential gene #11776.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 142;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 786  
ID ADE08443 standard; protein; 146 AA.  
DE Novel protein (useful for identifying genetic disorders) #598.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 146;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 787  
ID AAM93730 standard; protein; 147 AA.  
DE Human polypeptide, SEQ ID NO: 3691.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.8%; Score 6; DB 4; Length 147;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 788  
ID ADL31658 standard; protein; 147 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3691.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.8%; Score 6; DB 8; Length 147;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
RESULT 789  
ID ABP39482 standard; protein; 160 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4327.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 5; Length 160;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 790  
ID ADC86547 standard; protein; 160 AA.  
DE Human GPCR protein SEQ ID NO:1000.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATOR.  
Query Match 7.8%; Score 6; DB 7; Length 160;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 791  
ID ADS05359 standard; protein; 160 AA.  
DE Staphylococcus epidermidis polypeptide seqid 4654.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Query Match 7.8%; Score 6; DB 8; Length 160;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 792  
ID AAU32072 standard; protein; 164 AA.  
DE Novel human secreted protein #2563.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 164;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 793  
ID ABP08409 standard; protein; 164 AA.  
DE Human ORFX protein sequence SEQ ID NO:16800.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 6; DB 5; Length 164;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
RESULT 794  
ID ABB50914 standard; protein; 167 AA.  
DE Human secreted protein encoded by gene 96 SEQ ID NO:867.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 4; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 795  
ID AAG65162 standard; protein; 167 AA.  
DE Human 5-phosphatase 18.  
PN WO200164730-A1.  
PD 07-SEP-2001.  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
Query Match 7.8%; Score 6; DB 4; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 796  
ID ABO45171 standard; protein; 167 AA.  
DE Novel human secreted protein #96 fragment #2.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 6; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 797  
ID ABO26651 standard; protein; 167 AA.  
DE Protein associated with novel secreted protein gene 96 #2.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 7; Length 167;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 798  
ID ADC32791 standard; protein; 171 AA.  
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:2873.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 171;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
RESULT 799  
ID ADF60188 standard; protein; 171 AA.  
DE Human contig polypeptide sequence SEQ ID NO:2555.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 171;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
RESULT 800  
ID ADF28442 standard; protein; 171 AA.  
DE Human neurological therapy-related protein - SED ID 352.  
PN WO2003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 171;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
RESULT 801  
ID ABO72027 standard; protein; 171 AA.  
DE Pseudomonas aeruginosa polypeptide #4202.  
PN US6551795-B1..  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 171;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
RESULT 802  
ID ADJ49069 standard; protein; 173 AA.  
DE Oil-associated gene related protein #569.  
PN US2004035202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 7.8%; Score 6; DB 8; Length 173;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;

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RESULT 803
ID AAB60280 standard; protein; 174 AA.
DE Neurospora crassa Cdc68 protein fragment.
PN WO200077215-A1.
PD 21-DEC-2000.
PA (ANAD-) ANADYS PHARM INC.
Query Match 7.8%; Score 6; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
RESULT 804
ID ABM73677 standard; protein; 179 AA.
DE DNA clone originating in barley containing SNP sequence #87.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 7.8%; Score 6; DB 7; Length 179;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 805
ID ABU45301 standard; protein; 181 AA.
DE Protein encoded by Prokaryotic essential gene #30828.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 806
ID AAU38465 standard; protein; 182 AA.
DE Salmonella typhi cellular proliferation protein #356.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 807
ID ABUS4893 standard; protein; 182 AA.
DE Metabolic pathway (MP) protein #23.
PN US2002142422-A1.
PD 03-OCT-2002.
PA (LERC/) LERCHL J.
PA (RENZ/) RENZ A.
PA (EHRH/) EHRHARDT T.
PA (REIN/) REINDL A.
PA (CIRP/) CIRPUS P.
PA (BISC/) BISCHOFF F.
PA (FRAN/) FRANK M.
PA (FREU/) FREUND A.
PA (DUWE/) DUWENIG E.
PA (SCHM/) SCHMIDT R.
PA (RESK/) RESKI R.
Query Match 7.8%; Score 6; DB 6; Length 182;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 808
ID ABU48016 standard; protein; 182 AA.
DE Protein encoded by Prokaryotic essential gene #33543.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 182;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
RESULT 809
ID ADA34686 standard; protein; 185 AA.
DE Acinetobacter baumannii protein #1847.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.8%; Score 6; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
RESULT 810
ID ABB67680 standard; protein; 195 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29832.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Query Match 7.8%; Score 6; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 811
ID ADR08929 standard; protein; 201 AA.
DE Human protein useful for treating neurological disease Seq 2435.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.8%; Score 6; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 812
ID ABM67845 standard; protein; 202 AA.
DE Photorhabdus luminescens protein sequence #942.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.8%; Score 6; DB 6; Length 202;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 813
ID AAB93444 standard; protein; 203 AA.
DE Human protein sequence SEQ ID NO:12686.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.8%; Score 6; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 814
ID ABB95562 standard; protein; 203 AA.
DE Human polypeptide SEQ ID NO 1938.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 6; DB 5; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 815
ID ABUS56465 standard; protein; 203 AA.
DE Lung cancer-associated polypeptide #58.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.8%; Score 6; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 816
ID ADN05076 standard; protein; 203 AA.
DE Antipsoriatic protein sequence #717.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 7.8%; Score 6; DB 8; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
RESULT 817
ID AAUS0621 standard; protein; 207 AA.
DE Propionibacterium acnes immunogenic protein #11517.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 6; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 818
ID ABM47140 standard; protein; 207 AA.
DE Propionibacterium acnes secreted polypeptide #11816.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 6; DB 6; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
RESULT 819
ID AAB18245 standard; protein; 209 AA.
DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:102.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
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PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 7.8%; Score 6; DB 3; Length 209;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 820  
ID AAW2724 standard; protein; 210 AA.  
DE Amino acid sequence of the specification.  
PN WO9737019-A1.  
PD 09-OCT-1997.  
PA (NINA-) JAPAN NAT INST HEALTH SCI.  
PA (NICA-) JAPANESE FOUND CANCER RES.  
Query Match 7.8%; Score 6; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 821  
ID AAM40135 standard; protein; 210 AA.  
DE Human polypeptide SEQ ID NO 3280.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 210;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 822  
ID ABO01414 standard; protein; 210 AA.  
DE Human protein NOV40b.  
PN WO2003023008-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 6; DB 6; Length 210;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 823  
ID ADN96200 standard; protein; 210 AA.  
DE Human NOVX polypeptide #127.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON/) ZHONG M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (SPYT/) SPYTEK K A.  
PA (KEKU/) KEKUDA R.  
PA (TAUP/) TAUPIER R J.  
PA (ANDE/) ANDERSON D W.  
PA (VERN/) VERNET C A M.  
PA (CATT/) CATTERTON E.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (TCHE/) TCHERNEV V T.  
PA (PADI/) PADIGARU M.  
PA (GUSE/) GUSEV V Y.  
PA (MALV/) MALYANKAR U M.  
PA (BURG/) BURGESS C E.  
PA (GERL/) GERLACH V.  
PA (CASM/) CASMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.  
PA (ROTH/) ROTHENBERG M E.  
PA (LARO/) LAROCHELLE W J.  
PA (SHIM/) SHIMKETS R A.  
PA (CRAB/) CRABTREE J.  
PA (RASI/) RASTELLI L.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOGF L.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (MACD/) MACDOUGALL J R.  
PA (ELLE/) ELLERMAN K.  
PA (CHAP/) CHAPOVAL A.  
Query Match 7.8%; Score 6; DB 8; Length 210;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;

RESULT 824  
ID ADF07175 standard; protein; 212 AA.  
DE Bacterial polypeptide #3288.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 212;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
RESULT 825  
ID ABB61788 standard; protein; 213 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12156.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 213;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
RESULT 826  
ID AAR45007 standard; protein; 215 AA.  
DE Sequence encoded by a human CD30-L cDNA clone.  
PN WO9324135-A1.  
PD 09-DEC-1993.  
PA (IMMV ) IMMUNEX CORP.  
Query Match 7.8%; Score 6; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
RESULT 827  
ID ADL24285 standard; protein; 215 AA.  
DE Human CD30-L #1.  
PN WO2004019866-A2.  
PD 11-MAR-2004.  
PA (IMMV ) IMMUNEX CORP.  
Query Match 7.8%; Score 6; DB 8; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
RESULT 828  
ID ABR53784 standard; protein; 220 AA.  
DE Protein sequence #SEQ ID 2433.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 7.8%; Score 6; DB 6; Length 220;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 829  
ID ADK63828 standard; protein; 220 AA.  
DE Disease treating protein complex-derived protein #1461.  
PN EP1338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 7.8%; Score 6; DB 7; Length 220;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 830  
ID ADL05021 standard; protein; 224 AA.  
DE M. catarrhalis protein #787.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 8; Length 224;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 831  
ID ADA33598 standard; protein; 231 AA.  
DE Acinetobacter baumannii protein #759.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 6; Length 231;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
RESULT 832  
ID AEG30262 standard; protein; 233 AA.  
DE Novel human diagnostic protein #30253.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 233;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
RESULT 833

ID ADB64902 standard; protein; 233 AA.  
DE Human protein encoded by clone PLACE60107010.  
PN EPI1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 233;  
Pred. No. 6e+02;  
RESULT 834  
ID ADI21122 standard; protein; 233 AA.  
DE Novel human protein #97.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 233;  
Pred. No. 6e+02;  
RESULT 835  
ID ADS22095 standard; protein; 233 AA.  
DE Bacterial polypeptide #11128.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 233;  
Pred. No. 6e+02;  
RESULT 836  
ID AAR45009 standard; protein; 234 AA.  
DE Sequence encoded by a human CD30-L cDNA clone encoding additional N-terminal amino acids.  
PN WO9324135-A1.  
PD 09-DEC-1993.  
PA (IMMV-) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 2; Length 234;  
Pred. No. 6e+02;  
RESULT 837  
ID AAU33818 standard; protein; 234 AA.  
DE Staphylococcus aureus cellular proliferation protein #94.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 4; Length 234;  
Pred. No. 6e+02;  
RESULT 838  
ID AAU78086 standard; protein; 234 AA.  
DE Human CD30-ligand (CD30L) protein sequence.  
PN WO200211767-A2.  
PD 14-FEB-2002.  
PA (IMMV-) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 5; Length 234;  
Pred. No. 6e+02;  
RESULT 839  
ID ABP97382 standard; protein; 234 AA.  
DE Human CD153 protein.  
PN WO2003000286-A1.  
PD 03-JAN-2003.  
PA (SUNR-) SUNTORY LTD.  
PA (SUNT-) SUNTORY BIOMEDICAL RES LTD.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 6; Length 234;  
Pred. No. 6e+02;  
RESULT 840  
ID ABR42311 standard; protein; 234 AA.  
DE Human CD30LG protein.  
PN WO2003040307-A2.  
PD 15-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 6; Length 234;  
Pred. No. 6e+02;  
RESULT 841  
ID ABO01413 standard; protein; 234 AA.  
DE Human protein NOV40a.

PN WO2003023008-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 6; Length 234;  
Pred. No. 6e+02;  
RESULT 842  
ID ADC35198 standard; protein; 234 AA.  
DE Human TNF ligand family member #8.  
PN US2003100074-A1.  
PD 29-MAY-2003.  
PA (YUGG-) YU G.  
PA (NIJU-) NI J.  
PA (ROSE-) ROSEN C A.  
PA (NARD-) NARDELLI B.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 234;  
Pred. No. 6e+02;  
RESULT 843  
ID ADD25574 standard; protein; 234 AA.  
DE Binding domain-immunoglobulin fusion protein-associated protein #64.  
PN US2003118592-A1.  
PD 26-JUN-2003.  
PA (GENE-) GENE-CRAFT INC.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 234;  
Pred. No. 6e+02;  
RESULT 844  
ID ABW02274 standard; protein; 234 AA.  
DE Human CD30LG protein.  
PN US2003198640-A1.  
PD 23-OCT-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 234;  
Pred. No. 6e+02;  
RESULT 845  
ID ADH87718 standard; protein; 234 AA.  
DE Enterococcus faecalis polypeptide #2198.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC-) DOUCETTE-STAMM L A.  
PA (BUSH-) BUSH D.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 234;  
Pred. No. 6e+02;  
RESULT 846  
ID ADL24287 standard; protein; 234 AA.  
DE Human CD30-L #2.  
PN WO2004019866-A2.  
PD 11-MAR-2004.  
PA (IMMV-) IMMUNEX CORP.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 234;  
Pred. No. 6e+02;  
RESULT 847  
ID ADN96198 standard; protein; 234 AA.  
DE Human NOVX polypeptide #126.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON-) ZHONG M.  
PA (LILL-) LI L.  
PA (GORM-) GORMAN L.  
PA (SPYT-) SPYTEK K A.  
PA (KERU-) KERODA R.  
PA (TAUP-) TAUPIER R J.  
PA (ANDE-) ANDERSON D W.  
PA (VERN-) VERNET C A M.  
PA (CATT-) CATTERTON E.  
PA (MILL-) MILLER C E.  
PA (SHEN-) SHENOY S G.  
PA (PATT-) PATTURAJAN M.  
PA (PENA-) PENA C E A.  
PA (TCHE-) TCHERNEV V T.  
PA (PADI-) PADIGARU M.  
PA (GUSE-) GUSEV V Y.  
PA (MALY-) MALYANKAR U M.  
PA (BURG-) BURGESS C E.  
PA (GERL-) GERLACH V.

PA (CASM/) CASHMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.  
PA (ROTH/) ROTHENBERG M E.  
PA (LARO/) LAROCHELLE W J.  
PA (SHIM/) SHIMKETS R A.  
PA (CRAB/) CRABTREE J.  
PA (RAST/) RASTELLI L.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG P L.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (MACD/) MACDOUGALL J R.  
PA (ELLE/) ELLERMAN K.  
PA (CHAP/) CHAPOVAL A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6e+02; Score 6; DB 8; Length 234;  
RESULT 848  
ID ADQ59514 standard; protein; 234 AA.  
DE Human cancer-associated (CA) protein sequence SEQ ID NO:150.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6e+02; Score 6; DB 8; Length 234;  
RESULT 849  
ID AAU37009 standard; protein; 241 AA.  
DE Staphylococcus aureus cellular proliferation protein #1179.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Score 6; DB 4; Length 241;  
RESULT 850  
ID ABU16028 standard; protein; 241 AA.  
DE Protein encoded by Prokaryotic essential gene #1555.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Score 6; DB 6; Length 241;  
RESULT 851  
ID ABM73572 standard; protein; 241 AA.  
DE Staphylococcus aureus protein #2812.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Score 6; DB 6; Length 241;  
RESULT 852  
ID ABB47788 standard; protein; 243 AA.  
DE Listeria monocytogenes protein #492.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTEUR.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Score 6; DB 5; Length 243;  
RESULT 853  
ID AAU35290 standard; protein; 244 AA.  
DE Enterococcus faecalis cellular proliferation protein #577.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Score 6; DB 4; Length 244;  
RESULT 854  
ID ABU29336 standard; protein; 244 AA.  
DE Protein encoded by Prokaryotic essential gene #14863.  
PN WO200277183-A2.  
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Score 6; DB 6; Length 244;  
RESULT 855  
ID AAW64220 standard; protein; 245 AA.  
DE Human secreted protein from clone CG300\_3.  
PN WO9827205-A2.  
PD 25-JUN-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 2; Length 245;  
RESULT 856  
ID RAM93721 standard; protein; 245 AA.  
DE Human polypeptide, SEQ ID NO: 3671.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 4; Length 245;  
RESULT 857  
ID AAB90730 standard; protein; 245 AA.  
DE Human CG300\_3 protein sequence SEQ ID 159.  
PN WO200119988-A1.  
PD 22-MAR-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 4; Length 245;  
RESULT 858  
ID ADL31638 standard; protein; 245 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3671.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 8; Length 245;  
RESULT 859  
ID AAB11054 standard; protein; 246 AA.  
DE S. mutans sortase transamidase srta protein.  
PN WO200062804-A2.  
PD 26-OCT-2000.  
PA (REGC) UNIV CALIFORNIA.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 3; Length 246;  
RESULT 860  
ID AAE36578 standard; protein; 246 AA.  
DE Streptococcus mutans Srta enzyme.  
PN WO2003020885-A2.  
PD 13-MAR-2003.  
PA (REGC) UNIV CALIFORNIA.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 6; Length 246;  
RESULT 861  
ID ABU61757 standard; protein; 246 AA.  
DE Sortase-transamidase homologue from Streptococcus mutans.  
PN US2003022179-A1.  
PD 30-JAN-2003.  
PA (SCHN/) SCHNEEWIND O.  
PA (MAZM/) MAZMANIAN S.  
PA (LIUG/) LIU G.  
PA (TONT/) TON-THAT H.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 6; Length 246;  
RESULT 862  
ID ABU44402 standard; protein; 246 AA.  
DE Protein encoded by Prokaryotic essential gene #29929.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Score 6; DB 6; Length 246;  
RESULT 863  
ID AAR92054 standard; protein; 248 AA.  
DE Xylanase precursor.

PN AU9525086-A.  
PD 08-FEB-1996.  
PA (SOLV ) SOLVAY SA.  
Query Match 7.8%; Score 6; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 864  
ID AAW44262 standard; protein; 248 AA.  
DE Glycosyl hydrolase family 11 xylanase derived from *Bacillus* sp.  
PN WO9743409-A2.  
PD 20-NOV-1997.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.8%; Score 6; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 865  
ID AAW44265 standard; protein; 248 AA.  
DE Xylanase activity positive clone protein SEQ ID NO:12.  
PN WO9743409-A2.  
PD 20-NOV-1997.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.8%; Score 6; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 866  
ID AAB42838 standard; protein; 249 AA.  
DE Human ORFX ORF2602 polypeptide sequence SEQ ID NO:5204.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 6; DB 3; Length 249;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 867  
ID AAE35948 standard; protein; 250 AA.  
DE Zea mays (Zm) Bax inhibitor (BI)-1.  
PN WO2002101079-A2.  
PD 19-DEC-2002.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 7.8%; Score 6; DB 6; Length 250;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 868  
ID AAY00252 standard; protein; 251 AA.  
DE *Enterococcus faecalis* protein EF130.  
PN WO9850554-A2.  
PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 869  
ID ABP43471 standard; protein; 251 AA.  
DE *E faecalis* EF130 protein.  
PN US2002045737-A1.  
PD 18-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 5; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 870  
ID ABU8499 standard; protein; 251 AA.  
DE *E. faecalis* novel protein #243.  
PN US2003017495-A1.  
PD 23-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 6; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 871  
ID ABU3750 standard; protein; 251 AA.  
DE *Enterococcus faecalis* EF040 polypeptide #243.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 6; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 872  
ID ADH88100 standard; protein; 251 AA.  
DE *Enterococcus faecalis* polypeptide #2580.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
Query Match 7.8%; Score 6; DB 7; Length 251;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
RESULT 873  
ID ABO66470 standard; protein; 254 AA.  
DE *Klebsiella pneumoniae* polypeptide seqid 12987.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 254;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 874  
ID ABU15858 standard; protein; 257 AA.  
DE Protein encoded by *Prokaryotic essential gene* #1385.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 257;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 875  
ID ABU39498 standard; protein; 257 AA.  
DE Protein encoded by *Prokaryotic essential gene* #25025.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 257;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 876  
ID AAU35177 standard; protein; 259 AA.  
DE *Enterococcus faecalis* cellular proliferation protein #464.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 259;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
RESULT 877  
ID ABU29157 standard; protein; 259 AA.  
DE Protein encoded by *Prokaryotic essential gene* #14684.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 259;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
RESULT 878  
ID AAG90297 standard; protein; 260 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4051.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 7.8%; Score 6; DB 4; Length 260;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
RESULT 879  
ID ADB64936 standard; protein; 262 AA.  
DE Human protein encoded by clone PROST20015210.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Query Match 7.8%; Score 6; DB 7; Length 262;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 880  
ID AAU34360 standard; protein; 267 AA.  
DE *Staphylococcus aureus* cellular proliferation protein #636.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 881  
ID AAB18237 standard; protein; 269 AA.  
DE *Plasmodium falciparum* chromosome 2 related protein SEQ ID NO:94.

PN WO200025728-A2.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 7.8%; Score 6; DB 3; Length 269;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 882  
ID AAU37278 standard; protein; 269 AA.  
DE Staphylococcus aureus cellular proliferation protein #1448.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 269;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 883  
ID ABM72048 standard; protein; 269 AA.  
DE Staphylococcus aureus protein #1288.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.8%; Score 6; DB 6; Length 269;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 884  
ID AAG27984 standard; protein; 273 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33032.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 273;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
RESULT 885  
ID ABM67790 standard; protein; 273 AA.  
DE Photobacterium luminescens protein sequence #887.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 7.8%; Score 6; DB 6; Length 273;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
RESULT 886  
ID ADP04485 standard; protein; 275 AA.  
DE Bacterial polypeptide #598.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 275;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 887  
ID ADP06864 standard; protein; 275 AA.  
DE Bacterial polypeptide #2977.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 275;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 888  
ID ADQ65898 standard; protein; 275 AA.  
DE Novel human protein sequence #871.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.8%; Score 6; DB 8; Length 275;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 889  
ID ADI28917 standard; protein; 276 AA.  
DE Sarcocystis neuroma antigenic protein SnSAG1.  
PN WO2004005489-A2.  
PD 15-JAN-2004.  
PA (KENT) UNIV KENTUCKY RES FOUND.  
Query Match 7.8%; Score 6; DB 8; Length 276;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 890

ID ADR44985 standard; protein; 276 AA.  
DE Sarcocystis neuroma (Sn) SAG1 antigenic protein.  
PN US2004162418-A1.  
PD 19-AUG-2004.  
PA (HOWE/) HOWE D K.  
Query Match 7.8%; Score 6; DB 8; Length 276;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 891  
ID AAG27983 standard; protein; 277 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33031.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 277;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
RESULT 892  
ID AAR22996 standard; protein; 288 AA.  
DE Yeast proteasome YC1 subunit.  
PN JP04077497-A.  
PD 11-MAR-1992.  
PA (SAKA) OTSUKA PHARM CO LTD.  
Query Match 7.8%; Score 6; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 893  
ID ADS28887 standard; protein; 288 AA.  
DE Bacterial polypeptide #17920.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 288;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 894  
ID ABO61862 standard; protein; 290 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8379.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 290;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
RESULT 895  
ID ABO62719 standard; protein; 291 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9236.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 291;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 896  
ID ADR94661 standard; protein; 291 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 3296.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 8; Length 291;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 897  
ID AAG28282 standard; protein; 299 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33441.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 299;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 898  
ID ABO66231 standard; protein; 301 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12748.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 301;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

RESULT 899  
ID ADI21046 standard; protein; 302 AA.  
DE Novel human protein #21.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 302;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 900  
ID AAW20903 standard; protein; 303 AA.  
DE H. pylori secreted or periplasmic protein, 14cp112lorf6.  
PN WO9640893-A1.  
PD 19-DEC-1996.  
PA (ASTR ) ASTRA AB.  
Query Match 7.8%; Score 6; DB 2; Length 303;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 901  
ID AAG46594 standard; protein; 305 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58635.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 305;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
RESULT 902  
ID ABG27928 standard; protein; 305 AA.  
DE Novel human diagnostic protein #27919.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 305;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
RESULT 903  
ID ABB33878 standard; protein; 306 AA.  
DE Lactococcus lactis protein yifg.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 7.8%; Score 6; DB 5; Length 306;  
Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
RESULT 904  
ID AAB06590 standard; protein; 309 AA.  
DE Human protein having hydrophobic domain, HP10785.  
PN WO200149728-A2.  
PD 12-JUL-2001.  
PA (PROT-) PROTEGENE INC.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
Query Match 7.8%; Score 6; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 905  
ID AAG28281 standard; protein; 310 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33440.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 310;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 906  
ID AAU29393 standard; protein; 310 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #14.  
PN WO200168858-A2.  
PD 20-SEP-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match 7.8%; Score 6; DB 4; Length 310;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 907  
ID ABB93747 standard; protein; 310 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2958.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 7.8%; Score 6; DB 5; Length 310;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 908  
ID ABG60681 standard; protein; 310 AA.

DE Novel G protein coupled receptor (ngCPR-x) #14.  
PN US2002058306-A1.  
PD 16-MAY-2002.  
PA (VOGE/) VOGELI G.  
Query Match 7.8%; Score 6; DB 5; Length 310;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 909  
ID ABO82227 standard; protein; 311 AA.  
DE Pseudomonas aeruginosa polypeptide #14402.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 311;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 910  
ID ABP73849 standard; protein; 314 AA.  
DE Candida albicans essential protein SEQ ID NO 7686.  
PN WO200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 5; Length 314;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
RESULT 911  
ID ADF04258 standard; protein; 319 AA.  
DE Bacterial polypeptide #371.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 319;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 912  
ID ABG05691 standard; protein; 320 AA.  
DE Novel human diagnostic protein #5682.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 320;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 913  
ID AAG27982 standard; protein; 321 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33030.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 914  
ID ABB63129 standard; protein; 321 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16179.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 321;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 915  
ID AAG28280 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33439.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 322;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 916  
ID AAU46913 standard; protein; 327 AA.  
DE Propionibacterium acnes immunogenic protein #7809.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 7.8%; Score 6; DB 4; Length 327;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
RESULT 917  
ID ABM43432 standard; protein; 327 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #8108.  
PN WO2003033515-A1.  
PD 24-APR-2003.

PA (CORI-) CORIXA CORP. 7.8%; Score 6; DB 6; Length 327;  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
 RESULT 918  
 ID ABP75866 standard; protein; 330 AA.  
 DE Human secretory polypeptide SPTM SEQ ID NO 1050.  
 PN WO200283876-A2.  
 PD 24-OCT-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 RESULT 919  
 ID AAG67466 standard; protein; 331 AA.  
 DE Breast amplified G protein coupled receptor (BCA-GPCR)-2.  
 PN WO200168704-A2.  
 PD 20-SEP-2001.  
 PA (TULA-) TULARIK INC.  
 PA (POWE/) POWERS S.  
 PA (YANG/) YANG J.  
 PA (CUTL/) CUTLER G.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 RESULT 920  
 ID ABB49192 standard; protein; 331 AA.  
 DE Listeria monocytogenes protein #1896.  
 PN WO200177335-A2.  
 PD 18-OCT-2001.  
 PA (INSP) INST PASTEUR.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 RESULT 921  
 ID ABR63704 standard; protein; 331 AA.  
 DE Human G-protein coupled receptor BCA-GPCR-2.  
 PN WO2003054542-A1.  
 PD 03-JUL-2003.  
 PA (TULA-) TULARIK INC.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 RESULT 922  
 ID ABG02033 standard; protein; 332 AA.  
 DE Novel human diagnostic protein #2024.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
 RESULT 923  
 ID AAY44245 standard; protein; 336 AA.  
 DE Human cell signalling protein-8.  
 PN WO9958558-A2.  
 PD 18-NOV-1999.  
 PA (INCY-) INCYTE PHARM INC.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 RESULT 924  
 ID AAG30338 standard; protein; 337 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36251.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 RESULT 925  
 ID ADC23919 standard; protein; 338 AA.  
 DE Protein sequence (SeqID 186) exhibiting nitrilase activity.  
 PN WO2003000840-A2.  
 PD 03-JAN-2003.  
 PA (MADD/) MADDEN D.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 926  
 ID ADH36020 standard; protein; 338 AA.  
 DE Chemical process monitoring-related nitrilase protein sequence SeqID186.  
 PN WO2003098187-A2.  
 PD 27-NOV-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 927  
 ID ADG93721 standard; protein; 338 AA.  
 DE Nitrilase enzyme amino acid sequence SeqID186.  
 PN WO2003097810-A2.  
 PD 27-NOV-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 928  
 ID ADI62318 standard; protein; 338 AA.  
 DE Nitrilase polypeptide #93.  
 PN WO2003106415-A2.  
 PD 24-DEC-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 929  
 ID ADI64439 standard; protein; 338 AA.  
 DE Nitrilase seq id 94.  
 PN US2004014195-A1.  
 PD 22-JAN-2004.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 930  
 ID ABR53456 standard; protein; 340 AA.  
 DE Protein sequence #SEQ ID 1777.  
 PN EP1258494-A1.  
 PD 20-NOV-2002.  
 PA (CELL-) CELLZOME AG.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 931  
 ID ADK64610 standard; protein; 340 AA.  
 DE Disease treating protein complex-derived protein #1070.  
 PN EP1338608-A2.  
 PD 27-AUG-2003.  
 PA (CELL-) CELLZOME AG.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 932  
 ID ADN19288 standard; protein; 340 AA.  
 DE Bacterial polypeptide #1941.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
 RESULT 933  
 ID ABB90323 standard; protein; 342 AA.  
 DE Human polypeptide SEQ ID NO 2699.  
 PN WO200190304-A2.  
 PD 29-NOV-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 RESULT 934  
 ID ADC87149 standard; protein; 344 AA.  
 DE Human GPCR protein SEQ ID NO:1602.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Query Match 7.8%; Score 6; DB 7; Length 344;

Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 935  
ID ABB52512 standard; protein; 345 AA.  
DE Escherichia coli polypeptide SEQ ID NO 378.  
PN WO200166572-A2.  
PD 13-SEP-2001.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match 7.8%; Score 6; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 936  
ID AAG46593 standard; protein; 346 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58634.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 346;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
RESULT 937  
ID ABB90159 standard; protein; 346 AA.  
DE Human polypeptide SEQ ID NO 2535.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 5; Length 346;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
RESULT 938  
ID ABB65881 standard; protein; 350 AA.  
DE Droscophila melanogaster polypeptide SEQ ID NO 24435.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 939  
ID ABU23172 standard; protein; 350 AA.  
DE Protein encoded by Prokaryotic essential gene #8699.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 350;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 940  
ID ADS29964 standard; protein; 351 AA.  
DE Bacterial polypeptide #18997.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 351;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 941  
ID ABG16162 standard; protein; 353 AA.  
DE Novel human diagnostic protein #16153.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 353;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 942  
ID ABU10305 standard; protein; 357 AA.  
DE Chicken bves (cbves) carboxyl domain.  
PN US6503540-B1.  
PD 07-JAN-2003.  
PA (REES/) REESE D E.  
PA (BADE/) BADER D M.  
Query Match 7.8%; Score 6; DB 7; Length 357;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 943  
ID ADK52127 standard; protein; 359 AA.  
DE Human atopic dermatitis/psoriasis-associated protein #42.  
PN WO2004016785-A1.

PD 26-FEB-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 7.8%; Score 6; DB 8; Length 359;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 944  
ID ADO29599 standard; protein; 361 AA.  
DE Mouse GPCR P2RY4, SEQ ID NO:701.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 7.8%; Score 6; DB 8; Length 361;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 945  
ID ADN24861 standard; protein; 362 AA.  
DE Bacterial polypeptide #7514.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 362;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 946  
ID ADN47009 standard; protein; 364 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID887.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 7.8%; Score 6; DB 8; Length 364;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 947  
ID ADN22102 standard; protein; 367 AA.  
DE Bacterial polypeptide #4755.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 367;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 948  
ID AAB94843 standard; protein; 368 AA.  
DE Human protein sequence SEQ ID NO:16018.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.8%; Score 6; DB 4; Length 368;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 949  
ID ADE31201 standard; protein; 370 AA.  
DE Human diagnostic and therapeutic polypeptide (DITRP), SEQ ID NO 333.  
PN WO2003062376-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 370;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
RESULT 950  
ID ABO81668 standard; protein; 373 AA.  
DE Pseudomonas aeruginosa polypeptide #13843.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 951  
ID ADP99028 standard; protein; 377 AA.  
DE C. albicans specific gene, orf6.2502, protein sequence.  
PN WO2004056965-A2.

PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 8; Length 377;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 952  
ID AAU33703 standard; protein; 381 AA.  
DE Pseudomonas aeruginosa cellular proliferation protein #147.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 381;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 953  
ID ABU40179 standard; protein; 381 AA.  
DE Protein encoded by Prokaryotic essential gene #25706.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 381;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 954  
ID ABU15637 standard; protein; 381 AA.  
DE Protein encoded by Prokaryotic essential gene #1164.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 381;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 955  
ID ABB54077 standard; protein; 382 AA.  
DE Lactococcus lactis protein nusa.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 7.8%; Score 6; DB 5; Length 382;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 956  
ID ADM48197 standard; protein; 382 AA.  
DE Polypeptide sequence #247 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match 7.8%; Score 6; DB 8; Length 382;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 957  
ID ABP69714 standard; protein; 383 AA.  
DE Human polypeptide SEQ ID NO 1761.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 5; Length 383;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 958  
ID ADN21352 standard; protein; 383 AA.  
DE Bacterial polypeptide #4005.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 383;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 959  
ID AAG22096 standard; protein; 393 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24894.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 393;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 960  
ID AAG22095 standard; protein; 394 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24893.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 394;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 961  
ID ADS24265 standard; protein; 394 AA.  
DE Bacterial polypeptide #13298.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 394;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 962  
ID ABU23064 standard; protein; 397 AA.  
DE Protein encoded by Prokaryotic essential gene #8591.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 397;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 963  
ID ADN21290 standard; protein; 397 AA.  
DE Bacterial polypeptide #3943.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 397;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 964  
ID ABG93164 standard; protein; 398 AA.  
DE S. cerevisiae BAX-associated protein fragment SEQ ID 286.  
PN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC ) JANSSEN PHARM NV.  
Query Match 7.8%; Score 6; DB 5; Length 398;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 965  
ID ADA35124 standard; protein; 398 AA.  
DE Acinetobacter baumannii protein #2285.  
PN US562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 6; Length 398;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 966  
ID ABR63122 standard; protein; 402 AA.  
DE Cattle plasminogen activator inhibitor-1.  
PN WO2003071267-A1.  
PD 28-AUG-2003.  
PA (UYVA-) UNIV VANDERBILT.  
PA (DECL/) DECLERCK P J.  
Query Match 7.8%; Score 6; DB 7; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 967  
ID ADG47611 standard; protein; 402 AA.  
DE Bovine plasminogen activator inhibitor-1 (BovPAII).  
PN US6541452-B1.  
PD 01-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 7; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1e+03;

RESULT 968  
ID AAG22094 standard; protein; 404 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24892.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 404;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 969  
ID ABU34333 standard; protein; 411 AA.  
DE Protein encoded by Prokaryotic essential gene #19860.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 411;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 970  
ID AAR66223 standard; protein; 417 AA.  
DE Cystathionine gamma lyase.  
PN JP06292586-A.  
PD 21-OCT-1994.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 7.8%; Score 6; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 971  
ID ADN27129 standard; protein; 420 AA.  
DE Bacterial polypeptide #9782.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 420;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 972  
ID ABG33823 standard; protein; 421 AA.  
DE Novel human diagnostic protein #23814.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 421;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 973  
ID ADB70152 standard; protein; 425 AA.  
DE C. neoformans amino acid sequence SEQ ID NO:3196.  
PN WO2003052076-A2.  
PD 26-JUN-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 7; Length 425;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 974  
ID ABO62928 standard; protein; 425 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9445.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 425;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 975  
ID AAG29446 standard; protein; 426 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35039.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 976  
ID AAY59728 standard; protein; 431 AA.  
DE Human normal ovarian tissue derived protein 5.  
PN DE19816395-A1.  
PD 07-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 7.8%; Score 6; DB 2; Length 431;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 977  
ID AAR13493 standard; protein; 434 AA.  
DE P. denitrificans COB B.  
PN WO9111518-A.  
PD 08-AUG-1991.  
PA (RHON ) RHONE-POULENC BIOCH.  
Query Match 7.8%; Score 6; DB 2; Length 434;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 978  
ID ADS23740 standard; protein; 446 AA.  
DE Bacterial polypeptide #12773.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 446;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 979  
ID AAU38019 standard; protein; 447 AA.  
DE Streptococcus pneumoniae cellular proliferation protein #448.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 980  
ID AAU37897 standard; protein; 447 AA.  
DE Streptococcus pneumoniae cellular proliferation protein #326.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 981  
ID ABU46174 standard; protein; 447 AA.  
DE Protein encoded by Prokaryotic essential gene #31701.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 982  
ID AAY1551 standard; protein; 448 AA.  
DE Florida bitterbush delta-6 fatty acid desaturase.  
PN WO200032790-A2.  
PD 08-JUN-2000.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 7.8%; Score 6; DB 3; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 983  
ID ADB79971 standard; protein; 449 AA.  
DE Mycobacterium tuberculosis nutrient starvation-inducible protein #5.  
PN WO2003004520-A2.  
PD 16-JAN-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Query Match 7.8%; Score 6; DB 7; Length 449;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 984  
ID AAR07295 standard; protein; 450 AA.  
DE Nucleoprotein N of Mokola Virus.  
PN WO9011358-A.  
PD 04-OCT-1990.  
PA (INSP ) INST PASTEUR.  
Query Match 7.8%; Score 6; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 985  
ID ABB55123 standard; protein; 453 AA.  
DE Lactococcus lactis protein ysdA.  
PN FR2807446-A1.

PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 7.8%; Score 6; DB 5; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 986  
ID ABB54687 standard; protein; 454 AA.  
DE Lactococcus lactis protein yniG.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 7.8%; Score 6; DB 5; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 987  
ID ABB20916 standard; protein; 462 AA.  
DE Protein encoded by Prokaryotic essential gene #6443.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 988  
ID ABO63192 standard; protein; 462 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9709.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 989  
ID ABG27022 standard; protein; 463 AA.  
DE Novel human diagnostic protein #27013.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 990  
ID AAB41219 standard; protein; 472 AA.  
DE Human ORFX ORF983 polypeptide sequence SEQ ID NO:1966.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 6; DB 3; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 991  
ID ABB97828 standard; protein; 472 AA.  
DE Human secretory polypeptide (SPTM) 80.  
PN WO200220756-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.8%; Score 6; DB 5; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 992  
ID ADE08673 standard; protein; 472 AA.  
DE Novel protein (useful for identifying genetic disorders) #828.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 993  
ID ABG29474 standard; protein; 474 AA.  
DE Novel human diagnostic protein #29465.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 474;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 994  
ID ADS44078 standard; protein; 486 AA.  
DE Bacterial polypeptide #22508.  
PN US2003233675-A1.  
PD 18-DEC-2003.

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 995  
ID ABU10301 standard; protein; 487 AA.  
DE Fragment of chicken bves (cbves).  
PN US6503540-B1.  
PD 07-JAN-2003.  
PA (REES/) REESE D E.  
PA (BADE/) BADER D M.  
Query Match 7.8%; Score 6; DB 7; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 996  
ID ABO66846 standard; protein; 488 AA.  
DE Klebsiella pneumoniae polypeptide seqid 13363.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 488;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 997  
ID ABB63372 standard; protein; 504 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16908.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 998  
ID ADS44277 standard; protein; 504 AA.  
DE Bacterial polypeptide #22707.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 7.8%; Score 6; DB 8; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 999  
ID ABB59492 standard; protein; 525 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 5268.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 525;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1000  
ID ABM5858 standard; protein; 539 AA.  
DE Mouse protein sequence mCPI3326.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 7.8%; Score 6; DB 7; Length 539;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1001  
ID ABG91046 standard; protein; 542 AA.  
DE Chlamydia trachomatis apolipoprotein N-acetyltransferase protein.  
PN WO200262380-A2.  
PD 15-AUG-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 7.8%; Score 6; DB 5; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1002  
ID ADD43852 standard; protein; 542 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 147.  
PN WO2003049762-A2.  
PD 19-JUN-2003.

PA (CHIR-) CHIRON SPA.  
Query Match 7.8%; Score 6; DB 7; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1003  
ID ABB68867 standard; protein; 545 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33393.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1004  
ID AAU38979 standard; protein; 545 AA.  
DE Drosophila G-protein coupled receptor, GPCR #57.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1005  
ID AAB95605 standard; protein; 545 AA.  
DE Human protein sequence SEQ ID NO:18299.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.8%; Score 6; DB 4; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1006  
ID AAE38161 standard; protein; 545 AA.  
DE Fruit fly G protein-coupled receptor (GPCR) protein #10.  
PN WO2003052078-A2.  
PD 26-JUN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 7.8%; Score 6; DB 7; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1007  
ID ADC31778 standard; protein; 545 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1860.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 7; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1008  
ID ADC35919 standard; protein; 545 AA.  
DE Drosophila G protein coupled receptor seq id 59.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 7.8%; Score 6; DB 7; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1009  
ID ADK52117 standard; protein; 545 AA.  
DE Human atopic dermatitis/psoriasis-associated protein #32.  
PN WO2004016785-A1.  
PD 26-FEB-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 7.8%; Score 6; DB 8; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1010  
ID ADN05311 standard; protein; 545 AA.  
DE Antipsoriatic protein sequence #829.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.8%; Score 6; DB 8; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1011  
ID ABO74401 standard; protein; 548 AA.  
DE Pseudomonas aeruginosa polypeptide #6576.  
PN US6551795-B1.  
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 7.8%; Score 6; DB 7; Length 548;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1012  
ID ABG91054 standard; protein; 549 AA.  
DE Chlamydia trachomatis serovar D cute protein.  
PN WO200262380-A2.  
PD 15-AUG-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 7.8%; Score 6; DB 5; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1013  
ID ADJ33778 standard; protein; 559 AA.  
DE Protein of the invention SEQ ID NO:755.  
PN WO200187917-A1.  
PD 22-NOV-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 5; Length 559;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1014  
ID AAU31067 standard; protein; 560 AA.  
DE Novel human secreted protein #1558.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1015  
ID ADC38726 standard; protein; 560 AA.  
DE Human secreted protein #40.  
PN US2002193567-A1.  
PD 19-DEC-2002.  
PA (GEMY ) GENETICS INST INC.  
Query Match 7.8%; Score 6; DB 7; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1016  
ID AAG31172 standard; protein; 561 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37391.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.8%; Score 6; DB 3; Length 561;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1017  
ID AAR66929 standard; protein; 576 AA.  
DE AML chromosome inv(16) product.  
PN WO9504067-A1.  
PD 09-FEB-1995.  
PA (UNMI ) UNIV MICHIGAN.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.8%; Score 6; DB 2; Length 576;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1018  
ID ABR43182 standard; protein; 583 AA.  
DE Human REMAP-14 protein SEQ ID NO:14.  
PN WO2003025130-A2.  
PD 27-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.8%; Score 6; DB 6; Length 583;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1019  
ID AAR96246 standard; protein; 585 AA.  
DE Malic enzyme #1.  
PN JP08089250-A.  
PD 09-APR-1996.  
PA (MITK ) MITSUI TOATSU CHEM INC.  
Query Match 7.8%; Score 6; DB 2; Length 585;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1020  
ID AAR96247 standard; protein; 592 AA.  
DE Malic enzyme #2.  
PN JP08089250-A.  
PD 09-APR-1996.  
PA (MITK ) MITSUI TOATSU CHEM INC.

Query Match 7.8%; Score 6; DB 2; Length 592;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 RESULT 1021  
 ID ADL05729 standard; protein; 598 AA.  
 DE M. catarrhalis protein #1495.  
 PN US6673910-B1.  
 PD 06-JAN-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 7.8%; Score 6; DB 8; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 RESULT 1022  
 ID ADB64938 standard; protein; 602 AA.  
 DE Human protein encoded by clone PROST20016760.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 7.8%; Score 6; DB 7; Length 602;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1023  
 ID ADF30481 standard; protein; 621 AA.  
 DE Rat angiogenesis modulating protein #17.  
 PN US2003162706-A1.  
 PD 28-AUG-2003.  
 PA (PROC) PROCTER & GAMBLE CO.  
 Query Match 7.8%; Score 6; DB 7; Length 621;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1024  
 ID ABP65819 standard; protein; 624 AA.  
 DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:563.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC PROD NESTLE SA.  
 Query Match 7.8%; Score 6; DB 5; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1025  
 ID ADN19456 standard; protein; 624 AA.  
 DE Bacterial polypeptide #2109.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 7.8%; Score 6; DB 8; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1026  
 ID AAG29253 standard; protein; 631 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 34774.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 7.8%; Score 6; DB 3; Length 631;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1027  
 ID ADF23256 standard; protein; 631 AA.  
 DE AT4931670 protein #SEQ ID 2.  
 PN CN1369502-A.  
 PD 18-SEP-2002.  
 PA (UYBE-) UNIV BEIJING.  
 Query Match 7.8%; Score 6; DB 7; Length 631;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1028  
 ID AAY65616 standard; protein; 636 AA.  
 DE Zea mays chlorophyll localised malic acid enzyme.  
 PN JP1308994-A.  
 PD 09-NOV-1999.  
 PA (MITA) MITSUI CHEM INC.  
 Query Match 7.8%; Score 6; DB 3; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1029  
 ID AAR70096 standard; protein; 638 AA.  
 DE Malic acid enzyme isolated from a rice plant.

PN JP07023790-A.  
 PD 27-JAN-1995.  
 PA (NISC) NISSAN CHEM IND LTD.  
 Query Match 7.8%; Score 6; DB 2; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1030  
 ID ADI82510 standard; protein; 638 AA.  
 DE Human modifier of p21 (MP21) protein sequence SeqID76.  
 PN WO2004005486-A2.  
 PD 15-JAN-2004.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 7.8%; Score 6; DB 8; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 RESULT 1031  
 ID AAY35056 standard; protein; 643 AA.  
 DE Chlamydia pneumoniae transmembrane protein sequence.  
 PN WO9927105-A2.  
 PD 03-JUN-1999.  
 PA (GEST) GENSET.  
 Query Match 7.8%; Score 6; DB 2; Length 643;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1032  
 ID AAG39461 standard; protein; 643 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48826.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 7.8%; Score 6; DB 3; Length 643;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1033  
 ID ABU26526 standard; protein; 643 AA.  
 DE Protein encoded by Prokaryotic essential gene #12053.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 6; Length 643;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1034  
 ID ADN21267 standard; protein; 645 AA.  
 DE Bacterial polypeptide #3920.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 7.8%; Score 6; DB 8; Length 645;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1035  
 ID AAG39460 standard; protein; 653 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48825.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 7.8%; Score 6; DB 3; Length 653;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1036  
 ID AAG39459 standard; protein; 654 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48824.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 7.8%; Score 6; DB 3; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1037  
 ID ABU27648 standard; protein; 655 AA.  
 DE Protein encoded by Prokaryotic essential gene #13175.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 6; Length 655;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1038  
 ID ANU34917 standard; protein; 659 AA.  
 DE Enterococcus faecalis cellular proliferation protein #204.

PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 4; Length 659;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1039  
 ID ABG21920 standard; protein; 667 AA.  
 DE Novel human diagnostic protein #21911.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 7.8%; Score 6; DB 4; Length 667;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1040  
 ID AAB95883 standard; protein; 681 AA.  
 DE Human protein sequence SEQ ID NO:18994.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 7.8%; Score 6; DB 4; Length 681;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1041  
 ID AAB10556 standard; protein; 684 AA.  
 DE Human aspartate protease psl 5 protein.  
 PN WO200043505-A2.  
 PD 27-JUL-2000.  
 PA (MEMO-) MEMOREC MEDICAL MOLECULAR RES COLOGNE ST.  
 PA (HOFM/) HOFMANN K.  
 Query Match 7.8%; Score 6; DB 3; Length 684;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1042  
 ID ADS42758 standard; protein; 684 AA.  
 DE Bacterial polypeptide #21188.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 7.8%; Score 6; DB 8; Length 684;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 RESULT 1043  
 ID ABG69602 standard; protein; 689 AA.  
 DE Human NOV5 protein.  
 PN WO200250277-A2.  
 PD 27-JUN-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 7.8%; Score 6; DB 5; Length 689;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1044  
 ID ADN19373 standard; protein; 694 AA.  
 DE Bacterial polypeptide #2026.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 7.8%; Score 6; DB 8; Length 694;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1045  
 ID AAR1384 standard; protein; 712 AA.  
 DE Tribolium semaphorin I protein.  
 PN WO9507706-A1.  
 PD 23-MAR-1995.  
 PA (RECC) UNIV CALIFORNIA.  
 Query Match 7.8%; Score 6; DB 2; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1046  
 ID ADS44332 standard; protein; 712 AA.  
 DE Bacterial polypeptide #22762.

PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 7.8%; Score 6; DB 8; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1047  
 ID ABU29206 standard; protein; 719 AA.  
 DE Protein encoded by Prokaryotic essential gene #14733.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1048  
 ID ADH97068 standard; protein; 719 AA.  
 DE S. pneumoniae RDR alpha subunit protein #2.  
 PN WO2003102190-A2.  
 PD 11-DEC-2003.  
 PA (AFFI-) AFFINIUM PHARM INC.  
 Query Match 7.8%; Score 6; DB 8; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1049  
 ID ADH97066 standard; protein; 719 AA.  
 DE S. pneumoniae RDR alpha subunit protein #1.  
 PN WO2003102190-A2.  
 PD 11-DEC-2003.  
 PA (AFFI-) AFFINIUM PHARM INC.  
 Query Match 7.8%; Score 6; DB 8; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1050  
 ID ADH87842 standard; protein; 722 AA.  
 DE Enterococcus faecalis polypeptide #2322.  
 PN US6617156-B1.  
 PD 09-SEP-2003.  
 PA (DOUC/) DOUCETTE-STAMM L A.  
 PA (BUSH/) BUSH D.  
 Query Match 7.8%; Score 6; DB 7; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1051  
 ID ABR58376 standard; protein; 724 AA.  
 DE Human NOV5b.  
 PN WO2003029423-A2.  
 PD 10-APR-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 7.8%; Score 6; DB 6; Length 724;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1052  
 ID ADF78959 standard; protein; 731 AA.  
 DE Rice cell cycle gene cullin 3, protein.  
 PN US2003186362-A1.  
 PD 02-OCT-2003.  
 PA (MORG/) MORGANTE M.  
 PA (FAMC/) FAMODU O O.  
 PA (WENG/) WENG Z.  
 Query Match 7.8%; Score 6; DB 8; Length 731;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 RESULT 1053  
 ID ADB70247 standard; protein; 761 AA.  
 DE C. neoformans amino acid sequence SEQ ID NO:3291.  
 PN WO2003052076-A2.  
 PD 26-JUN-2003.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 7; Length 761;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 RESULT 1054  
 ID ADJ83031 standard; protein; 761 AA.  
 DE Human NOVX NOV5 protein.  
 PN US2003170630-A1.  
 PD 11-SEP-2003.

PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASH/) CASHMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Length 761;  
RESULT 1055  
ID ABU15226 standard; protein; 765 AA.  
DE Protein encoded by Prokaryotic essential gene #753.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Length 765;  
RESULT 1056  
ID ABU48326 standard; protein; 765 AA.  
DE Protein encoded by Prokaryotic essential gene #33853.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Length 765;  
RESULT 1057  
ID ABB61410 standard; protein; 798 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11022.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Length 798;  
RESULT 1058  
ID ABP96601 standard; protein; 805 AA.  
DE HIV-PFIC2-alpha construct protein sequence.  
PN WO2003016472-A2.  
PD 27-FEB-2003.  
PA (PEPG-) PEPCOR CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Length 805;  
RESULT 1059  
ID ABU19894 standard; protein; 807 AA.  
DE Protein encoded by Prokaryotic essential gene #5421.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Length 807;  
RESULT 1060  
ID AAR66931 standard; protein; 816 AA.  
DE AMML chromosome inv(16) product.  
PN WO9504067-A1.  
PD 09-FEB-1995.  
PA (UNMI) UNIV MICHIGAN.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Length 816;  
RESULT 1061  
ID ABU48633 standard; protein; 823 AA.  
DE Protein encoded by Prokaryotic essential gene #34160.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 823;  
RESULT 1062  
ID ADN47384 standard; protein; 828 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SegID1262.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 828;  
RESULT 1063  
ID ADJ49851 standard; protein; 841 AA.  
DE Oil-associated gene related protein #1351.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 841;  
RESULT 1064  
ID ADJ49518 standard; protein; 841 AA.  
DE Oil-associated gene related protein #1018.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 841;  
RESULT 1065  
ID ABB66422 standard; protein; 844 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 26058.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 844;  
RESULT 1066  
ID ADJ50264 standard; protein; 847 AA.  
DE Oil-associated gene related protein #1764.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 847;  
RESULT 1067  
ID AAB54359 standard; protein; 855 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:811.  
PN WO200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2e+03; Length 855;  
RESULT 1068

ID AAB96597 standard; protein; 872 AA.  
DE Putative P. abyssi superfamily II DNA and RNA helicase #8.  
PN PR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Query Match 7.8%; Score 6; DB 4; Length 872;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1069  
ID AAR66930 standard; protein; 885 AA.  
DE AAML chromosome inv(16) product.  
PN WO9504067-A1.  
PD 09-FEB-1995.  
PA (UNMI ) UNIV MICHIGAN  
PA (TEXA ) UNIV TEXAS SVSTEM.  
Query Match 7.8%; Score 6; DB 2; Length 885;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1070  
ID AAY90238 standard; protein; 885 AA.  
DE Mature Chlamydia antigen CPN100635.  
PN WO200032794-A2.  
PD 08-JUN-2000.  
PA (CONN-) CONNAUGHT LAB LTD.  
Query Match 7.8%; Score 6; DB 3; Length 885;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1071  
ID ABB57134 standard; protein; 889 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:312.  
PN WO2001818-A2.  
PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 7.8%; Score 6; DB 5; Length 889;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1072  
ID ADN04279 standard; protein; 889 AA.  
DE Antisporiatric protein sequence #334.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.8%; Score 6; DB 8; Length 889;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1073  
ID ADP24012 standard; protein; 889 AA.  
DE PRO polypeptide SEQ ID NO:1190.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.8%; Score 6; DB 8; Length 889;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1074  
ID AAW88429 standard; protein; 914 AA.  
DE Chlamydia pneumoniae surface exposed protein Omp5.  
PN WO9858953-A2.  
PD 30-DEC-1998.  
PA (BIRK/) BIRKELUND S.  
PA (CHRI/) CHRISTIANSEN G.  
Query Match 7.8%; Score 6; DB 2; Length 914;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1075  
ID AAW88418 standard; protein; 928 AA.  
DE Chlamydia pneumoniae surface exposed protein Omp5.  
PN WO9858953-A2.  
PD 30-DEC-1998.  
PA (BIRK/) BIRKELUND S.  
PA (CHRI/) CHRISTIANSEN G.  
Query Match 7.8%; Score 6; DB 2; Length 928;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1076  
ID AAY90237 standard; protein; 928 AA.  
DE Chlamydia antigen CPN100635.  
PN WO200032794-A2.  
PD 08-JUN-2000.  
PA (CONN-) CONNAUGHT LAB LTD.

Query Match 7.8%; Score 6; DB 3; Length 928;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1077  
ID ABB90573 standard; protein; 928 AA.  
DE Chlamydia pneumoniae cp0010 protein, SEQ ID NO:95.  
PN WO200202606-A2.  
PD 10-JAN-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.8%; Score 6; DB 5; Length 928;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1078  
ID AAM78649 standard; protein; 931 AA.  
DE Human protein SEQ ID NO 1311.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 931;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1079  
ID ABM80675 standard; protein; 931 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81297, SEQ:1747.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.8%; Score 6; DB 8; Length 931;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1080  
ID ADJ83096 standard; protein; 933 AA.  
DE Fruit fly adenylate cyclase isoform 39E protein - SEQ ID 87.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHP/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERRHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match 7.8%; Score 6; DB 7; Length 933;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1081  
ID ABB12315 standard; peptide; 949 AA.  
DE Human protocadherin homologue, SEQ ID NO:2685.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 949;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1082  
ID AAM79633 standard; protein; 949 AA.  
DE Human protein SEQ ID NO 3279.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.

Query Match  
Best Local Similarity 7.8%; Score 6; DB 4; Length 949;  
RESULT 1083  
ID AD512208 standard; protein; 949 AA.  
DE Human therapeutic contig protein - SEQ ID 2445.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 949;  
RESULT 1084  
ID ADO42010 standard; protein; 992 AA.  
DE Human cell adhesion and extracellular matrix protein 39 SeqID39.  
PN WO2004048529-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 992;  
RESULT 1085  
ID ABM83663 standard; protein; 992 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3912.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 992;  
RESULT 1086  
ID ADJ49445 standard; protein; 1032 AA.  
DE Oil-associated gene related protein #945.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR-) LAURIE C C.  
PA (RAVA-) RAVANELLO M.  
PA (SAVA-) SAVAGE T.  
PA (LEDE-) LEDEUX J R.  
PA (ROGE-) ROGERS J A.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 1032;  
RESULT 1087  
ID ADN96156 standard; protein; 1118 AA.  
DE Human NOVX polypeptide #105.  
PN US2004087490-A1.  
PD 08-APR-2004.  
PA (ZHON-) ZHONG M.  
PA (LILL-) LI L.  
PA (GORM-) GORMAN L.  
PA (SPYT-) SPYTEK K A.  
PA (KEKU-) KEKUDA R.  
PA (TAUP-) TAUPIER R J.  
PA (ANDE-) ANDERSON D W.  
PA (VERN-) VERNET C A M.  
PA (CATT-) CATTERTON E.  
PA (MILL-) MILLER C E.  
PA (SHEN-) SHENOY S G.  
PA (PATT-) PATTURAJAN M.  
PA (PENA-) PENA C E A.  
PA (TCHE-) TCHERNEV V T.  
PA (PADI-) PADIGARU M.  
PA (GUSE-) GUSEV V Y.  
PA (MALY-) MALYANKAR U M.  
PA (BURG-) BURGESS C E.  
PA (GERL-) GERLACH V.  
PA (CASM-) CASMAN S J.  
PA (RIEG-) RIEGER D K.  
PA (GROS-) GROSSE W M.  
PA (SMIT-) SMITHSON G.  
PA (PEYM-) PEYMAN J A.  
PA (STAR-) STARLING J G.  
PA (ROTH-) ROTHENBERG M E.  
PA (LARO-) LAROCHELLE W J.  
PA (SHIM-) SHIMKETS R A.  
PA (CRAB-) CRABTREE J.  
PA (RAST-) RASTELLI L.  
PA (VOSS-) VOSS E Z.  
PA (BOLD-) BOLDOG F L.  
PA (EDIN-) EDINGER S R.  
PA (MILL-) MILLET I.  
PA (MACD-) MACDOUGALL J R.  
PA (ELLE-) ELLERMAN K.  
PA (CHAP-) CHAPOVAL A.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 1118;  
RESULT 1088  
ID ADN20724 standard; protein; 1124 AA.  
DE Bacterial polypeptide #3377.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 8; Length 1124;  
RESULT 1089  
ID RAB02007 standard; protein; 1144 AA.  
DE Type III adenylyl cyclase.  
PN US6107076-A.  
PD 22-AUG-2000.  
PA (TEXA-) UNIV TEXAS SYSTEM.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 3; Length 1144;  
RESULT 1090  
ID ADJ83095 standard; protein; 1144 AA.  
DE Human adenylylase cyclase 3 protein - SEQ ID 86.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO-) ALSOBROOK J P.  
PA (TCHE-) TCHERNEV V T.  
PA (LIUX-) LIU X.  
PA (SPYT-) SPYTEK K A.  
PA (ZERH-) ZERHUSEN B D.  
PA (PATT-) PATTURAJAN M.  
PA (LEPL-) LEPLEY D M.  
PA (BURG-) BURGESS C E.  
PA (SHIM-) SHIMKETS R A.  
PA (GROS-) GROSSE W M.  
PA (SZEK-) SZEKERES E S.  
PA (VERN-) VERNET C A M.  
PA (LILL-) LI L.  
PA (CASM-) CASMAN S J.  
PA (BOLD-) BOLDOG F L.  
PA (GORM-) GORMAN L.  
PA (GANG-) GANGOLLI E A.  
PA (FERN-) FERNANDES E R.  
PA (RIEG-) RIEGER D K.  
PA (EDIN-) EDINGER S R.  
PA (GUNT-) GUNTHER E.  
PA (MILL-) MILLET I.  
PA (SCIO-) SCIORE P.  
PA (ELLE-) ELLERMAN K.  
PA (MACD-) MACDOUGALL J R.  
PA (SMIT-) SMITHSON G.  
Query Match  
Best Local Similarity 7.8%; Score 6; DB 7; Length 1144;  
RESULT 1091  
ID ADJ83094 standard; protein; 1144 AA.  
DE Rat adenylylase cyclase type III protein - SEQ ID 85.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO-) ALSOBROOK J P.  
PA (TCHE-) TCHERNEV V T.  
PA (LIUX-) LIU X.  
PA (SPYT-) SPYTEK K A.  
PA (ZERH-) ZERHUSEN B D.  
PA (PATT-) PATTURAJAN M.

PA (LEPL/) LEPLEY D M. 7.8%; Score 6; DB 7; Length 1144;  
 PA (BURG/) BURGESS C E. 7.8%; Score 6; DB 7; Length 1144;  
 PA (SHIM/) SHIMKETS R A. 7.8%; Score 6; DB 7; Length 1144;  
 PA (GROS/) GROSSE W M. 7.8%; Score 6; DB 7; Length 1144;  
 PA (SZEK/) SZEKERES E S. 7.8%; Score 6; DB 7; Length 1144;  
 PA (VERN/) VERNET C A M. 7.8%; Score 6; DB 7; Length 1144;  
 PA (LILL/) LI L. 7.8%; Score 6; DB 7; Length 1144;  
 PA (CASN/) CASMAN S J. 7.8%; Score 6; DB 7; Length 1144;  
 PA (BOLD/) BOLDOG F L. 7.8%; Score 6; DB 7; Length 1144;  
 PA (GORM/) GORMAN L. 7.8%; Score 6; DB 7; Length 1144;  
 PA (GANG/) GANGOLLI E A. 7.8%; Score 6; DB 7; Length 1144;  
 PA (FERN/) FERNANDES E R. 7.8%; Score 6; DB 7; Length 1144;  
 PA (RIEG/) RIEGER D K. 7.8%; Score 6; DB 7; Length 1144;  
 PA (EDIN/) EDINGER S R. 7.8%; Score 6; DB 7; Length 1144;  
 PA (GUNT/) GUNTHER E. 7.8%; Score 6; DB 7; Length 1144;  
 PA (MILL/) MILLET I. 7.8%; Score 6; DB 7; Length 1144;  
 PA (SCIO/) SCIORE P. 7.8%; Score 6; DB 7; Length 1144;  
 PA (ELLE/) ELLERMAN K. 7.8%; Score 6; DB 7; Length 1144;  
 PA (MACD/) MACDOUGALL J R. 7.8%; Score 6; DB 7; Length 1144;  
 PA (SMIT/) SMITHSON G. 7.8%; Score 6; DB 7; Length 1144;  
 Query Match 7.8%; Score 6; DB 7; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1092  
 ID ADJ82968 standard; protein; 1144 AA.  
 DE Human adenylate cyclase 3 ADCY3 protein.  
 PN WO2004005483-A2.  
 PD 15-JAN-2004.  
 PA (EXEL-) EXELIXIS INC. 7.8%; Score 6; DB 8; Length 1144;  
 Query Match 7.8%; Score 6; DB 8; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1093  
 ID ADQ89906 standard; protein; 1144 AA.  
 DE Antagonist of cell cycle progression polypeptide #168.  
 PN WO2004063362-A2.  
 PD 29-JUL-2004.  
 PA (CYCL-) CYCLACEL LTD. 7.8%; Score 6; DB 8; Length 1144;  
 Query Match 7.8%; Score 6; DB 8; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1094  
 ID ADR73440 standard; protein; 1144 AA.  
 DE Human adenylate cyclase 3, ADCY3, protein.  
 PN WO2004076682-A2.  
 PD 10-SEP-2004.  
 PA (SURRE-) SURREMED INC. 7.8%; Score 6; DB 8; Length 1144;  
 Query Match 7.8%; Score 6; DB 8; Length 1144;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1095  
 ID AAR74209 standard; protein; 1165 AA.  
 DE Laminin B1k chain.  
 PN WO9511972-A1.  
 PD 04-MAY-1995.  
 PA (GEHO-) GEN HOSPITAL CORP. 7.8%; Score 6; DB 2; Length 1165;  
 PA (UYOR-) UNIV OREGON HEALTH SCI. 7.8%; Score 6; DB 2; Length 1165;  
 Query Match 7.8%; Score 6; DB 2; Length 1165;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1096  
 ID AAB48462 standard; protein; 1170 AA.  
 DE Human laminin 5 polypeptide, SEQ ID NO: 14.  
 PN WO200066731-A2.  
 PD 09-NOV-2000.  
 PA (BIOS-) BIOSTATUM INC. 7.8%; Score 6; DB 3; Length 1170;  
 Query Match 7.8%; Score 6; DB 3; Length 1170;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1097  
 ID AAW37870 standard; protein; 1172 AA.  
 DE Human protein comprising secretory signal amino acid sequence 7.  
 PN WO9811217-A2.  
 PD 19-MAR-1998.  
 PA (SAGA-) SAGAMI CHEM RES CENTRE.  
 PA (PROT-) PROTEGENE INC. 7.8%; Score 6; DB 2; Length 1172;  
 Query Match 7.8%; Score 6; DB 2; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1098

ID ABG77169 standard; protein; 1172 AA.  
 DE Prostate adenocarcinoma associated protein #4.  
 PN US2002119463-A1.  
 PD 29-AUG-2002.  
 PA (FARI/) FARIS M. 7.8%; Score 6; DB 5; Length 1172;  
 PA (TURN/) TURNER C M. 7.8%; Score 6; DB 5; Length 1172;  
 Query Match 7.8%; Score 6; DB 5; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1099  
 ID ABUS6661 standard; protein; 1172 AA.  
 DE Lung cancer-associated polypeptide #254.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.8%; Score 6; DB 6; Length 1172;  
 Query Match 7.8%; Score 6; DB 6; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1100  
 ID ABUS6417 standard; protein; 1172 AA.  
 DE Lung cancer-associated polypeptide #10.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.8%; Score 6; DB 6; Length 1172;  
 Query Match 7.8%; Score 6; DB 6; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1101  
 ID ABUS7624 standard; protein; 1172 AA.  
 DE Differentially expressed breast cancer associated protein #11.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN/) CHEN H. 7.8%; Score 6; DB 6; Length 1172;  
 Query Match 7.8%; Score 6; DB 6; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1102  
 ID ABR58375 standard; protein; 1172 AA.  
 DE Human NOV5a.  
 PN WO2003029423-A2.  
 PD 10-APR-2003.  
 PA (CURA-) CURAGEN CORP. 7.8%; Score 6; DB 6; Length 1172;  
 Query Match 7.8%; Score 6; DB 6; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1103  
 ID ADC01885 standard; protein; 1172 AA.  
 DE Human laminin beta 3 subunit.  
 PN US2003103975-A1.  
 PD 05-JUN-2003.  
 PA (JONE/) JONES J C R. 7.8%; Score 6; DB 7; Length 1172;  
 PA (GONZ/) GONZALES M. 7.8%; Score 6; DB 7; Length 1172;  
 Query Match 7.8%; Score 6; DB 7; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1104  
 ID ADN39002 standard; protein; 1172 AA.  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:320.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.8%; Score 6; DB 7; Length 1172;  
 Query Match 7.8%; Score 6; DB 7; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1105  
 ID ABM80221 standard; protein; 1172 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO36468, SEQ:554.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH-) GENENTECH INC. 7.8%; Score 6; DB 8; Length 1172;  
 Query Match 7.8%; Score 6; DB 8; Length 1172;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 RESULT 1106  
 ID ADJ48738 standard; protein; 1174 AA.  
 DE Oil-associated gene related protein #238.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C. 7.8%; Score 6; DB 8; Length 1172;  
 PA (RAVA/) RAVANELLO M. 7.8%; Score 6; DB 8; Length 1172;  
 PA (SAVA/) SAVAGE T. 7.8%; Score 6; DB 8; Length 1172;

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PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 7.8%; Score 6; DB 8; Length 1174;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1107
ID ADA55131 standard; protein; 1196 AA.
DE Human protein, SEQ ID 2699.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.8%; Score 6; DB 6; Length 1196;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
RESULT 1108
ID ABP69358 standard; protein; 1223 AA.
DE Human polypeptide SEQ ID NO 1405.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.8%; Score 6; DB 5; Length 1223;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
RESULT 1109
ID AAU96923 standard; protein; 1223 AA.
DE Human alpha-2/delta-4 protein subunit 1.
PN WO200226821-A2.
PD 04-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 6; DB 5; Length 1223;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
RESULT 1110
ID ADI27951 standard; protein; 1223 AA.
DE Human alpha-2/delta-4 protein.
PN US2003165891-A1.
PD 04-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 6; DB 8; Length 1223;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
RESULT 1111
ID ADN24522 standard; protein; 1241 AA.
DE Bacterial polypeptide #7175.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOI/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.8%; Score 6; DB 8; Length 1241;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
RESULT 1112
ID ADN21766 standard; protein; 1261 AA.
DE Bacterial polypeptide #4419.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOI/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.8%; Score 6; DB 8; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
RESULT 1113
ID AAE22909 standard; protein; 1274 AA.
DE Human transporter and ion channel (TRICH) 8.
PN WO200222684-A2.
PD 21-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.8%; Score 6; DB 5; Length 1274;
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1114
ID ADC22810 standard; protein; 1286 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #82.
PN US655339-B1.

PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 7.8%; Score 6; DB 7; Length 1286;
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1115
ID ADH14283 standard; protein; 1286 AA.
DE Vector pCMV DNA ORF 3.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 7.8%; Score 6; DB 7; Length 1286;
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1116
ID ABU19860 standard; protein; 1287 AA.
DE Protein encoded by Prokaryotic essential gene #5387.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 1287;
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1117
ID ABB64155 standard; protein; 1297 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19257.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 6; DB 4; Length 1297;
Best Local Similarity 100.0%; Pred. No. 3e+03;
RESULT 1118
ID ABB99695 standard; protein; 1325 AA.
DE Amino acid sequence of a mutant ABCC5 transporter polypeptide.
PN WO200294378-A2.
PD 28-NOV-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 7.8%; Score 6; DB 6; Length 1325;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
RESULT 1119
ID ABM82693 standard; protein; 1397 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2942.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.8%; Score 6; DB 8; Length 1397;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
RESULT 1120
ID ADQ15222 standard; protein; 1410 AA.
DE Melon Vat-like protein, seq id 6.
PN FR2849863-A1.
PD 16-JUL-2004.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 7.8%; Score 6; DB 8; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
RESULT 1121
ID ADN03630 standard; protein; 1419 AA.
DE Antipsoriatic protein sequence #12.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.8%; Score 6; DB 8; Length 1419;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
RESULT 1122
ID ABP69396 standard; protein; 1426 AA.
DE Human polypeptide SEQ ID NO 1443.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.8%; Score 6; DB 5; Length 1426;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
RESULT 1123
ID ADJ76344 standard; protein; 1436 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1596.
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PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC. 7.8%; Score 6; DB 8; Length 1436;  
Query Match 100.0%; Pred. No. 3.3e+03;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1124  
ID AAN80597 standard; protein; 1437 AA.  
DE Human multidrug resistance-associated protein.  
PN WO9846736-A1.  
PD 22-OCT-1998.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 6; DB 2; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1125  
ID AAY43542 standard; protein; 1437 AA.  
DE A human MPR-related ABC transporter designated MOAT-C.  
PN WO9949795-A1.  
PD 07-OCT-1999.  
PA (FOXC-) FOX CHASE CANCER CENT.  
Query Match 7.8%; Score 6; DB 2; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1126  
ID AAB10225 standard; protein; 1437 AA.  
DE Human MRP-beta protein.  
PN US6077936-A.  
PD 20-JUN-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 6; DB 3; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1127  
ID ABP52112 standard; protein; 1437 AA.  
DE Homo sapiens ABC transporter ABCC5 protein SEQ ID NO:64.  
PN EP1217066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match 7.8%; Score 6; DB 5; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1128  
ID ABUS6560 standard; protein; 1437 AA.  
DE Lung cancer-associated polypeptide #153.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.8%; Score 6; DB 6; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1129  
ID ABUS6500 standard; protein; 1437 AA.  
DE Lung cancer-associated polypeptide #93.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.8%; Score 6; DB 6; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1130  
ID ABUS6693 standard; protein; 1437 AA.  
DE Lung cancer-associated polypeptide #286.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.8%; Score 6; DB 6; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1131  
ID ABB99693 standard; protein; 1437 AA.  
DE Amino acid sequence of human ABCC5 transporter polypeptide.  
PN WO200294378-A2.  
PD 28-NOV-2002.  
PA (ACTI-) ACTIVE PASS PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1132  
ID ADJ68757 standard; protein; 1437 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID563.  
PN WO2003087768-A2.

PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
Query Match 7.8%; Score 6; DB 7; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1133  
ID ADN39066 standard; protein; 1437 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:384.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.8%; Score 6; DB 7; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1134  
ID ADN39950 standard; protein; 1437 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C320.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.8%; Score 6; DB 7; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1135  
ID ADN39949 standard; protein; 1437 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C319.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 7.8%; Score 6; DB 7; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1136  
ID ADJ75629 standard; protein; 1437 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:881.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 7.8%; Score 6; DB 8; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1137  
ID ADP44532 standard; protein; 1437 AA.  
DE Human ABCC5 polypeptide.  
PN US2004115649-A1.  
PD 17-JUN-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 7.8%; Score 6; DB 8; Length 1437;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1138  
ID AAB47021 standard; protein; 1453 AA.  
DE Multidrug-resistance associated polypeptide-beta.  
PN US6162616-A.  
PD 19-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 1453;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1139  
ID ABB60944 standard; protein; 1503 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 9624.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.8%; Score 6; DB 4; Length 1503;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
RESULT 1140  
ID AAY06597 standard; protein; 1765 AA.  
DE Mouse sodium channel NaN.  
PN WO9938889-A2.  
PD 05-AUG-1999.  
PA (UYVA ) UNIV YALE.  
Query Match 7.8%; Score 6; DB 2; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1141  
ID AAB20124 standard; protein; 1765 AA.  
DE Mouse sodium channel NaN.  
PN WO200105831-A1.

PD 25-JAN-2001.  
PA (OYTA ) UNIV YALE.  
Query Match 7.8%; Score 6; DB 4; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1142  
ID ADD32196 standard; protein; 1765 AA.  
DE Mouse Na v 1.9 sodium channel protein SEQ ID NO:6.  
PN WO2003080570-A2.  
PD 02-OCT-2003.  
PA (TRAN-) TRANSMOLECULAR INC.  
Query Match 7.8%; Score 6; DB 7; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1143  
ID AAW98354 standard; protein; 1797 AA.  
DE H. pylori GHPO 739 protein.  
PN WO9843478-A1.  
PD 08-OCT-1998.  
PA (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.8%; Score 6; DB 2; Length 1797;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
RESULT 1144  
ID AAU84350 standard; protein; 1857 AA.  
DE Protein MYH11 differentially expressed in breast cancer tissue.  
PN WO200210436-A2.  
PD 07-FEB-2002.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
PA (BAAK/) BAAK J.  
Query Match 7.8%; Score 6; DB 5; Length 1857;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
RESULT 1145  
ID AAM25750 standard; protein; 1879 AA.  
DE Human protein sequence SEQ ID NO:1265.  
PN WO200153455-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.8%; Score 6; DB 4; Length 1879;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
RESULT 1146  
ID ABO44412 standard; protein; 1911 AA.  
DE Novel human protein kinase #32.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 1911;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
RESULT 1147  
ID AAB5656 standard; protein; 1920 AA.  
DE Novel protein kinase, SEQ ID NO: 183.  
PN WO200073469-A2.  
PD 07-DEC-2000.  
PA (SUGE-) SUGEN INC.  
Query Match 7.8%; Score 6; DB 4; Length 1920;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
RESULT 1148  
ID ABR92127 standard; protein; 1938 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:164.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 1938;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
RESULT 1149  
ID ABO44404 standard; protein; 1939 AA.  
DE Novel human protein kinase #24.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 1939;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
RESULT 1150  
ID ABU10398 standard; protein; 1945 AA.  
DE Human smooth muscle myosin heavy chain (hSMMyHC) variant #1.  
PN US2003032018-A1.  
PD 13-FEB-2003.  
PA (CYTO-) CYTOKINETICS INC.  
Query Match 7.8%; Score 6; DB 6; Length 1945;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
RESULT 1151  
ID ADI29263 standard; protein; 1952 AA.  
DE Human MARK3-associated protein #46.  
PN US2003232771-A1.  
PD 18-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 7.8%; Score 6; DB 8; Length 1952;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
RESULT 1152  
ID ABO44396 standard; protein; 1971 AA.  
DE Novel human protein kinase #16.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 1971;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
RESULT 1153  
ID AAW00024 standard; protein; 1972 AA.  
DE Smooth muscle myosin heavy chain SM1 isoform protein.  
PN WO9623089-A1.  
PD 01-AUG-1996.  
PA (VSES-) VESSEL RES LAB CO LTD.  
PA (OSAP ) OSAKA PREFECTURAL GOVERNMENT.  
Query Match 7.8%; Score 6; DB 2; Length 1972;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1154  
ID ABR92126 standard; protein; 1972 AA.  
DE Human cervical cancer cell marker protein SEQ ID NO:162.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.8%; Score 6; DB 6; Length 1972;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1155  
ID ADE58724 standard; protein; 1972 AA.  
DE Human Protein P35749, SEQ ID NO 4602.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.8%; Score 6; DB 7; Length 1972;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1156  
ID ADE58721 standard; protein; 1972 AA.  
DE Human Protein P35749, SEQ ID NO-4598.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.8%; Score 6; DB 7; Length 1972;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1157  
ID ADE63520 standard; protein; 1972 AA.  
DE Human Protein NP\_002465, SEQ ID NO 9464.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.8%; Score 6; DB 7; Length 1972;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1158  
ID ADE63516 standard; protein; 1972 AA.  
DE Human Protein P35749, SEQ ID NO 9460.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.8%; Score 6; DB 7; Length 1972;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1159  
 ID ABO44388 standard; protein; 1999 AA.  
 DE Novel human protein kinase #8.  
 PN US6541252-B1.  
 PD 01-APR-2003.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Query Match 7.8%; Score 6; DB 7; Length 1999;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1160  
 ID ABO44409 standard; protein; 2004 AA.  
 DE Novel human protein kinase #29.  
 PN US6541252-B1.  
 PD 01-APR-2003.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Query Match 7.8%; Score 6; DB 7; Length 2004;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1170  
 ID ABB64300 standard; protein; 2030 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 19692.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE) PE CORP NY.  
 Query Match 7.8%; Score 6; DB 4; Length 2030;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 RESULT 1171  
 ID ABO44401 standard; protein; 2032 AA.  
 DE Novel human protein kinase #21.  
 PN US6541252-B1.  
 PD 01-APR-2003.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Query Match 7.8%; Score 6; DB 7; Length 2032;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 RESULT 1172  
 ID AAR04032 standard; protein; 2037 AA.  
 DE Full length T4 encoded by plasmid pBG381.  
 PN WO8911860-A.  
 PD 14-DEC-1989.  
 PA (BIOJ) BIOGEN NV INC.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (BIOJ) BIOGEN INC.  
 PA (BIOJ) BIOGEN INC.  
 Query Match 7.8%; Score 6; DB 2; Length 2037;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 RESULT 1173  
 ID ABO44411 standard; protein; 2048 AA.  
 DE Novel human protein kinase #31.  
 PN US6541252-B1.  
 PD 01-APR-2003.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Query Match 7.8%; Score 6; DB 7; Length 2048;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 RESULT 1174  
 ID AAR07641 standard; protein; 2050 AA.  
 DE Deduced sequence of pBG381 comprising truncated T4 glycoprotein.  
 PN WO9008198-A.  
 PD 26-JUL-1990.  
 PA (HARD) HARVARD COLLEGE.  
 Query Match 7.8%; Score 6; DB 2; Length 2050;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 RESULT 1175  
 ID ABO44393 standard; protein; 2064 AA.  
 DE Novel human protein kinase #13.  
 PN US6541252-B1.  
 PD 01-APR-2003.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Query Match 7.8%; Score 6; DB 7; Length 2064;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 RESULT 1176  
 ID ADH48388 standard; protein; 2070 AA.  
 DE Human KRP protein SEQ ID NO:46.  
 PN WO2004001008-A2.  
 PD 31-DEC-2003.  
 PA (INCY-) INCYTE CORP.

Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1159  
 ID ADK70527 standard; protein; 1972 AA.  
 DE Respiratory disease differentially expressed protein #93.  
 PN WO2003101283-A2.  
 PD 11-DEC-2003.  
 PA (INCY-) INCYTE CORP.  
 Query Match 7.8%; Score 6; DB 8; Length 1972;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1160  
 ID ADN03745 standard; protein; 1972 AA.  
 DE Antipsoriatic protein sequence #69.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 7.8%; Score 6; DB 8; Length 1972;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1161  
 ID ABB92318 standard; protein; 1973 AA.  
 DE Herbicidically active polypeptide SEQ ID NO 1529.  
 PN WO200210210-A2.  
 PD 07-FEB-2002.  
 PA (FARB) BAYER AG.  
 Query Match 7.8%; Score 6; DB 5; Length 1973;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1162  
 ID ABU10399 standard; protein; 1979 AA.  
 DE Human smooth muscle myosin heavy chain (hSMMyHC) variant #2.  
 PN US2003032018-A1.  
 PD 13-FEB-2003.  
 PA (CYTO-) CYTOKINETICS INC.  
 Query Match 7.8%; Score 6; DB 6; Length 1979;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1163  
 ID ADS11120 standard; protein; 1981 AA.  
 DE Human therapeutic protein - SEQ ID 1357.  
 PN WO2004080148-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC.  
 Query Match 7.8%; Score 6; DB 8; Length 1981;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1164  
 ID ABU16052 standard; protein; 1983 AA.  
 DE Protein encoded by Prokaryotic essential gene #1579.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 6; Length 1983;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1165  
 ID ABR62800 standard; protein; 1983 AA.  
 DE VISA Staphylococcus aureus FmtB-like protein SAV1758.  
 PN WO2003062466-A2.  
 PD 31-JUL-2003.  
 PA (UYBR-) UNIV BRISTOL.  
 Query Match 7.8%; Score 6; DB 7; Length 1983;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1166  
 ID ADQ26947 standard; protein; 1995 AA.  
 DE Human myosin heavy chain.  
 PN DE10260633-A1.  
 PD 24-JUN-2004.  
 PA (RAUT/) RAUTENSTRAUSS B.  
 Query Match 7.8%; Score 6; DB 8; Length 1995;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 RESULT 1167  
 ID ABB66040 standard; protein; 1998 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 24912.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE) PE CORP NY.  
 Query Match 7.8%; Score 6; DB 4; Length 1998;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Query Match 7.8%; Score 6; DB 8; Length 2070;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
RESULT 1177  
ID AAU34319 standard; protein; 2076 AA.  
DE Staphylococcus aureus cellular proliferation protein #595.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 2076;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
RESULT 1178  
ID ABO44403 standard; protein; 2076 AA.  
DE Novel human protein kinase #23.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2076;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
RESULT 1179  
ID ABO44385 standard; protein; 2092 AA.  
DE Novel human protein kinase #5.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2092;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
RESULT 1180  
ID ABO44395 standard; protein; 2108 AA.  
DE Novel human protein kinase #15.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2108;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
RESULT 1181  
ID ADC98049 standard; protein; 2108 AA.  
DE Human XPP protein - SEQ ID 2.  
PN WO2003033680-A2.  
PD 24-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2108;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
RESULT 1182  
ID AAE21714 standard; protein; 2135 AA.  
DE Human PKIN-9 protein.  
PN WO200218557-A2.  
PD 07-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.8%; Score 6; DB 5; Length 2135;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1183  
ID ABO44387 standard; protein; 2136 AA.  
DE Novel human protein kinase #7.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2136;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1184  
ID ABO44408 standard; protein; 2141 AA.  
DE Novel human protein kinase #28.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2141;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1185  
ID ABP57679 standard; protein; 2149 AA.  
DE Saccharopolyspora busb butenyl-spinosyn biosynthetic gene product.  
PN WO200279477-A2.  
PD 10-OCT-2002.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 7.8%; Score 6; DB 6; Length 2149;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1186  
ID AAY39298 standard; protein; 2152 AA.  
DE SpnB a polyketide synthase.  
PN WO946387-A1.  
PD 16-SEP-1999.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 7.8%; Score 6; DB 2; Length 2152;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1187  
ID AAB70966 standard; protein; 2152 AA.  
DE S. spinosa protein fragment encoded by ORF19, SEQ ID 44.  
PN DE19957268-A1.  
PD 08-MAR-2001.  
PA (FARB) BAYER AG.  
Query Match 7.8%; Score 6; DB 4; Length 2152;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1188  
ID ABO44406 standard; protein; 2157 AA.  
DE Novel human protein kinase #26.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2157;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1189  
ID ABO44400 standard; protein; 2169 AA.  
DE Novel human protein kinase #20.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2169;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
RESULT 1190  
ID ABO44398 standard; protein; 2185 AA.  
DE Novel human protein kinase #18.  
PN US6541252-B1.  
PD 01-APR-2003.  
PA (LEXI-) LEXICON GENETICS INC.  
Query Match 7.8%; Score 6; DB 7; Length 2185;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
RESULT 1191  
ID AAU37320 standard; protein; 2186 AA.  
DE Staphylococcus aureus cellular proliferation protein #1490.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.8%; Score 6; DB 4; Length 2186;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
RESULT 1192  
ID ABJ19059 standard; protein; 2186 AA.  
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 336.  
PN WO200259148-A2.  
PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
Query Match 7.8%; Score 6; DB 6; Length 2186;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
RESULT 1193  
ID ABM71190 standard; protein; 2186 AA.  
DE Staphylococcus aureus protein #430.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.8%; Score 6; DB 6; Length 2186;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
RESULT 1194  
ID ABR62805 standard; protein; 2186 AA.  
DE Methicillin resistant Staphylococcus aureus ORF SA1577-fmtB protein.  
PN WO2003062466-A2.  
PD 31-JUL-2003.  
PA (UYBR-) UNIV BRISTOL.  
Query Match 7.8%; Score 6; DB 7; Length 2186;  
Best Local Similarity 100.0%; Pred. No. 4.9e+03;

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RESULT 1195
ID ABP56875 standard; protein; 2189 AA.
DE Staphylococcus epidermidis Ekes_MRSA protein SEQ ID NO:2.
PN WO2002102829-A2.
PD 27-DEC-2002.
PA (INHI-) INHIBITEK INC.
PA (QUE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA (UYPA-) UNIV PAVIA.
Query Match 7.8%; Score 6; DB 6; Length 2189;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
RESULT 1196
ID ABR62792 standard; protein; 2196 AA.
DE MRSA FmcB-like protein SA1577.
PN WO2003062466-A2.
PD 31-JUL-2003.
PA (OYBR-) UNIV BRISTOL.
Query Match 7.8%; Score 6; DB 7; Length 2196;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
RESULT 1197
ID ABO44392 standard; protein; 2201 AA.
DE Novel human protein kinase #12.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2201;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
RESULT 1198
ID ABO44390 standard; protein; 2217 AA.
DE Novel human protein kinase #10.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2217;
Best Local Similarity 100.0%; Pred. No. 5e+03;
RESULT 1199
ID ABO44384 standard; protein; 2229 AA.
DE Novel human protein kinase #4.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2229;
Best Local Similarity 100.0%; Pred. No. 5e+03;
RESULT 1200
ID ABO44382 standard; protein; 2245 AA.
DE Novel human protein kinase #2.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2245;
Best Local Similarity 100.0%; Pred. No. 5e+03;
RESULT 1201
ID ABO44405 standard; protein; 2294 AA.
DE Novel human protein kinase #25.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2294;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
RESULT 1202
ID ABO44397 standard; protein; 2322 AA.
DE Novel human protein kinase #17.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2322;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
RESULT 1203
ID ABO44389 standard; protein; 2354 AA.
DE Novel human protein kinase #9.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2354;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
RESULT 1204
ID ABP71619 standard; protein; 2382 AA.
DE Human WNK1 protein.
PN WO2003007793-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (LIFT-) LIFTON R P.
PA (WILS-) WILSON F H.
PA (CHOR-) CHOATE K.
PA (NELS-) NELSON-WILLIAMS C.
PA (ISHI-) ISHIKAWA K.
Query Match 7.8%; Score 6; DB 6; Length 2382;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
RESULT 1205
ID ABO44381 standard; protein; 2382 AA.
DE Novel human protein kinase #1.
PN US6541252-B1.
PD 01-APR-2003.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.8%; Score 6; DB 7; Length 2382;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
RESULT 1206
ID ADJ69598 standard; protein; 2382 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1404.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.8%; Score 6; DB 7; Length 2382;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
RESULT 1207
ID ADS11119 standard; protein; 2388 AA.
DE Human therapeutic protein - SEQ ID 1356.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.8%; Score 6; DB 8; Length 2388;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
RESULT 1208
ID ADE52217 standard; protein; 2606 AA.
DE PG1EN-EH3.His vector and E3Bi sequence, SEQ ID 5.
PN WO2003090513-A2.
PD 06-NOV-2003.
PA (WILL-) WILLIAMS HOSPITAL ROGER.
Query Match 7.8%; Score 6; DB 7; Length 2606;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
RESULT 1209
ID ADE52214 standard; protein; 2606 AA.
DE PG1EN-EH3.His vector and E3Bi sequence, SEQ ID 2.
PN WO2003090513-A2.
PD 06-NOV-2003.
PA (WILL-) WILLIAMS HOSPITAL ROGER.
Query Match 7.8%; Score 6; DB 7; Length 2606;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
RESULT 1210
ID AAU35978 standard; protein; 2890 AA.
DE Helicobacter pylori cellular proliferation protein #291.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 4; Length 2890;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
RESULT 1211
ID AAU35817 standard; protein; 2890 AA.
DE Helicobacter pylori cellular proliferation protein #130.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.8%; Score 6; DB 4; Length 2890;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
RESULT 1212
ID ABU30983 standard; protein; 2890 AA.
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DE Protein encoded by Prokaryotic essential gene #16510.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (EUIT-) ELITRA PHARM INC.  
 Query Match 7.8%; Score 6; DB 6; Length 2890;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 RESULT 1213  
 ID ADH11258 standard; protein; 3614 AA.  
 DE Vertebrate UNC-53 protein homologue related amino acid sequence.  
 PN WO9824810-A2.  
 PD 11-JUN-1998.  
 PA (JANC) JANSSEN PHARM NV.  
 Query Match 7.8%; Score 6; DB 2; Length 3614;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 RESULT 1214  
 ID ABP76679 standard; protein; 19938 AA.  
 DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.  
 PN WO200268436-A1.  
 PD 06-SEP-2002.  
 PA (COMB-) COMBINATURE BIOPHARM AG.  
 Query Match 7.8%; Score 6; DB 6; Length 19938;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
 RESULT 1215  
 ID ADM33096 standard; peptide; 6 AA.  
 DE Human immunodeficiency virus 1 cell entry inhibitor peptide #124.  
 PN WO2004024173-A2.  
 PD 23-MAR-2004.  
 PA (CREA-) CREABILIS THERAPEUTICS SRL.  
 Query Match 6.5%; Score 5; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1216  
 ID ADE78187 standard; peptide; 7 AA.  
 DE Synthetic peptide (SeqID 438) that binds atherosclerotic lesions.  
 PN WO2003014145-A2.  
 PD 20-FEB-2003.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS PHARMA GMBH.  
 PA (Scri) SCRIPPS RES INST.  
 Query Match 6.5%; Score 5; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1217  
 ID ADE77755 standard; peptide; 7 AA.  
 DE Synthetic peptide (SeqID 6) that binds atherosclerotic lesions.  
 PN WO2003014145-A2.  
 PD 20-FEB-2003.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS PHARMA GMBH.  
 PA (Scri) SCRIPPS RES INST.  
 Query Match 6.5%; Score 5; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1218  
 ID ADR69555 standard; peptide; 7 AA.  
 DE Novel hybrid antigen-related peptide SeqID345.  
 PN WO2004071457-A2.  
 PD 26-AUG-2004.  
 PA (MOJA-) MOJAVE THERAPEUTICS INC.  
 Query Match 6.5%; Score 5; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1219  
 ID ADM68731 standard; peptide; 8 AA.  
 DE Human MAGE-2-derived antigenic peptide SeqID80.  
 PN WO2004029071-A2.  
 PD 08-APR-2004.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 Query Match 6.5%; Score 5; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1220  
 ID ADR69562 standard; peptide; 8 AA.  
 DE Novel hybrid antigen-related peptide SeqID501.  
 PN WO2004071457-A2.  
 PD 26-AUG-2004.  
 PA (MOJA-) MOJAVE THERAPEUTICS INC.  
 Query Match 6.5%; Score 5; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1221  
 ID ADR69563 standard; peptide; 8 AA.  
 DE Novel hybrid antigen-related peptide SeqID502.  
 PN WO2004071457-A2.  
 PD 26-AUG-2004.  
 PA (MOJA-) MOJAVE THERAPEUTICS INC.  
 Query Match 6.5%; Score 5; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1222  
 ID ADR69738 standard; peptide; 8 AA.  
 DE Novel hybrid antigen-related peptide #1318.  
 PN WO2004071457-A2.  
 PD 26-AUG-2004.  
 PA (MOJA-) MOJAVE THERAPEUTICS INC.  
 Query Match 6.5%; Score 5; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1223  
 ID AAG88479 standard; peptide; 9 AA.  
 DE HER2/NEU DR supermotif binding peptide core sequence #96.  
 PN WO200141787-A1.  
 PD 14-JUN-2001.  
 PA (EPIM-) EPIMUNE INC.  
 Query Match 6.5%; Score 5; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1224  
 ID ADE78189 standard; peptide; 9 AA.  
 DE Synthetic peptide (SeqID 440) that binds atherosclerotic lesions.  
 PN WO2003014145-A2.  
 PD 20-FEB-2003.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS PHARMA GMBH.  
 PA (Scri) SCRIPPS RES INST.  
 Query Match 6.5%; Score 5; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1225  
 ID ADE77757 standard; peptide; 9 AA.  
 DE Synthetic peptide (SeqID 8) that binds atherosclerotic lesions.  
 PN WO2003014145-A2.  
 PD 20-FEB-2003.  
 PA (NOVS) NOVARTIS AG.  
 PA (NOVS) NOVARTIS PHARMA GMBH.  
 PA (Scri) SCRIPPS RES INST.  
 Query Match 6.5%; Score 5; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1226  
 ID ADK04181 standard; peptide; 9 AA.  
 DE Hepatitis C virus CTL epitope peptide #2011.  
 PN WO2004011650-A2.  
 PD 05-FEB-2004.  
 PA (INTE-) INTERCELL AG.  
 Query Match 6.5%; Score 5; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1227  
 ID ADM68730 standard; peptide; 9 AA.  
 DE Human MAGE-2-derived antigenic peptide SeqID79.  
 PN WO2004029071-A2.  
 PD 08-APR-2004.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 Query Match 6.5%; Score 5; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1228  
 ID ADM68729 standard; peptide; 9 AA.  
 DE Human MAGE-2-derived antigenic peptide SeqID78.  
 PN WO2004029071-A2.  
 PD 08-APR-2004.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 Query Match 6.5%; Score 5; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 RESULT 1229  
 ID ADO69362 standard; peptide; 9 AA.  
 DE Human 213P1F11 HLA motif bearing epitope #5452.  
 PN US2004019915-A1.

PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 6.5%; Score 5; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1230  
ID ADO65155 standard; peptide; 9 AA.  
DE Human 213P1P11 HLA motif bearing epitope #1245.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 6.5%; Score 5; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1231  
ID AAY81292 standard; peptide; 10 AA.  
DE Protein VIII zone-1 library variant peptide, SEQ ID NO:143.  
PN WO200006717-A2.  
PD 10-FEB-2000.  
PA (GETH/) GENENTECH INC.  
Query Match 6.5%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1232  
ID AAU68189 standard; peptide; 10 AA.  
DE Human Breast cancer-associated protein isoform, BPI-218 peptide.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match 6.5%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1233  
ID AAU68047 standard; peptide; 10 AA.  
DE Human Breast cancer-associated protein isoform, BPI-302 peptide #7.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match 6.5%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1234  
ID AAU68096 standard; peptide; 10 AA.  
DE Human Breast cancer-associated protein isoform, BPI-311 peptide #6.  
PN WO200171357-A2.  
PD 27-SEP-2001.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match 6.5%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1235  
ID AAG88845 standard; peptide; 10 AA.  
DE HER2/neu epitope B7 supermotif peptide #5.  
PN WO200141787-A1.  
PD 14-JUN-2001.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1236  
ID AAB76168 standard; peptide; 10 AA.  
DE Tumour associated antigen Her2/neu immunogenic peptide.  
PN WO200100225-A1.  
PD 04-JAN-2001.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1237  
ID AAM43188 standard; peptide; 10 AA.  
DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 497.  
PN WO200142278-A2.  
PD 14-JUN-2001.  
PA (PROT-) PROTEOM LTD.  
Query Match 6.5%; Score 5; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1238  
ID ABR91494 standard; peptide; 10 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:328.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1239  
ID ADM33152 standard; peptide; 10 AA.  
DE Human MAGE-C2 peptide #9.  
PN US2003170256-A1.  
PD 11-SEP-2003.  
PA (LUCA/) LUCAS S.  
PA (DSME/) DE SMET C.  
PA (BOON/) BOON-FALLEUR T.  
Query Match 6.5%; Score 5; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1240  
ID ADK04197 standard; peptide; 10 AA.  
DE Hepatitis C virus CTL epitope peptide #2027.  
PN WO2004011650-A2.  
PD 05-FEB-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1241  
ID ADM68728 standard; peptide; 10 AA.  
DE Human MAGE-2-derived antigenic peptide SeqID77.  
PN WO2004029071-A2.  
PD 08-APR-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1242  
ID ADM68739 standard; peptide; 10 AA.  
DE Human MAGE-2-derived antigenic peptide SeqID88.  
PN WO2004029071-A2.  
PD 08-APR-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1243  
ID ADN64612 standard; peptide; 10 AA.  
DE HLA binding peptide #1212.  
PN WO2004031211-A2.  
PD 15-APR-2004.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1244  
ID ADO65924 standard; peptide; 10 AA.  
DE Human 213P1P11 HLA motif bearing epitope #2014.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1245  
ID ADO74645 standard; peptide; 10 AA.

DE Human 213P1P11 HLA motif bearing epitope #8744.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOWITS A.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1246  
ID ADO65435 standard; peptide; 10 AA.  
DE Human 213P1P11 HLA motif bearing epitope #1525.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOWITS A.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1247  
ID ADP80201 standard; peptide; 10 AA.  
DE Human HLA-B44 epitope vaccine peptide SeqID457.  
PN WO2004052917-A2.  
PD 24-JUN-2004.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 1248  
ID ABR91498 standard; peptide; 11 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:332.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
RESULT 1249  
ID AAY93003 standard; peptide; 12 AA.  
DE Transforming growth factor inhibitory peptide P49.  
PN WO200031135-A1.  
PD 02-JUN-2000.  
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
Query Match 6.5%; Score 5; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
RESULT 1250  
ID ABP61679 standard; peptide; 13 AA.  
DE Human KRPI tryptic digest peptide #158.  
PN WO200254081-A2.  
PD 11-JUL-2002.  
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
Query Match 6.5%; Score 5; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 1251  
ID AAM00699 standard; peptide; 14 AA.  
DE Human protein fragment SEQ ID NO: 1249.  
PN WO200151670-A2.  
PD 19-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 5; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1252  
ID AAM00411 standard; peptide; 14 AA.  
DE Human protein fragment SEQ ID NO: 959.  
PN WO200151670-A2.  
PD 19-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 5; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1253  
ID AAM00412 standard; peptide; 14 AA.  
DE Human protein fragment SEQ ID NO: 960.  
PN WO200151670-A2.  
PD 19-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.5%; Score 5; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1254  
ID ABR91535 standard; peptide; 14 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:369.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1255  
ID ABR64069 standard; peptide; 14 AA.  
DE E. coli phosphoglyceromutase 1 tryptic peptide #9.  
PN WO2003025006-A2.  
PD 27-MAR-2003.  
PA (AFFI-) AFFINIUM PHARM INC.  
Query Match 6.5%; Score 5; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1256  
ID ADB98806 standard; peptide; 14 AA.  
DE LRP5 peptide #4.  
PN WO200292000-A2.  
PD 21-NOV-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (AMHP) WYETH.  
Query Match 6.5%; Score 5; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1257  
ID ADD18061 standard; peptide; 14 AA.  
DE Human G-protein coupled receptor phosphorylation peptide SeqID118.  
PN WO2003016478-A2.  
PD 27-FEB-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.5%; Score 5; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
RESULT 1258  
ID AAY98848 standard; peptide; 15 AA.  
DE HLA class II binding antigen epitope peptide #37.  
PN WO961916-A1.  
PD 02-DEC-1999.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1259  
ID AAG88490 standard; peptide; 15 AA.  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #101.  
PN WO200141787-A1.  
PD 14-JUN-2001.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1260  
ID AAG89018 standard; peptide; 15 AA.  
DE HER2/NEU DR supermotif primary binding peptide #12.  
PN WO200141787-A1.  
PD 14-JUN-2001.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1261  
ID AAG88382 standard; peptide; 15 AA.  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #47.  
PN WO200141787-A1.  
PD 14-JUN-2001.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 6.5%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1262  
ID AAG88480 standard; peptide; 15 AA.  
DE HER2/NEU DR supermotif binding peptide exemplary sequence #96.  
PN WO200141787-A1.  
PD 14-JUN-2001.  
PA (EPIN-) EPIMUNE INC.  
Query Match 6.5%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1263  
ID ABB05807 standard; peptide; 15 AA.  
DE Human sigma receptor 10.67 N-terminal peptide SEQ ID NO:7.  
PN WO200196524-A2.  
PD 20-DEC-2001.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 6.5%; Score 5; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1264  
ID ABB83075 standard; peptide; 15 AA.  
DE Synoviolin related peptide Syno-P3.  
PN WO200252007-A1.  
PD 04-JUL-2002.  
PA (LOCO-) LOCOMOGENE INC.  
Query Match 6.5%; Score 5; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1265  
ID ADO76610 standard; peptide; 15 AA.  
DE Human 213P1F11 HLA motif bearing epitope #10709.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 6.5%; Score 5; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1266  
ID ADO76588 standard; peptide; 15 AA.  
DE Human 213P1F11 HLA motif bearing epitope #10687.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 6.5%; Score 5; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1267  
ID ADO76396 standard; peptide; 15 AA.  
DE Human 213P1F11 HLA motif bearing epitope #10495.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 6.5%; Score 5; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 1268  
ID AAY95828 standard; peptide; 16 AA.  
DE Native human MAC-1 (CD11 alpha) signal peptide.  
PN WO200047741-A1.  
PD 17-AUG-2000.  
PA (AMGE-) AMGEN INC.

Query Match 6.5%; Score 5; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1269  
ID ADD90457 standard; protein; 16 AA.  
DE Novel human secreted protein seq id 53 protein feature seq id 272.  
PN US2003199683-A1.  
PD 23-OCT-2003.  
PA (RUBE/) RUBEN S M.  
PA (FENG/) FENG P.  
PA (LAFU/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (KYAW/) KYAW H.  
PA (LIYV/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (CART/) CARTER K C.  
PA (ENDR/) ENDRESS G A.  
PA (WEIY/) WEI Y.  
PA (FANP/) FAN P.  
PA (ROSE/) ROSEN C A.  
Query Match 6.5%; Score 5; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1270  
ID ADF70221 standard; peptide; 16 AA.  
DE Human protease-42 N-myristoylation peptide SeqID51.  
PN WO2003078594-A2.  
PD 25-SEP-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.5%; Score 5; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1271  
ID ADF12260 standard; peptide; 16 AA.  
DE Neurospora crassa poly A element TAD fragment seq id 6.  
PN US2003121063-A1.  
PD 26-JUN-2003.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 6.5%; Score 5; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1272  
ID ADG90276 standard; peptide; 16 AA.  
DE Human secreted protein gene 43 extra polypeptide #1.  
PN US2003166541-A1.  
PD 04-SEP-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 7; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1273  
ID ADM68732 standard; peptide; 16 AA.  
DE Human WAGE-2 minigene 14-derived peptide SeqID81.  
PN WO2004029071-A2.  
PD 08-APR-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 6.5%; Score 5; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1274  
ID AAB28046 standard; peptide; 17 AA.  
DE Human secreted protein SEQ ID NO: 94.  
PN WO200055177-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1275  
ID AAE19470 standard; peptide; 17 AA.  
DE Limulus polyphemus polypheumisin-like peptide #1.  
PN WO200200687-A2.  
PD 03-JAN-2002.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match 6.5%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1276  
ID AAE19471 standard; peptide; 17 AA.  
DE Limulus polyphemus polypheumisin-like peptide #2.

PN W0200200687-A2.  
PD 03-JAN-2002.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
Query Match 6.5%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1277  
ID AAU90064 standard; peptide; 17 AA.  
DE Insulin/insulin-like growth factor receptor-binding peptide #2020.  
PD 04-OCT-2001.  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 6.5%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1278  
ID AAU90053 standard; peptide; 17 AA.  
DE Insulin/insulin-like growth factor receptor-binding peptide #2009.  
PN W020017271-A2.  
PD 04-OCT-2001.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 6.5%; Score 5; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1279  
ID ABR75732 standard; peptide; 17 AA.  
DE Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:243.  
PN W02003038444-A2.  
PD 08-MAY-2003.  
PA (PFIZ) PFIZER PROD INC.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
Query Match 6.5%; Score 5; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1280  
ID ADN07384 standard; peptide; 17 AA.  
DE Liver response-associated feature LRF223.  
PN US2003228583-A1.  
PD 11-DEC-2003.  
PA (AMAC/) AMACHER D E.  
PA (FASU/) FASULO L M.  
PA (HERA/) HERATH H M A C.  
PA (HOLT/) HOLT G D.  
PA (STIG/) STIGER T R.  
Query Match 6.5%; Score 5; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
RESULT 1281  
ID AAU03222 standard; peptide; 18 AA.  
DE BWP-8 fragment 85-102.  
PN EP691349-A2.  
PD 10-JAN-1996.  
PA (FARH) HOECHST JAPAN LTD.  
Query Match 6.5%; Score 5; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1282  
ID AAU53126 standard; peptide; 18 AA.  
DE Human thrombopoietin C-terminal peptide fragment 1.  
PN W09806849-A1.  
PD 19-FEB-1998.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 6.5%; Score 5; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1283  
ID ABG32241 standard; peptide; 18 AA.  
DE Tomato lycopene epsilon cyclase catalytic domain.  
PN W0200261050-A2.  
PD 08-AUG-2002.  
PA (UYMA-) UNIV MARYLAND BALTIMORE.  
Query Match 6.5%; Score 5; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1284  
ID ABG32239 standard; peptide; 18 AA.  
DE A. thaliana lycopene epsilon cyclase catalytic domain.  
PN W0200261050-A2.  
PD 08-AUG-2002.

PA (UYMA-) UNIV MARYLAND BALTIMORE.  
Query Match 6.5%; Score 5; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1285  
ID ABG32240 standard; peptide; 18 AA.  
DE Potato lycopene epsilon cyclase catalytic domain.  
PN W0200261050-A2.  
PD 08-AUG-2002.  
PA (UYMA-) UNIV MARYLAND BALTIMORE.  
Query Match 6.5%; Score 5; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1286  
ID ABG32242 standard; peptide; 18 AA.  
DE Marigold lycopene epsilon cyclase catalytic domain.  
PN W0200261050-A2.  
PD 08-AUG-2002.  
PA (UYMA-) UNIV MARYLAND BALTIMORE.  
Query Match 6.5%; Score 5; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1287  
ID ABR64073 standard; peptide; 18 AA.  
DE E. coli phosphoglyceromutase 1 tryptic peptide #13.  
PN W02003025006-A2.  
PD 27-MAR-2003.  
PA (AFPI-) AFFINIUM PHARM INC.  
Query Match 6.5%; Score 5; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1288  
ID ADO27348 standard; peptide; 18 AA.  
DE Hepatitis C virus E1 glycoprotein lead peptide SeqID 50.  
PN W02004044220-A2.  
PD 27-MAY-2004.  
PA (TULA) TULANE EDUCATIONAL FUND.  
PA (UYRQ) UNIV ROCKEFELLER.  
Query Match 6.5%; Score 5; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1289  
ID ADO27347 standard; peptide; 18 AA.  
DE Hepatitis C virus E1 glycoprotein lead peptide SeqID 49.  
PN W02004044220-A2.  
PD 27-MAY-2004.  
PA (TULA) TULANE EDUCATIONAL FUND.  
PA (UYRQ) UNIV ROCKEFELLER.  
Query Match 6.5%; Score 5; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 1290  
ID AAB51951 standard; protein; 19 AA.  
DE Human secreted protein sequence encoded by gene 23 SEQ ID NO:83.  
PN W0200058334-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1291  
ID ADE36949 standard; peptide; 19 AA.  
DE Interfacial biomaterial ligand polystyrene binding peptide SEQ ID NO:10.  
PN W02003072542-A2.  
PD 04-SEP-2003.  
PA (UYDU-) UNIV DUKE.  
Query Match 6.5%; Score 5; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1292  
ID ADR69755 standard; peptide; 19 AA.  
DE Novel hybrid antigen-related peptide #1335.  
PN W02004071457-A2.  
PD 26-AUG-2004.  
PA (MOJA-) MOJAVE THERAPEUTICS INC.  
Query Match 6.5%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
RESULT 1293  
ID AAR84422 standard; peptide; 20 AA.  
DE Hepatitis C virus E1 region (265-284) peptide.  
PN W09512677-A2.

PD 11-MAY-1995.  
PA (INNO-) INNOGENETICS NV.  
Query Match 6.5%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1294  
ID AAR30973 standard; peptide; 20 AA.  
DE HCV E1 peptide E1-45 for competition studies.  
PN WO9604385-A2.  
PD 15-FEB-1996.  
PA (INNO-) INNOGENETICS NV.  
Query Match 6.5%; Score 5; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1295  
ID AAM20136 standard; protein; 20 AA.  
DE Peptide #6570 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1296  
ID ABB40352 standard; peptide; 20 AA.  
DE Peptide #7858 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1297  
ID AAM34057 standard; protein; 20 AA.  
DE Peptide #8094 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1298  
ID ABB24740 standard; protein; 20 AA.  
DE Protein #6739 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1299  
ID AAM3875 standard; protein; 20 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34181.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1300  
ID AAM61161 standard; protein; 20 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33266.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1301  
ID ABG55626 standard; peptide; 20 AA.  
DE Human liver peptide, SEQ ID No 34274.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1302  
ID ABG43763 standard; peptide; 20 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33428.  
PN WO200186003-A2.  
PD 15-NOV-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1303  
ID AAU71025 standard; peptide; 20 AA.  
DE M. tuberculosis RV0284 protein immunogenic peptide P38.  
PN WO200179274-A2.  
PD 25-OCT-2001.  
PA (STAT-) STATENS SERUM INST.  
Query Match 6.5%; Score 5; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1304  
ID AAO18693 standard; peptide; 20 AA.  
DE Hepatitis C virus E1 protein derived peptide E1-45.  
PN WO20025548-A2.  
PD 18-JUL-2002.  
PA (INNO-) INNOGENETICS NV.  
Query Match 6.5%; Score 5; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1305  
ID ADD55572 standard; peptide; 20 AA.  
DE Hepatitis C virus E1 epitope peptide #14.  
PN WO2003051912-A2.  
PD 26-JUN-2003.  
PA (INNO-) INNOGENETICS NV.  
Query Match 6.5%; Score 5; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1306  
ID ADP71154 standard; peptide; 20 AA.  
DE HCV E1 protein, peptide E1-45.  
PN US2004126395-A1.  
PD 01-JUL-2004.  
PA (MAER/) MAERTENS G.  
PA (DEPL/) DEPLA E.  
PA (BOSM/) BOSMAN F.  
Query Match 6.5%; Score 5; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 1307  
ID AAM88554 standard; protein; 21 AA.  
DE Secreted protein encoded by gene 21 clone HSDGP60.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1308  
ID ABB50321 standard; protein; 21 AA.  
DE Human secreted protein encoded by gene 21 SEQ ID NO:269.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1309  
ID ABG66496 standard; peptide; 21 AA.  
DE Ige Fc epsilon RI binding peptide IGE134 #37.  
PN WO200226781-A2.  
PD 04-APR-2002.  
PA (GETH) GENENTECH INC.  
Query Match 6.5%; Score 5; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1310  
ID ABO44578 standard; protein; 21 AA.  
DE Novel human secreted protein #21.  
PN US2003085160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1311  
ID ABO26058 standard; protein; 21 AA.  
DE Human protein from novel secreted protein gene 21.  
PN US6525174-B1.

PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1312  
ID ADE48087 standard; peptide; 21 AA.  
DE Hyaluronidase fragment #8.  
PN US2003009296-A1.  
PD 09-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.5%; Score 5; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1313  
ID ABO60589 standard; protein; 21 AA.  
DE Human genome derived single exon protein #6823.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 6.5%; Score 5; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
RESULT 1314  
ID RAW03582 standard; peptide; 22 AA.  
DE Human m2 muscarinic acetylcholine GPR N-terminal sequence.  
PN US508384-A.  
PD 16-APR-1996.  
PA (UYNY) UNIV NEW YORK STATE.  
Query Match 6.5%; Score 5; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 1315  
ID AAY52259 standard; peptide; 22 AA.  
DE H. pylori ygd protein fragment containing conserved motif 3.  
PN WO954470-A2.  
PD 28-OCT-1999.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 6.5%; Score 5; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 1316  
ID AAB57740 standard; peptide; 22 AA.  
DE D.melanogaster Jock peptide #6.  
PN US6150160-A.  
PD 21-NOV-2000.  
PA (UYJO) UNIV JOHNS HOPKINS.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 6.5%; Score 5; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
RESULT 1317  
ID AAY11429 standard; protein; 23 AA.  
DE Human 5, EST secreted protein SEQ ID No 251.  
PN WO9906551-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 6.5%; Score 5; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1318  
ID AAU90690 standard; peptide; 23 AA.  
DE Insulin/insulin-like growth factor receptor-binding peptide #2646.  
PN WO20017271-A2.  
PD 04-OCT-2001.  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 6.5%; Score 5; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1319  
ID AAU88261 standard; peptide; 23 AA.  
DE Insulin/insulin-like growth factor receptor-binding peptide #217.  
PN WO20017271-A2.  
PD 04-OCT-2001.  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 6.5%; Score 5; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;

RESULT 1320  
ID ADA04526 standard; peptide; 23 AA.  
DE IR/IGF-IR related peptide SEQ ID NO:1157.  
PN WO2003027246-A2.  
PD 03-APR-2003.  
PA (NOVO) NOVO NORDISK AS.  
PA (DGIB-) DGI BIOTECHNOLOGIES.  
Query Match 6.5%; Score 5; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1321  
ID AAE33949 standard; peptide; 23 AA.  
DE Dilapidated malaria peptide.  
PN WO200276485-A2.  
PD 03-OCT-2002.  
PA (BUDZ/) BUDZYNSKI W A.  
Query Match 6.5%; Score 5; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1322  
ID AAE38456 standard; peptide; 23 AA.  
DE CD2AP peptide #5.  
PN WO2003068808-A1.  
PD 21-AUG-2003.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 6.5%; Score 5; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1323  
ID ADD18049 standard; peptide; 23 AA.  
DE Human G-protein coupled receptor related transmembrane peptide SeqID106.  
PN WO2003016478-A2.  
PD 27-FEB-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.5%; Score 5; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1324  
ID ADH95739 standard; protein; 23 AA.  
DE Insulin/insulin-like growth factor receptor binding protein, SEQ ID 1157.  
PN WO2003070747-A2.  
PD 28-AUG-2003.  
PA (NOVO) NOVO NORDISK AS.  
PA (DGIB-) DGI BIOTECHNOLOGIES.  
Query Match 6.5%; Score 5; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1325  
ID ADL68430 standard; peptide; 23 AA.  
DE IGF-IR/IR binding peptide seq id 1157.  
PN US2004023887-A1.  
PD 05-FEB-2004.  
PA (PILL/) PILLIUTLA R.  
PA (DEDO/) DEDOVA O.  
PA (BLUM/) BLUME A J.  
PA (GOLD/) GOLDSTEIN N I.  
PA (BRIS/) BRISSETTE R.  
PA (WANG/) WANG P.  
PA (LIUH/) LIU H.  
PA (HSIA/) HSIAO K.  
PA (LENN/) LENNICK M.  
PA (FLET/) FLETCHER P.  
Query Match 6.5%; Score 5; DB 8; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1326  
ID ADM38275 standard; peptide; 23 AA.  
DE Representative peptide #3.  
PN US2003236190-A1.  
PD 25-DEC-2003.  
PA (PILL/) PILLIUTLA R.  
PA (BRIS/) BRISSETTE R.  
PA (BLUM/) BLUME A J.  
PA (SCHA/) SCHAFER L.  
PA (BRAN/) BRANDT J.  
PA (GOLD/) GOLDSTEIN N I.  
PA (SPET/) SPETZLER J.  
PA (OSTE/) OSTERGAARD S.  
PA (HANS/) HANSEN P H.

Query Match 6.5%; Score 5; DB 8; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
RESULT 1327  
ID AAB57698 standard; peptide; 24 AA.  
DE N.crassa TAD peptide #6.  
PN US6150160-A.  
PD 21-NOV-2000.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 6.5%; Score 5; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 1328  
ID AAB48671 standard; peptide; 24 AA.  
DE Human CDB6 constant Domain fragment, SEQ ID NO:20.  
PN WO200066162-A1.  
PD 09-NOV-2000.  
PA (UYPE-) UNIV PENNSYLVANIA.  
PA (SEKA/) SERALY R P.  
PA (HOLT/) HOLTERMAN M.  
Query Match 6.5%; Score 5; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 1329  
ID ABR91576 standard; peptide; 24 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:410.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 1330  
ID ABO57390 standard; protein; 24 AA.  
DE Human genome derived single exon protein #3624.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 6.5%; Score 5; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 1331  
ID AAR10510 standard; protein; 25 AA.  
DE Fragment of subtilisin secretion signal.  
PN EP409098-A.  
PD 23-JAN-1991.  
PA (ENIE ) ENIRICRCH SPA.  
Query Match 6.5%; Score 5; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1332  
ID AAR39772 standard; peptide; 25 AA.  
DE Melittin delta 14 (deletion analogue).  
PN US235038-A.  
PD 10-AUG-1993.  
PA (TORR-) TORRY PINES INST MOLECULAR STUDIES.  
Query Match 6.5%; Score 5; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1333  
ID AAM13922 standard; protein; 25 AA.  
DE Peptide #356 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1334  
ID ABB32867 standard; peptide; 25 AA.  
DE Peptide #373 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1335  
ID AAM26328 standard; protein; 25 AA.

DE Peptide #365 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1336  
ID ABB27696 standard; peptide; 25 AA.  
DE Human peptide #347 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1337  
ID ABB18349 standard; protein; 25 AA.  
DE Protein #348 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1338  
ID AAM66053 standard; protein; 25 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26359.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1339  
ID AAM53669 standard; protein; 25 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 25774.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1340  
ID ABG47719 standard; peptide; 25 AA.  
DE Human liver peptide, SEQ ID NO 26367.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1341  
ID AAM01665 standard; protein; 25 AA.  
DE Peptide #347 encoded by probe for measuring human breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1342  
ID ABG13692 standard; protein; 25 AA.  
DE Novel human diagnostic protein #13683.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1343  
ID AAB62888 standard; protein; 25 AA.  
DE Mature bovine beta-lactoglobulin (BLG) tryptic digest peptide 3.  
PN WO200118528-A1.  
PD 15-MAR-2001.  
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
Query Match 6.5%; Score 5; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1344  
ID ABG35701 standard; peptide; 25 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25366.

PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1345  
ID ABR91360 standard; peptide; 25 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:194.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1346  
ID ABR91580 standard; peptide; 25 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:414.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1347  
ID ABR91363 standard; peptide; 25 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:197.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
RESULT 1348  
ID AAY70373 standard; peptide; 26 AA.  
DE Maize ZmKCSI peptide-4.  
PN WO200008172-A1.  
PD 17-FEB-2000.  
PA (AGRI-) AGRIC TECHNOLOGY & GENETICS GMBH.  
Query Match 6.5%; Score 5; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 1349  
ID ABR91364 standard; peptide; 26 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:198.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 1350  
ID ABR91365 standard; peptide; 26 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:199.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 1351  
ID ABR91362 standard; peptide; 26 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:196.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 1352  
ID ADM10549 standard; peptide; 26 AA.  
DE Nucleic acid-peptide library peptide sequence #11.  
PN WO2003089454-A2.  
PD 30-OCT-2003.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 6.5%; Score 5; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 1353  
ID ADI19974 standard; peptide; 26 AA.  
DE Bovine lactalbumin peptide #3.  
PN US2003219838-A1.

PD 27-NOV-2003.  
PA (JOHN/) JOHNSON R S.  
Query Match 6.5%; Score 5; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 1354  
ID AAM33910 standard; peptide; 27 AA.  
DE Fragment from LITMUS 39 based plasmid pLit.GFP-2A23H-CP.  
PN WO9739134-A1.  
PD 23-OCT-1997.  
PA (SCCR-) SCOTTISH CROP RES INST.  
Query Match 6.5%; Score 5; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1355  
ID AAM20101 standard; protein; 27 AA.  
DE Peptide #6535 encoded by probe for measuring cervical gene expression.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1356  
ID ABB40292 standard; peptide; 27 AA.  
DE Peptide #7798 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1357  
ID AAM33975 standard; protein; 27 AA.  
DE Peptide #8012 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1358  
ID ABB24700 standard; protein; 27 AA.  
DE Protein #6699 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1359  
ID AAM73788 standard; protein; 27 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34094.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1360  
ID AAM61085 standard; protein; 27 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33190.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1361  
ID ABG55535 standard; peptide; 27 AA.  
DE Human liver peptide, SEQ ID No 34183.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1362  
ID ABG43674 standard; peptide; 27 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33339.  
PN WO200186003-A2.  
PD 15-NOV-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 5; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1363  
ID ABR91366 standard; peptide; 27 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:200.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1364  
ID ADF28635 standard; peptide; 27 AA.  
DE Neural IgCAM-like protein transmembrane domain - SED ID 545.  
PN WO2003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 5; DB 7; Length 27;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
RESULT 1365  
ID ABG78097 standard; peptide; 28 AA.  
DE ITALY, LOR-2, STRIPE, TRASH, BUSF, LRSG and STMST-related peptide #45.  
PN US2002072089-A1.  
PD 13-JUN-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (MACE/) MACBETH K J.  
PA (BUSF/) BUSFIELD S J.  
PA (PANI/) PAN Y.  
PA (WHIT/) WHITE D.  
PA (KHOD/) KHODADOUST M M.  
PA (GUWV/) GU W.  
Query Match 6.5%; Score 5; DB 5; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 1366  
ID ADR45673 standard; peptide; 28 AA.  
DE Human G protein-coupled receptor IL-8RA, transmembrane domain 2.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.5%; Score 5; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 1367  
ID AAR60524 standard; protein; 29 AA.  
DE Secretion sequence.  
PN EP614982-A1.  
PD 14-SEP-1994.  
PA (ENTIE ) ENIRICERCH SPA.  
Query Match 6.5%; Score 5; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1368  
ID AAN94837 standard; peptide; 29 AA.  
DE WO9856926 Seq ID 3.  
PN WO9856926-A1.  
PD 17-DEC-1998.  
PA (TAKI ) TAKARA SHUZO CO LTD.  
Query Match 6.5%; Score 5; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1369  
ID ADB25860 standard; peptide; 29 AA.  
DE Dimeric coiled-coil peptide dCoil-adLH29.  
PN US2002119572-A1.  
PD 29-AUG-2002.  
PA (JACO/) JACOBSON J M.  
PA (SCHW/) SCHWARTZ J J.  
PA (HAWA/) HAWAD K.  
PA (ZHAN/) ZHANG S.  
Query Match 6.5%; Score 5; DB 6; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1370  
ID ABM74029 standard; protein; 29 AA.  
DE DNA clone originating in barley containing SNP sequence #439.  
PN WO2003057877-A1.

PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Query Match 6.5%; Score 5; DB 7; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1371  
ID AAY64891 standard; protein; 30 AA.  
DE Human 5' EST related polypeptide SEQ ID NO:1052.  
PN WO9953051-A2.  
PD 21-OCT-1999.  
PA (GEST ) GENSET.  
Query Match 6.5%; Score 5; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1372  
ID AAU84616 standard; peptide; 30 AA.  
DE HCV HepC1a segment 19.  
PN WO200190197-A1.  
PD 29-NOV-2001.  
PA (AUSU ) UNIV AUSTRALIAN NAT.  
Query Match 6.5%; Score 5; DB 5; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1373  
ID AAU84615 standard; peptide; 30 AA.  
DE HCV HepC1a segment 18.  
PN WO200190197-A1.  
PD 29-NOV-2001.  
PA (AUSU ) UNIV AUSTRALIAN NAT.  
Query Match 6.5%; Score 5; DB 5; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1374  
ID ABR91368 standard; peptide; 30 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:202.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1375  
ID ADH39846 standard; peptide; 30 AA.  
DE Subtilisin E signal peptide.  
PN US2003215906-A1.  
PD 20-NOV-2003.  
PA (LIMB/) LIM B L.  
Query Match 6.5%; Score 5; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1376  
ID AAM24746 standard; peptide; 31 AA.  
DE Heel domain of OP-2.  
PN WO9640771-A1.  
PD 19-DEC-1996.  
PA (CREA-) CREATIVE BIOMOLECULES INC.  
Query Match 6.5%; Score 5; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1377  
ID AAY02266 standard; protein; 31 AA.  
DE A F-box protein sequence.  
PN WO9918989-A1.  
PD 22-APR-1999.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 6.5%; Score 5; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1378  
ID AAM19230 standard; protein; 31 AA.  
DE Peptide #5664 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1379  
ID AAE08038 standard; peptide; 31 AA.  
DE Mouse F-box protein, F13.  
PN US6232081-B1.  
PD 15-MAY-2001.

PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1380  
ID ABB38458 standard; peptide; 31 AA.  
DE Peptide #5964 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1381  
ID AAM31899 standard; protein; 31 AA.  
DE Peptide #5936 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1382  
ID ABB23622 standard; protein; 31 AA.  
DE Protein #5621 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1383  
ID AAM71602 standard; protein; 31 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31908.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1384  
ID AAM5069 standard; protein; 31 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31174.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1385  
ID AAG53284 standard; peptide; 31 AA.  
DE Human liver peptide, SEQ ID No 31932.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1386  
ID ABG41414 standard; peptide; 31 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31079.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 5; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1387  
ID AAE39646 standard; peptide; 31 AA.  
DE Mouse F-box protein, F13 (omicron).  
PN US6573094-B1.  
PD 03-JUN-2003.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 6.5%; Score 5; DB 7; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1388  
ID ADR68965 standard; peptide; 31 AA.  
DE Mouse F13 (omicron) F-box domain peptide.  
PN US2004166530-A1.  
PD 26-AUG-2004.  
PA (HARP/) HARPER J W.

PA (ELLE/) ELLEDGE S J.  
Query Match 6.5%; Score 5; DB 8; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1389  
ID AAR57991 standard; protein; 32 AA.  
DE B.licheniformis alpha-amylase signal sequence in pBlapr.  
PN WO9418314-A1.  
PD 18-AUG-1994.  
PA (GEMV ) GENENCOR INT INC.  
Query Match 6.5%; Score 5; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1390  
ID AAR85822 standard; peptide; 32 AA.  
DE Peptide xi from the WD-40 domain-contg. YCW2 protein.  
PN WO9521252-A2.  
PD 10-AUG-1995.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Query Match 6.5%; Score 5; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1391  
ID AAW88722 standard; protein; 32 AA.  
DE Secretd protein encoded by gene 189 clone HHSAX25.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1392  
ID ABB50489 standard; protein; 32 AA.  
DE Human secreted protein encoded by gene 189 SEQ ID NO:437.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1393  
ID ABB50714 standard; protein; 32 AA.  
DE Human secreted protein encoded by gene 55 SEQ ID NO:665.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1394  
ID AAG80082 standard; peptide; 32 AA.  
DE Chemokine CCR3 extracellular loop domain #1.  
PN WO200172830-A2.  
PD 04-OCT-2001.  
PA (IPPF-) IPF PHARM GMBH.  
Query Match 6.5%; Score 5; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1395  
ID AAO13527 standard; protein; 32 AA.  
DE Human polypeptide SEQ ID NO 27419.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 5; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1396  
ID AAG65885 standard; protein; 32 AA.  
DE B. licheniformis alpha-amylase fragment.  
PN US6297037-B1.  
PD 02-OCT-2001.  
PA (BARN/) BARNETT C C.  
PA (MITC/) MITCHINSON C.  
PA (POWE/) POWER S D.  
PA (REQU/) REQUADT C A.  
Query Match 6.5%; Score 5; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1397

ID ABO44971 standard; protein; 32 AA.  
DE Novel human secreted protein #55 fragment #2.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1398  
ID ABO44746 standard; protein; 32 AA.  
DE Novel human secreted protein #189.  
PN US2003085160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1399  
ID ABO26226 standard; protein; 32 AA.  
DE Human protein from novel secreted protein gene 189.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 7; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1400  
ID ABO26451 standard; protein; 32 AA.  
DE Protein associated with novel secreted protein gene 55 #2.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 7; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1401  
ID ADF90370 standard; peptide; 32 AA.  
DE ICAM-2 transmembrane domain.  
PN US2003190684-A1.  
PD 09-OCT-2003.  
PA (FISH/) FISHER J.  
PA (LORE/) LORENS J.  
PA (PAYA/) PAVAN D.  
PA (ROSS/) ROSSI A.  
Query Match 6.5%; Score 5; DB 7; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1402  
ID ABO54160 standard; protein; 32 AA.  
DE Human genome derived single exon protein #394.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 6.5%; Score 5; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1403  
ID AAR57989 standard; protein; 33 AA.  
DE B.subtilis alkaline protease aprE signal sequence-mature protein.  
PN WO9418314-A1.  
PD 18-AUG-1994.  
PA (GEMV) GENENCOR INT INC.  
Query Match 6.5%; Score 5; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1404  
ID AAY49759 standard; peptide; 33 AA.  
DE Compact structure forming exemplification peptide #52.  
PN WO9951625-A2.  
PD 14-OCT-1999.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.5%; Score 5; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1405  
ID AAY3819 standard; peptide; 33 AA.  
DE Transmembrane domain of ICAM-2.  
PN WO9954494-A2.  
PD 28-OCT-1999.

PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.5%; Score 5; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1406  
ID AAB44770 standard; protein; 33 AA.  
DE Human secreted protein sequence encoded by gene 9 SEQ ID NO:69.  
PN WO200058336-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1407  
ID AAY88075 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane region peptide fragment.  
PN WO200023463-A2.  
PD 27-APR-2000.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 6.5%; Score 5; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1408  
ID AAM19101 standard; protein; 33 AA.  
DE Peptide #5535 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1409  
ID AAB35066 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain.  
PN WO200072008-A2.  
PD 30-NOV-2000.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1410  
ID AAB45934 standard; peptide; 33 AA.  
DE Transdominant effector peptide associated screening peptide #14.  
PN US6153380-A.  
PD 28-NOV-2000.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1411  
ID AAB35094 standard; peptide; 33 AA.  
DE Filamentous phage protein display related sequence #1.  
PN WO200071694-A1.  
PD 30-NOV-2000.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1412  
ID ABB38307 standard; peptide; 33 AA.  
DE Peptide #5813 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1413  
ID AAM31744 standard; protein; 33 AA.  
DE Peptide #5781 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1414  
ID ABG99131 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain.  
PN WO200166565-A2.  
PD 13-SEP-2001.

PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1415  
ID ABB23485 standard; protein; 33 AA.  
DE Protein #5484 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1416  
ID AAM71451 standard; protein; 33 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31757.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1417  
ID AAM58927 standard; protein; 33 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31032.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1418  
ID ABG53146 standard; peptide; 33 AA.  
DE Human liver peptide, SEQ ID No 31794.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1419  
ID AAG5883 standard; protein; 33 AA.  
DE B. subtilis alkaline protease aprE fragment.  
PN US6297037-B1.  
PD 02-OCT-2001.  
PA (BARN/) BARNETT C C.  
PA (MITC/) MITCHINSON C.  
PA (POWE/) POWER S D.  
PA (REQU/) REQUAD C A.  
Query Match 6.5%; Score 5; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1420  
ID ABG41255 standard; peptide; 33 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 30920.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1421  
ID ABB07745 standard; peptide; 33 AA.  
DE Transmembrane domain of ICAM-2 protein (residues 224-256).  
PN WO200210417-A2.  
PD 07-FEB-2002.  
PA (XENC-) XENCOR INC.  
Query Match 6.5%; Score 5; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1422  
ID AAU76172 standard; protein; 33 AA.  
DE Intercellular adhesion molecule-2 transmembrane anchoring sequence.  
PN US2002001830-A1.  
PD 03-JAN-2002.  
PA (LUOY/) LUO Y.  
PA (YUPW/) YU P W.  
PA (LORE/) LORENS J.  
Query Match 6.5%; Score 5; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1423

ID AAE28677 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain.  
PN WO200268453-A2.  
PD 06-SEP-2002.  
PA (XENC-) XENCOR INC.  
Query Match 6.5%; Score 5; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1424  
ID ABG92957 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain sequence peptide.  
PN WO200262822-A2.  
PD 15-AUG-2002.  
PA (UYRP) UNIV ROCHESTER.  
Query Match 6.5%; Score 5; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1425  
ID ABG98455 standard; peptide; 33 AA.  
DE Transmembrane domain for use in controlling signal pathways #2.  
PN US2002127564-A1.  
PD 12-SEP-2002.  
PA (NOLA/) NOLAN G P.  
Query Match 6.5%; Score 5; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1426  
ID ABU64892 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain.  
PN US2002172968-A1.  
PD 21-NOV-2002.  
PA (LIUH/) LIU H.  
PA (DAHI/) DAHIYAT B I.  
PA (LIHM/) LI M.  
Query Match 6.5%; Score 5; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1427  
ID ABU64787 standard; peptide; 33 AA.  
DE Human ICAM-2 membrane anchor peptide, #2.  
PN US2002186640-A1.  
PD 14-NOV-2002.  
PA (LIHM/) LI M.  
PA (DAHI/) DAHIYAT B I.  
Query Match 6.5%; Score 5; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1428  
ID ABP56553 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain SEQ ID NO:19.  
PN WO200286096-A2.  
PD 31-OCT-2002.  
PA (UYRP) UNIV ROCHESTER MEDICAL CENT.  
Query Match 6.5%; Score 5; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1429  
ID ABR39521 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain fragment (residues 224-256).  
PN WO2003017937-A2.  
PD 06-MAR-2003.  
PA (UYHA-) UNIV HAWAII.  
Query Match 6.5%; Score 5; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1430  
ID ABU14020 standard; peptide; 33 AA.  
DE ICAM-2 residues 224-256, transmembrane domain.  
PN US6455247-B1.  
PD 24-SEP-2002.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.5%; Score 5; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1431  
ID ABP72873 standard; peptide; 33 AA.  
DE Human ICAM-2 membrane anchoring signal sequence.  
PN WO2003020896-A2.  
PD 13-MAR-2003.  
PA (RIGE-) RIGEL PHARM INC.

Query Match  
Best Local Similarity 6.5%; Score 5; DB 6; Length 33;  
RESULT 1432  
ID AB09644 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain.  
PN US2003017601-A1.  
PD 23-JAN-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 6; Length 33;  
RESULT 1433  
ID AAE32695 standard; peptide; 33 AA.  
DE ICAM-2 targeting peptide #2.  
PN WO200286450-A2.  
PD 31-OCT-2002.  
PA (HARD) HARVARD COLLEGE.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 6; Length 33;  
RESULT 1434  
ID ADA07047 standard; peptide; 33 AA.  
DE ICAM-1 transmembrane domain peptide.  
PN WO200290535-A1.  
PD 14-NOV-2002.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 6; Length 33;  
RESULT 1435  
ID ADA0698 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain.  
PN US2003022196-A1.  
PD 30-JAN-2003.  
PA (LORE/) LORENS J.  
PA (KINS/) KINSELLA T M.  
PA (MASU/) MASUDA E.  
PA (HITO/) HITOSHI Y.  
PA (LIAO/) LIAO X C.  
PA (PEAR/) PEARSAI D.  
PA (FRIE/) FRIERA A.  
PA (CHUP/) CHU P.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1436  
ID ADA08288 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane anchoring signal.  
PN US6562617-B1.  
PD 13-MAY-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1437  
ID ADB66843 standard; peptide; 33 AA.  
DE Fusion nucleic acid retroviral vector associated peptide #13.  
PN US200309932-A1.  
PD 29-MAY-2003.  
PA (LORE/) LORENS J B.  
PA (FERE/) FERRICK D A.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1438  
ID AAE38941 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain.  
PN US6548249-B1.  
PD 15-APR-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1439  
ID AAE39825 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain peptide.  
PN US2003170641-A1.  
PD 11-SEP-2003.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1440  
ID ADD28901 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain.  
PN US2003104384-A1.  
PD 05-JUN-2003.  
PA (NOLA/) NOLAN G P.  
PA (ROTH/) ROTHENBERG S M.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1441  
ID ADE10737 standard; peptide; 33 AA.  
DE Structurally biased peptide library membrane anchoring sequence #4.  
PN US2003143562-A1.  
PD 31-JUL-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1442  
ID ADF32299 standard; peptide; 33 AA.  
DE ICAM-2 membrane anchoring peptide domain.  
PN US6548632-B1.  
PD 15-APR-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1443  
ID ADJ3812 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain.  
PN US2003211535-A1.  
PD 13-NOV-2003.  
PA (LORE/) LORENS J.  
PA (BOGE/) BOGENBERGER J M.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 33;  
RESULT 1444  
ID ADG14185 standard; peptide; 33 AA.  
DE Human BMP8/OP2 protein heel region.  
PN US2003185792-A1.  
PD 02-OCT-2003.  
PA (CURI-) CURIS INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 8; Length 33;  
RESULT 1445  
ID ADI36216 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane domain.  
PN US2003219723-A1.  
PD 27-NOV-2003.  
PA (LUHH/) LU H H.  
PA (HUAN/) HUANG P.  
PA (KINS/) KINSELLA T.  
PA (MART/) MARTINEZ A.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 8; Length 33;  
RESULT 1446  
ID ADK15756 standard; peptide; 33 AA.  
DE Fusion protein library-related human peptide #10.  
PN US2003224412-A1.  
PD 04-DEC-2003.  
PA (ANDE/) ANDERSON D.  
PA (PEEL/) PELLIE B R.  
PA (BOGE/) BOGENBERGER J M.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 8; Length 33;  
RESULT 1447  
ID ADM24749 standard; peptide; 33 AA.  
DE Human ICAM-2 transmembrane sequence.  
PN US2003211462-A1.  
PD 13-NOV-2003.  
PA (SHEN/) SHEN M.  
PA (YUSS/) YU S.  
PA (WUXX/) WU X.  
PA (PAYA/) PAYAN D.

Query Match  
Best Local Similarity 6.5%; Score 5; DB 8; Length 33;  
RESULT 1448  
ID ADL23786 standard; peptide; 33 AA.  
DE ICAM-2 transmembrane domain sequence.  
PN WO2004019890-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 8; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1449  
ID ADN41111 standard; protein; 33 AA.  
DE Novel human secreted protein seqid 233.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAPL/) LAPLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 8; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1450  
ID AAY02700 standard; protein; 34 AA.  
DE Human secreted protein encoded by gene 51 clone HUKEX85,  
PN WO902546-A1.  
PD 21-JAN-1999.  
PA (HWA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1451  
ID ABP66698 standard; protein; 34 AA.  
DE Human breast specific protein SEQ ID NO 200.  
PN WO200266605-A2.  
PD 29-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1452  
ID ADA07379 standard; protein; 34 AA.  
DE Human secreted protein from gene 51.  
PN US2003064412-A1.  
PD 03-APR-2003.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAPL/) LAPLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1453  
ID AAR57990 standard; protein; 35 AA.  
DE B.licheniformis alpha-amylase signal sequence in pA4BL.  
PN WO9418314-A1.  
PD 18-AUG-1994.  
PA (GEMV) GENENCOR INT INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1454  
ID AAW6863 standard; peptide; 35 AA.  
DE Nucleic acid binding domain from apoB-100, residues 2353-2387.  
PN WO9856938-A1.  
PD 17-DEC-1998.  
PA (BAYU) BAYLOR COLLEGE MEDICINE.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1455  
ID AAG65884 standard; protein; 35 AA.  
DE B.licheniformis alpha-amylase fragment.  
PN US6297037-B1.  
PD 02-OCT-2001.  
PA (BARN/) BARNETT C C.  
PA (MITC/) MITCHINSON C.  
PA (POME/) POWER S D.  
PA (REQU/) REQUADT C A.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1456  
ID ABP77794 standard; protein; 35 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 2118.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1457  
ID ABP68409 standard; protein; 36 AA.  
DE Human colon specific protein, SEQ ID 150.  
PN WO200277234-A2.  
PD 03-OCT-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1458  
ID AAW93461 standard; peptide; 37 AA.  
DE Human hCG beta-subunit peptide structure XVia.  
PN US5891992-A.  
PD 06-APR-1999.  
PA (OHIS) UNIV OHIO STATE RES FOUND.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1459  
ID AAY87497 standard; peptide; 37 AA.  
DE Human chorionic gonadotropin beta subunit-derived peptide XVia.  
PN US6039948-A.  
PD 21-MAR-2000.  
PA (OHIS) UNIV OHIO STATE.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1460  
ID AAB20566 standard; protein; 37 AA.  
DE Human chorionic gonadotropin beta subunit derived polypeptide (XVIA).  
PN US6096318-A.  
PD 01-AUG-2000.  
PA (OHIS) UNIV OHIO STATE.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1461  
ID AAU21887 standard; protein; 37 AA.  
DE Human cardiovascular system antigen polypeptide SEQ ID No 661.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 6.5%; Score 5; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1462  
ID AAU01169 standard; peptide; 37 AA.  
DE Structure XVia, peptide used to produce modified HCG peptides.  
PN US6217881-B1.  
PD 17-APR-2001.

PA (OHIS ) UNIV OHIO STATE RES FOUND.  
Query Match 6.5%; Score 5; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1463  
ID AAB48403 standard; peptide; 37 AA.  
DE Human chorionic gonadotropin beta subunit structure XV1a.  
PN US6143305-A.  
PD 07-NOV-2000.  
PA (OHIS ) UNIV OHIO STATE.  
Query Match 6.5%; Score 5; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1464  
ID AAU02865 standard; protein; 37 AA.  
DE Human Chorionic Gonadotrophin (HCG) beta-subunit fragment #14.  
PN WO200124765-A2.  
PD 12-APR-2001.  
PA (OHIS ) UNIV OHIO STATE RES FOUND.  
Query Match 6.5%; Score 5; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1465  
ID AAB04141 standard; peptide; 37 AA.  
DE Peptide fragment of beta subunit of human chorionic gonadotropin.  
PN US6146633-A.  
PD 14-NOV-2000.  
PA (OHIS ) UNIV OHIO STATE.  
Query Match 6.5%; Score 5; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1466  
ID ADE45855 standard; protein; 37 AA.  
DE Human cardiovascular system related polypeptide #36.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1467  
ID ADJ07273 standard; peptide; 37 AA.  
DE Human cardiovascular system associated polypeptide SeqID661.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 8; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1468  
ID AAY12631 standard; protein; 39 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 296 from WO 9906553.  
PN WO9906553-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 6.5%; Score 5; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1469  
ID AAB52117 standard; protein; 39 AA.  
DE Human secreted protein encoded by cDNA #15.  
PN WO200061624-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1470  
ID AAU01783 standard; peptide; 39 AA.  
DE Human secreted protein #62.  
PN WO200123546-A1.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1471  
ID ABJ19737 standard; peptide; 39 AA.  
DE Human secreted protein amino acid sequence - SEQ ID No 205.  
PN WO200277188-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 6.5%; Score 5; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1472  
ID ABP99831 standard; protein; 39 AA.  
DE Human secreted protein SEQ ID NO 775.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1473  
ID ADC20554 standard; protein; 39 AA.  
DE Human secreted protein - amino acid sequence #235.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 7; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1474  
ID ABB15215 standard; protein; 41 AA.  
DE Human nervous system related polypeptide SEQ ID NO 3872.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1475  
ID ABP80379 standard; protein; 41 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 7288.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.5%; Score 5; DB 6; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1476  
ID AAW27841 standard; protein; 42 AA.  
DE Staphylococcus aureus protein of unknown function.  
PN WO9730070-A1.  
PD 21-AUG-1997.  
PA (SMIX ) SMITHKLINE BEECHAM CORP.  
Query Match 6.5%; Score 5; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1477  
ID AAY19539 standard; protein; 42 AA.  
DE Amino acid sequence of a human secreted protein.  
PN WO9822243-A1.  
PD 06-MAY-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1478  
ID AAM17255 standard; protein; 42 AA.  
DE Peptide #3689 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1479  
ID ABB36254 standard; peptide; 42 AA.  
DE Peptide #3760 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1480  
ID AAM29750 standard; protein; 42 AA.  
DE Peptide #3787 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1481  
ID ABB31065 standard; peptide; 42 AA.  
DE Peptide #3716 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1482  
ID AAM69421 standard; protein; 42 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29727.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1483  
ID AAM57029 standard; protein; 42 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29134.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1484  
ID AAG51093 standard; peptide; 42 AA.  
DE Human liver peptide, SEQ ID No 29741.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1485  
ID AAM04946 standard; protein; 42 AA.  
DE Peptide #3628 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1486  
ID AAG39039 standard; peptide; 42 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28704.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 5; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1487  
ID ABR91588 standard; peptide; 42 AA.  
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:422.  
PN WO2002102324-A2.  
PD 27-DEC-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 6.5%; Score 5; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1488  
ID ADN04586 standard; protein; 42 AA.  
DE Antipeptidic protein sequence #482.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.5%; Score 5; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1489  
ID ADO19898 standard; protein; 42 AA.  
DE Human PRO polypeptide #409.  
PN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.5%; Score 5; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1490  
ID ADP55022 standard; protein; 42 AA.  
DE Human PRO protein sequence SEQ ID NO:998.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.5%; Score 5; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1491  
ID ADP24559 standard; protein; 42 AA.  
DE PRO polypeptide SEQ ID NO:1737.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.5%; Score 5; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1492  
ID AAR28988 standard; protein; 43 AA.  
DE Thyroid N-acetyl-glucosamine receptor fragment TGR-CL11.  
PN WO9219733-A1.  
PD 12-NOV-1992.  
PA (CNRS ) CENT NAT RECH SCI.  
Query Match 6.5%; Score 5; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1493  
ID AAW88581 standard; protein; 43 AA.  
DE Secreted protein encoded by gene 48 clone HCNAP62.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1494  
ID AAM16809 standard; protein; 43 AA.  
DE Peptide #3243 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1495  
ID ABB50348 standard; protein; 43 AA.  
DE Human secreted protein encoded by gene 48 SEQ ID NO:296.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1496  
ID ABB35792 standard; peptide; 43 AA.  
DE Peptide #3298 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1497  
ID AAM29291 standard; protein; 43 AA.  
DE Peptide #3328 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1498  
ID ABB1187 standard; peptide; 43 AA.  
DE Human pheromone receptor VIRL1 homologue, SEQ ID NO:1557.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1499

ID ABB30627 standard; peptide; 43 AA.  
DE Peptide #3278 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1500  
ID ABB21214 standard; protein; 43 AA.  
DE Protein #3213 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 6.5%; Score 5; DB 4; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2005, 04:04:42 ; Search time 41 Seconds  
(without alignments)  
140.195 Million cell updates/sec

Title: US-10-063-563-56

Perfect score: 77

Sequence: 1 MGVKQLKRMFEPTRIAT.....LSFIPFARDAVKCFACVLA 77

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	10.4	441	4	US-09-489-039A-10091
2	7	9.1	168	4	US-09-270-767-32997
3	7	9.1	168	4	US-09-270-767-48214
4	7	9.1	172	4	US-09-270-767-36922
5	7	9.1	172	4	US-09-270-767-52139
6	7	9.1	199	4	US-09-489-039A-10661
7	7	9.1	220	4	US-09-198-452A-461
8	7	9.1	220	4	US-09-438-185A-442
9	6	7.8	27	3	US-08-470-953A-9
10	6	7.8	42	4	US-09-270-767-56935
11	6	7.8	74	4	US-09-270-767-34586
12	6	7.8	74	4	US-09-270-767-49803
13	6	7.8	78	4	US-09-248-796A-24206
14	6	7.8	78	4	US-09-248-796A-26253
15	6	7.8	91	4	US-09-270-767-41301
16	6	7.8	91	4	US-09-270-767-56517
17	6	7.8	96	4	US-09-107-433-4292
18	6	7.8	112	4	US-09-107-532A-5370
19	6	7.8	120	4	US-09-489-039A-7830
20	6	7.8	123	4	US-09-489-039A-11581
21	6	7.8	124	1	US-08-462-949-28
22	6	7.8	124	1	US-08-023-764B-28
23	6	7.8	124	3	US-08-904-871-10
24	6	7.8	125	1	US-08-225-989-20
25	6	7.8	125	1	US-08-570-923-20
26	6	7.8	125	1	US-08-580-014-20
27	6	7.8	125	3	US-09-079-785-20

28	6	7.8	125	4	US-09-628-126-20	Sequence 20, Appl
29	6	7.8	128	4	US-09-107-532A-6997	Sequence 6997, Ap
30	6	7.8	128	4	US-09-543-681A-4686	Sequence 4686, Ap
31	6	7.8	130	4	US-09-248-796A-25706	Sequence 25706, A
32	6	7.8	137	4	US-09-248-796A-15191	Sequence 15191, A
33	6	7.8	160	3	US-09-134-001C-4327	Sequence 4327, Ap
34	6	7.8	167	4	US-09-205-258-867	Sequence 867, App
35	6	7.8	171	4	US-09-252-991A-20773	Sequence 20773, A
36	6	7.8	184	4	US-09-902-540-12024	Sequence 12024, A
37	6	7.8	185	4	US-09-328-352-5973	Sequence 5973, Ap
38	6	7.8	196	4	US-09-270-767-38699	Sequence 38699, A
39	6	7.8	196	4	US-09-270-767-53916	Sequence 53916, A
40	6	7.8	212	4	US-09-543-681A-7460	Sequence 7460, Ap
41	6	7.8	215	1	US-08-225-989-23	Sequence 23, Appl
42	6	7.8	215	1	US-08-570-923-23	Sequence 23, Appl
43	6	7.8	215	1	US-08-580-014-23	Sequence 23, Appl
44	6	7.8	215	3	US-09-079-785-23	Sequence 23, Appl
45	6	7.8	215	4	US-09-628-126-23	Sequence 23, Appl
46	6	7.8	224	4	US-09-540-236-2707	Sequence 2707, Ap
47	6	7.8	230	4	US-09-248-796A-18348	Sequence 18348, A
48	6	7.8	231	4	US-09-328-352-4885	Sequence 4885, Ap
49	6	7.8	234	1	US-08-225-989-8	Sequence 8, Appli
50	6	7.8	234	1	US-08-570-923-8	Sequence 8, Appli
51	6	7.8	234	1	US-08-580-014-8	Sequence 8, Appli
52	6	7.8	234	3	US-09-079-785-8	Sequence 8, Appli
53	6	7.8	234	4	US-09-134-000C-5603	Sequence 5603, Ap
54	6	7.8	234	4	US-09-921-667-2	Sequence 2, Appli
55	6	7.8	234	4	US-09-628-126-8	Sequence 8, Appli
56	6	7.8	246	4	US-09-933-999A-7	Sequence 7, Appli
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173	5	6.5	12	6	5489533-15	Patent No. 5489533	246	5	6.5	33	4	US-09-495-880A-38	Sequence 38, App1

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290	5	6.5	60	4	US-09-621-976-5232	Sequence 5232, App	363	5	6.5	84	4	US-09-270-767-51969	Sequence 51969, A
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292	5	6.5	62	4	US-09-328-352-4341	Sequence 4341, Ap	365	5	6.5	85	4	US-09-621-976-5566	Sequence 5566, Ap
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294	5	6.5	63	4	US-09-270-767-53963	Sequence 53963, A	367	5	6.5	86	3	US-08-894-173-52	Sequence 52, Appl
295	5	6.5	64	4	US-09-489-039A-12018	Sequence 12018, A	368	5	6.5	86	3	US-09-398-193-52	Sequence 53, Appl
296	5	6.5	65	4	US-09-107-532A-4450	Sequence 4450, Ap	369	5	6.5	86	3	US-09-398-193-53	Sequence 53, Appl
297	5	6.5	65	4	US-09-513-999C-4409	Sequence 4409, Ap	370	5	6.5	86	4	US-09-205-258-1033	Sequence 1033, Ap
298	5	6.5	65	4	US-09-513-999C-4415	Sequence 4415, Ap	371	5	6.5	87	3	US-09-227-357-544	Sequence 544, App
299	5	6.5	66	4	US-09-205-258-381	Sequence 381, App	372	5	6.5	88	3	US-09-415-784-116	Sequence 116, App
300	5	6.5	67	4	US-09-248-796A-27201	Sequence 27201, A	373	5	6.5	88	4	US-09-415-785A-116	Sequence 116, App
301	5	6.5	67	4	US-09-513-999C-4575	Sequence 4575, Ap	374	5	6.5	88	4	US-08-944-465-116	Sequence 116, App
302	5	6.5	67	4	US-09-513-999C-5550	Sequence 5550, Ap	375	5	6.5	88	4	US-09-415-868-116	Sequence 116, App
303	5	6.5	68	4	US-09-270-767-34897	Sequence 34897, A	376	5	6.5	88	4	US-09-415-900-116	Sequence 116, App
304	5	6.5	68	4	US-09-270-767-50114	Sequence 50114, A	377	5	6.5	88	4	US-09-507-362-116	Sequence 116, App
305	5	6.5	68	4	US-09-270-767-59156	Sequence 59156, A	378	5	6.5	88	4	US-09-270-767-36403	Sequence 36403, A
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311	5	6.5	70	4	US-09-621-976-5489	Sequence 5489, Ap	384	5	6.5	90	3	US-08-444-818-87	Sequence 87, Appl
312	5	6.5	70	4	US-09-248-796A-24653	Sequence 24653, A	385	5	6.5	91	4	US-09-270-767-34625	Sequence 34625, A
313	5	6.5	70	4	US-09-774-639-162	Sequence 162, App	386	5	6.5	91	4	US-09-270-767-49842	Sequence 49842, A
314	5	6.5	71	4	US-09-252-991A-20047	Sequence 20047, A	387	5	6.5	92	4	US-09-328-352-6709	Sequence 6709, Ap
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316	5	6.5	71	4	US-09-248-796A-24708	Sequence 24708, A	389	5	6.5	93	4	US-09-134-000C-3436	Sequence 3436, Ap
317	5	6.5	71	4	US-09-107-433-4291	Sequence 4291, Ap	390	5	6.5	93	4	US-09-513-999C-7638	Sequence 7638, Ap
318	5	6.5	72	4	US-09-398-395A-37	Sequence 37, Appl	391	5	6.5	94	4	US-09-270-767-34084	Sequence 34084, A
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395	5	6.5	95	4	US-09-543-681A-8178	Sequence 8178, Ap	468	5	6.5	115	4	US-09-438-185A-161	Sequence 161, App
396	5	6.5	95	4	US-09-489-039A-9727	Sequence 9727, Ap	469	5	6.5	115	4	US-09-893-737-128	Sequence 128, App
397	5	6.5	96	4	US-09-902-540-11645	Sequence 11645, A	470	5	6.5	117	4	US-09-252-991A-16755	Sequence 16755, A
398	5	6.5	97	4	US-09-134-000C-3928	Sequence 3928, Ap	471	5	6.5	118	4	US-09-198-452A-477	Sequence 477, App
399	5	6.5	97	4	US-09-248-796A-21269	Sequence 21269, A	472	5	6.5	118	4	US-09-107-532A-7102	Sequence 7102, Ap
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401	5	6.5	98	4	US-09-583-110-3578	Sequence 3578, Ap	474	5	6.5	119	3	US-08-936-165A-311	Sequence 311, App
402	5	6.5	98	4	US-09-107-433-4198	Sequence 4189, Ap	475	5	6.5	119	4	US-09-543-681A-9227	Sequence 8227, Ap
403	5	6.5	99	3	US-09-227-357-630	Sequence 630, App	476	5	6.5	120	4	US-09-252-991A-24161	Sequence 24161, A
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412	5	6.5	102	3	US-08-479-744A-47	Sequence 47, Appl	485	5	6.5	125	1	US-08-474-087-10	Sequence 10, Appl
413	5	6.5	102	3	US-08-280-757B-47	Sequence 47, Appl	486	5	6.5	125	4	US-09-690-454-155	Sequence 155, App
414	5	6.5	102	3	US-08-931-858B-162	Sequence 162, App	487	5	6.5	125	4	US-09-328-352-5320	Sequence 5320, Ap
415	5	6.5	102	3	US-08-981-739-162	Sequence 162, App	488	5	6.5	125	4	US-09-328-352-5491	Sequence 5491, Ap
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419	5	6.5	102	4	US-09-220-616-162	Sequence 162, App	492	5	6.5	126	4	US-09-902-540-12158	Sequence 12158, A
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422	5	6.5	102	4	US-09-220-527-162	Sequence 162, App	495	5	6.5	127	4	US-09-621-976-6400	Sequence 6400, Ap
423	5	6.5	102	4	US-09-220-407-162	Sequence 162, App	496	5	6.5	127	4	US-09-270-767-61197	Sequence 61197, A
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425	5	6.5	102	4	US-09-425-516-47	Sequence 47, Appl	498	5	6.5	128	4	US-08-974-690C-238	Sequence 238, App
426	5	6.5	103	4	US-09-615-192A-398	Sequence 398, App	499	5	6.5	129	3	US-09-476-482-8	Sequence 8, Appl1
427	5	6.5	104	4	US-09-248-796A-24884	Sequence 24884, A	500	5	6.5	129	3	US-09-534-638-5	Sequence 5, Appl1
428	5	6.5	104	4	US-09-107-433-2674	Sequence 2674, Ap	501	5	6.5	129	3	US-09-732-210-143	Sequence 143, App
429	5	6.5	105	3	US-08-936-165A-467	Sequence 467, App	502	5	6.5	129	4	US-09-248-796A-20661	Sequence 20661, A
430	5	6.5	105	3	US-08-820-825-14	Sequence 14, Appl	503	5	6.5	130	4	US-09-270-767-59805	Sequence 59805, A
431	5	6.5	106	3	US-08-444-818-85	Sequence 85, Appl	504	5	6.5	130	4	US-09-248-796A-28096	Sequence 28096, A
432	5	6.5	106	3	US-09-307-817-14	Sequence 14, Appl	505	5	6.5	130	4	US-09-621-976-4177	Sequence 4177, Ap
433	5	6.5	106	4	US-09-734-036-14	Sequence 14, Appl	506	5	6.5	131	4	US-09-489-039A-10399	Sequence 10399, A
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436	5	6.5	106	4	US-09-270-767-41175	Sequence 41175, A	509	5	6.5	133	4	US-09-270-767-47817	Sequence 47817, A
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440	5	6.5	107	1	US-08-409-731A-2	Sequence 2, Appl1	513	5	6.5	134	3	US-08-793-381A-2	Sequence 2, Appl1
441	5	6.5	107	2	US-09-470-298B-2	Sequence 2, Appl1	514	5	6.5	134	4	US-09-513-999C-7854	Sequence 7854, Ap
442	5	6.5	107	2	US-09-023-073A-2	Sequence 2, Appl1	515	5	6.5	135	2	US-08-820-825-2	Sequence 2, Appl1
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444	5	6.5	107	4	US-08-728-742A-9	Sequence 9, Appl1	517	5	6.5	135	3	US-09-307-817-2	Sequence 2, Appl1
445	5	6.5	107	4	US-09-621-976-5595	Sequence 5595, Ap	518	5	6.5	135	3	US-09-734-036-2	Sequence 2, Appl1
446	5	6.5	108	4	US-09-482-273-123	Sequence 123, App	519	5	6.5	135	4	US-09-732-210-410	Sequence 410, App
447	5	6.5	110	3	US-09-240-274-67	Sequence 67, Appl	520	5	6.5	135	4	US-09-355-040-15	Sequence 15, Appl
448	5	6.5	110	3	US-09-134-001C-3010	Sequence 3010, Ap	521	5	6.5	135	4	US-09-513-999C-6294	Sequence 6294, Ap
449	5	6.5	110	4	US-09-087-031B-22	Sequence 22, Appl	522	5	6.5	137	2	US-08-379-057-18	Sequence 18, Appl
450	5	6.5	110	4	US-09-198-452A-943	Sequence 943, App	523	5	6.5	137	4	US-09-096-731A-35	Sequence 35, Appl
451	5	6.5	110	4	US-09-621-976-5906	Sequence 5906, Ap	524	5	6.5	137	4	US-09-270-767-42606	Sequence 42606, A
452	5	6.5	111	4	US-09-585-174-4	Sequence 4, Appl1	525	5	6.5	137	1	US-08-278-729A-7	Sequence 7, Appl1
453	5	6.5	111	4	US-09-489-039A-14265	Sequence 14265, A	526	5	6.5	139	1	US-08-278-729A-8	Sequence 8, Appl1
454	5	6.5	111	4	US-09-270-767-57264	Sequence 57264, A	527	5	6.5	139	1	US-08-155-343A-7	Sequence 7, Appl1
455	5	6.5	112	1	US-07-800-364B-15	Sequence 15, Appl	528	5	6.5	139	1	US-08-155-343A-8	Sequence 8, Appl1
456	5	6.5	112	2	US-08-678-194-6	Sequence 6, Appl1	529	5	6.5	139	1	US-08-406-672-7	Sequence 7, Appl1
457	5	6.5	112	3	US-08-890-011-6	Sequence 6, Appl1	530	5	6.5	139	1	US-08-406-672-8	Sequence 8, Appl1
458	5	6.5	112	3	US-09-262-72A-6	Sequence 6, Appl1	531	5	6.5	139	1	US-08-643-563A-7	Sequence 7, Appl1
459	5	6.5	112	4	US-09-513-999C-7870	Sequence 7870, Ap	532	5	6.5	139	1	US-08-643-563A-8	Sequence 8, Appl1
460	5	6.5	112	5	PCT-US91-0338B-13	Sequence 13, Appl	533	5	6.5	139	1	US-08-643-763A-7	Sequence 7, Appl1
461	5	6.5	113	4	US-09-621-976-4026	Sequence 4026, Ap	534	5	6.5	139	1	US-08-643-763A-8	Sequence 8, Appl1
462	5	6.5	113	2	US-08-580-988A-25	Sequence 25, Appl	535	5	6.5	139	1	US-08-462-623-7	Sequence 7, Appl1
463	5	6.5	115	2	US-07-903-029-6	Sequence 6, Appl1	536	5	6.5	139	1	US-08-462-623-8	Sequence 8, Appl1
464	5	6.5	115	4	US-09-198-452A-179	Sequence 179, App	537	5	6.5	139	1	US-08-462-623A-7	Sequence 7, Appl1
465	5	6.5	115	4	US-09-270-767-36838	Sequence 36838, A	538	5	6.5	139	1	US-08-451-953A-7	Sequence 7, Appl1



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686	5	6.5	164	3	US-08-858-207A-333	Sequence 333, App	759	5	6.5	179	4	US-09-248-796A-28194	Sequence 28194, A
687	5	6.5	164	4	US-09-328-352-6590	Sequence 6590, App	760	5	6.5	180	2	US-08-467-603-68	Sequence 68, Appl
688	5	6.5	164	4	US-09-543-681A-4317	Sequence 4317, App	761	5	6.5	180	2	US-08-466-793-68	Sequence 68, Appl
689	5	6.5	164	4	US-09-583-110-4128	Sequence 4128, App	762	5	6.5	180	2	US-08-491-861A-68	Sequence 68, Appl
690	5	6.5	164	4	US-09-270-767-46414	Sequence 46414, A	763	5	6.5	180	4	US-09-374-671A-68	Sequence 68, Appl
691	5	6.5	164	4	US-09-107-433-4978	Sequence 4978, App	764	5	6.5	181	4	US-08-635-886C-182	Sequence 182, App
692	5	6.5	165	4	US-09-270-767-41191	Sequence 41191, A	765	5	6.5	181	4	US-08-974-690C-182	Sequence 182, App
693	5	6.5	165	4	US-09-270-767-56407	Sequence 56407, A	766	5	6.5	181	4	US-09-902-540-14787	Sequence 14787, A
694	5	6.5	165	4	US-09-107-433-5133	Sequence 5133, App	767	5	6.5	181	4	US-09-902-540-15650	Sequence 15650, A
695	5	6.5	166	2	US-08-483-695-3	Sequence 3, Appl	768	5	6.5	182	4	US-09-328-352-6036	Sequence 6036, App
696	5	6.5	166	2	US-08-483-695-31	Sequence 31, Appl	769	5	6.5	182	4	US-09-107-532A-6641	Sequence 6641, App
697	5	6.5	166	2	US-08-483-695-33	Sequence 33, Appl	770	5	6.5	182	4	US-09-780-717-44	Sequence 44, Appl
698	5	6.5	166	2	US-07-965-285-3	Sequence 3, Appl	771	5	6.5	183	4	US-09-107-532A-5935	Sequence 5935, App
699	5	6.5	166	2	US-07-965-285-31	Sequence 31, Appl	772	5	6.5	183	4	US-09-543-681A-5268	Sequence 5268, App
700	5	6.5	166	2	US-07-965-285-33	Sequence 33, Appl	773	5	6.5	183	4	US-09-540-236-3419	Sequence 3419, App
701	5	6.5	166	2	US-08-487-231-3	Sequence 3, Appl	774	5	6.5	183	4	US-09-270-767-32627	Sequence 32627, A
702	5	6.5	166	2	US-08-487-231-31	Sequence 31, Appl	775	5	6.5	183	4	US-09-270-767-47844	Sequence 47844, A
703	5	6.5	166	2	US-08-487-231-33	Sequence 33, Appl	776	5	6.5	184	1	US-08-088-633-6	Sequence 6, Appl
704	5	6.5	166	3	US-09-201-912-3	Sequence 3, Appl	777	5	6.5	184	1	US-08-245-756-6	Sequence 6, Appl
705	5	6.5	166	3	US-09-201-912-31	Sequence 31, Appl	778	5	6.5	184	1	US-08-441-750-6	Sequence 6, Appl
706	5	6.5	166	3	US-09-201-912-33	Sequence 33, Appl	779	5	6.5	184	2	US-08-441-751-6	Sequence 6, Appl
707	5	6.5	166	3	US-09-199-637A-245	Sequence 245, App	780	5	6.5	184	4	US-09-252-991A-22978	Sequence 22978, A
708	5	6.5	166	4	US-09-732-210-1606	Sequence 1606, App	781	5	6.5	184	5	US-09-134-000C-3412	Sequence 3412, App
709	5	6.5	166	4	US-09-513-999C-18067	Sequence 18067, App	782	5	6.5	184	5	PCT-US92-02521-6	Sequence 6, Appl
710	5	6.5	167	4	US-09-318-786-31	Sequence 31, Appl	783	5	6.5	185	1	US-07-676-647-9	Sequence 9, Appl
711	5	6.5	167	4	US-09-134-000C-6787	Sequence 6787, App	784	5	6.5	185	1	US-08-449-329-9	Sequence 9, Appl
712	5	6.5	168	3	US-08-669-408B-4	Sequence 4, Appl	785	5	6.5	185	2	US-08-445-073-9	Sequence 9, Appl
713	5	6.5	168	3	US-08-858-207A-486	Sequence 486, App	786	5	6.5	185	2	US-08-585-258-9	Sequence 9, Appl
714	5	6.5	168	3	US-09-380-882-2	Sequence 2, Appl	787	5	6.5	185	3	US-09-211-590-9	Sequence 9, Appl
715	5	6.5	168	4	US-09-380-882-3	Sequence 3, Appl	788	5	6.5	185	4	US-09-270-767-45303	Sequence 45303, A
716	5	6.5	168	4	US-09-673-395A-159	Sequence 159, App	789	5	6.5	185	4	US-09-902-540-11070	Sequence 11070, A
717	5	6.5	168	4	US-09-270-767-41903	Sequence 41903, A	790	5	6.5	185	5	PCT-US91-03896-9	Sequence 9, Appl
718	5	6.5	169	4	US-08-635-886C-242	Sequence 242, App	791	5	6.5	186	4	US-09-252-991A-26353	Sequence 26353, A
719	5	6.5	169	4	US-08-974-690C-242	Sequence 242, App	792	5	6.5	186	4	US-09-710-279-2530	Sequence 2530, App
720	5	6.5	169	4	US-09-540-236-2468	Sequence 2468, App	793	5	6.5	186	4	US-09-438-185A-16	Sequence 16, Appl
721	5	6.5	169	4	US-09-248-796A-22546	Sequence 22546, A	794	5	6.5	187	4	US-09-328-352-5927	Sequence 5927, App
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727	5	6.5	172	4	US-09-489-039A-12818	Sequence 12818, A	800	5	6.5	190	4	US-09-328-352-6255	Sequence 6255, App
728	5	6.5	172	5	PCT-US94-07280-5	Sequence 5, Appl	801	5	6.5	190	4	US-09-583-110-3050	Sequence 3050, App
729	5	6.5	172	5	PCT-US95-01087-5	Sequence 5, Appl	802	5	6.5	191	3	US-09-134-001C-5345	Sequence 5345, App
730	5	6.5	173	4	US-09-270-767-38634	Sequence 38634, A	803	5	6.5	191	4	US-09-252-991A-32734	Sequence 32734, A
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732	5	6.5	173	4	US-09-710-279-2436	Sequence 2436, App	805	5	6.5	191	4	US-08-635-886C-185	Sequence 185, App
733	5	6.5	175	4	US-09-270-767-38377	Sequence 38377, A	806	5	6.5	191	4	US-09-489-039A-11356	Sequence 11356, A
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735	5	6.5	175	4	US-09-902-540-14268	Sequence 14268, A	808	5	6.5	191	4	US-08-974-690C-185	Sequence 185, App
736	5	6.5	176	4	US-09-107-532A-4940	Sequence 4940, App	809	5	6.5	191	4	US-09-248-796A-20091	Sequence 20091, A
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738	5	6.5	177	2	US-08-466-793-70	Sequence 70, Appl	811	5	6.5	192	1	US-08-086-428B-53	Sequence 53, Appl
739	5	6.5	177	2	US-08-491-861A-70	Sequence 70, Appl	812	5	6.5	192	1	US-08-086-428B-54	Sequence 54, Appl
740	5	6.5	177	4	US-08-671-548C-8	Sequence 8, Appl	813	5	6.5	192	1	US-08-086-428B-55	Sequence 55, Appl
741	5	6.5	177	4	US-09-374-671A-70	Sequence 70, Appl	814	5	6.5	192	1	US-08-086-428B-56	Sequence 56, Appl
742	5	6.5	177	4	US-09-198-452A-28	Sequence 28, Appl	815	5	6.5	192	1	US-08-086-428B-57	Sequence 57, Appl
743	5	6.5	177	4	US-09-248-796A-14725	Sequence 14725, A	816	5	6.5	192	1	US-08-086-428B-58	Sequence 58, Appl
744	5	6.5	178	1	US-08-625-891-1	Sequence 1, Appl	817	5	6.5	192	1	US-08-086-428B-59	Sequence 59, Appl
745	5	6.5	178	4	US-09-328-352-5842	Sequence 5842, App	818	5	6.5	192	1	US-08-086-428B-77	Sequence 77, Appl
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747	5	6.5	178	4	US-09-809-665A-12	Sequence 12, Appl	820	5	6.5	192	1	US-08-086-428B-79	Sequence 79, Appl
748	5	6.5	179	1	US-08-193-577-6	Sequence 6, Appl	821	5	6.5	192	1	US-08-086-428B-80	Sequence 80, Appl
749	5	6.5	179	2	US-08-467-603-72	Sequence 72, Appl	822	5	6.5	192	1	US-08-086-428B-89	Sequence 89, Appl
750	5	6.5	179	2	US-08-466-793-72	Sequence 72, Appl	823	5	6.5	192	1	US-08-086-428B-90	Sequence 90, Appl
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752	5	6.5	179	3	US-08-867-381A-52	Sequence 52, Appl	825	5	6.5	192	1	US-08-086-428B-95	Sequence 95, Appl
753	5	6.5	179	3	US-09-521-144-52	Sequence 52, Appl	826	5	6.5	192	1	US-08-440-103-37	Sequence 37, Appl
754	5	6.5	179	4	US-09-615-192A-376	Sequence 376, App	827	5	6.5	192	1	US-08-440-103-38	Sequence 38, Appl
755	5	6.5	179	4	US-09-374-671A-72	Sequence 72, Appl	828	5	6.5	192	1	US-08-440-103-40	Sequence 40, Appl
756	5	6.5	179	4	US-09-134-000C-5806	Sequence 5806, App	829	5	6.5	192	1	US-08-440-103-41	Sequence 41, Appl
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991	5	6.5	211	4	US-09-270-767-34278	Sequence 34278, A	1064	5	6.5	239	4	US-09-711-164-367	Sequence 367, App
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1013	5	6.5	219	2	US-08-855-140-4	Sequence 4, Appl	1086	5	6.5	246	4	US-10-047-676E-14	Sequence 14, Appl
1014	5	6.5	219	2	US-08-807-044-3	Sequence 3, Appl	1087	5	6.5	247	3	US-08-501-126-19	Sequence 19, Appl
1015	5	6.5	219	3	US-09-162-184-32	Sequence 32, Appl	1088	5	6.5	247	4	US-09-583-110-4595	Sequence 4595, Ap
1016	5	6.5	219	3	US-09-489-777A-32	Sequence 32, Appl	1089	5	6.5	248	4	US-09-914-259-42	Sequence 42, Appl
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1032	5	6.5	226	4	US-09-367-891A-2	Sequence 2, Appl	1105	5	6.5	253	3	US-09-240-915-7	Sequence 7, Appl
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1034	5	6.5	227	3	US-09-092-160-4	Sequence 4, Appl	1107	5	6.5	254	4	US-09-328-352-7193	Sequence 7193, Ap
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1038	5	6.5	228	4	US-08-976-063B-14	Sequence 14, Appl	1111	5	6.5	256	3	US-09-150-864A-6	Sequence 6, Appl
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1126	5	6.5	259	4	US-09-328-352-8034	Sequence 8034, Ap	1199	5	6.5	275	4	US-09-291-417D-87	Sequence 87, Appl
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1128	5	6.5	259	4	US-09-538-092-269	Sequence 269, App	1201	5	6.5	276	4	US-09-205-258-1027	Sequence 1027, Ap
1129	5	6.5	259	4	US-09-809-545A-26	Sequence 26, Appl	1202	5	6.5	276	4	US-09-134-000C-5919	Sequence 5919, Ap
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1139	5	6.5	262	3	US-08-889-425-2	Sequence 2, Appl1	1212	5	6.5	279	2	US-08-326-286-7	Sequence 7, Appl1
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1421	5	6.5	323	4	US-09-651-200-21	Sequence 21, Appl	1494	5	6.5	340	4	US-10-067-443-6	Sequence 6, Appli
1422	5	6.5	323	4	US-09-328-352-6181	Sequence 6181, Ap	1495	5	6.5	340	4	US-09-270-767-46274	Sequence 46274, A
1423	5	6.5	323	4	US-09-441-411-22	Sequence 22, Appl	1496	5	6.5	340	4	US-09-248-796A-14915	Sequence 14915, A
1424	5	6.5	323	4	US-09-949-016-8089	Sequence 8089, Ap	1497	5	6.5	340	4	US-09-538-092-1103	Sequence 1103, A
1425	5	6.5	323	5	PCT-US94-09642-2	Sequence 2, Appli	1498	5	6.5	341	3	US-09-134-001C-4832	Sequence 4832, Ap
1426	5	6.5	324	4	US-09-549-848B-34	Sequence 34, Appl	1499	5	6.5	341	4	US-09-205-258-1034	Sequence 1034, Ap
1427	5	6.5	324	4	US-09-910-174B-6	Sequence 6, Appli	1500	5	6.5	341	4	US-09-602-787A-202	Sequence 202, App
1428	5	6.5	324	4	US-09-620-461-6	Sequence 6, Appli							
1429	5	6.5	324	4	US-09-248-796A-19935	Sequence 19935, A							
1430	5	6.5	325	3	US-08-867-381A-50	Sequence 50, Appl							
1431	5	6.5	325	3	US-09-521-144-50	Sequence 50, Appl							
1432	5	6.5	325	4	US-09-270-767-43881	Sequence 43881, A							
1433	5	6.5	325	4	US-09-248-796A-14929	Sequence 14929, A							
1434	5	6.5	326	1	US-08-118-270-39	Sequence 39, Appl							
1435	5	6.5	326	4	US-09-248-796A-18723	Sequence 18723, A							
1436	5	6.5	326	5	PCT-US93-08528-39	Sequence 39, Appl							
1437	5	6.5	327	4	US-09-540-236-2439	Sequence 2439, Ap							
1438	5	6.5	328	4	US-09-252-991A-26995	Sequence 26995, A							
1439	5	6.5	329	2	US-08-456-104-2	Sequence 2, Appli							
1440	5	6.5	329	2	US-08-101-624-2	Sequence 2, Appli							
1441	5	6.5	329	2	US-08-781-802-8	Sequence 8, Appli							
1442	5	6.5	329	3	US-08-479-744A-2	Sequence 2, Appli							
1443	5	6.5	329	3	US-08-280-757B-2	Sequence 2, Appli							
1444	5	6.5	329	3	US-08-694-078-8	Sequence 8, Appli							
1445	5	6.5	329	3	US-09-058-260-8	Sequence 8, Appli							
1446	5	6.5	329	3	US-08-205-697A-23	Sequence 23, Appl							
1447	5	6.5	329	3	US-08-702-525-23	Sequence 23, Appl							
1448	5	6.5	329	3	US-08-403-253A-4	Sequence 4, Appli							
1449	5	6.5	329	4	US-09-667-135-32	Sequence 32, Appl							
1450	5	6.5	329	4	US-08-435-816A-4	Sequence 4, Appli							
1451	5	6.5	329	4	US-09-252-991A-20373	Sequence 20373, A							
1452	5	6.5	329	4	US-09-425-762-2	Sequence 2, Appli							
1453	5	6.5	329	4	US-09-837-867A-23	Sequence 23, Appl							
1454	5	6.5	329	4	US-09-489-039A-13017	Sequence 13017, A							
1455	5	6.5	329	4	US-09-489-039A-14206	Sequence 14206, A							
1456	5	6.5	329	4	US-09-206-132-2	Sequence 2, Appli							
1457	5	6.5	329	4	US-09-441-411-26	Sequence 26, Appl							
1458	5	6.5	329	4	US-09-425-516-2	Sequence 2, Appli							
1459	5	6.5	329	5	PCT-US95-02576-23	Sequence 23, Appl							
1460	5	6.5	330	4	US-09-252-991A-29761	Sequence 29761, A							
1461	5	6.5	331	4	US-09-328-352-6515	Sequence 6515, Ap							
1462	5	6.5	331	4	US-09-489-039A-9639	Sequence 9639, Ap							
1463	5	6.5	331	4	US-09-270-767-44232	Sequence 44232, A							
1464	5	6.5	331	4	US-09-902-540-15531	Sequence 15531, A							
1465	5	6.5	332	4	US-09-107-532A-7060	Sequence 7060, Ap							
1466	5	6.5	332	4	US-09-270-767-38031	Sequence 38031, A							
1467	5	6.5	332	4	US-09-270-767-53248	Sequence 53248, A							
1468	5	6.5	333	4	US-09-252-991A-20110	Sequence 20110, A							
1469	5	6.5	334	4	US-09-543-681A-5946	Sequence 5946, A							
1470	5	6.5	334	4	US-09-270-767-59047	Sequence 59047, A							
1471	5	6.5	335	3	US-09-095-117-2	Sequence 2, Appli							
1472	5	6.5	335	3	US-09-095-117-4	Sequence 4, Appli							
1473	5	6.5	335	4	US-09-270-767-60903	Sequence 60903, A							
1474	5	6.5	335	4	US-09-248-796A-15895	Sequence 15895, A							
1475	5	6.5	336	3	US-08-749-816-2	Sequence 2, Appli							
1476	5	6.5	336	3	US-09-141-206-7	Sequence 7, Appli							
1477	5	6.5	336	3	US-09-334-601-13	Sequence 13, Appl							
1478	5	6.5	336	3	US-09-144-914-2	Sequence 2, Appli							
1479	5	6.5	336	4	US-09-252-991A-18342	Sequence 18342, A							
1480	5	6.5	336	4	US-09-252-991A-20404	Sequence 20404, A							
1481	5	6.5	337	4	US-09-252-991A-23552	Sequence 23552, A							
1482	5	6.5	337	4	US-09-489-039A-13330	Sequence 13330, A							
1483	5	6.5	338	3	US-09-286-805-4	Sequence 4, Appli							
1484	5	6.5	338	4	US-09-328-352-5051	Sequence 5051, Ap							
1485	5	6.5	338	4	US-09-270-767-32510	Sequence 32510, A							
1486	5	6.5	338	4	US-09-248-796A-16390	Sequence 16390, A							
1487	5	6.5	339	3	US-08-444-818-156	Sequence 156, App							

RESULT 1

US-09-489-039A-10091 ; Sequence 10091, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 10091

; LENGTH: 441

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-10091

Query Match 10.4%; Score 8; DB 4; Length 441;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ALTLCSAP 34

Db 356 ALTLCSAP 363

RESULT 2

US-09-270-767-32997 ; Sequence 32997, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32997

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-32997

Query Match 9.1%; Score 7; DB 4; Length 168;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TRLIATI 20

Db 105 TRLIATI 111

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RESULT 3
US-09-270-767-48214
; Sequence 48214, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48214
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48214

Query Match          9.1%; Score 7; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TRIATI 20
Db 105 TRIATI 111

RESULT 4
US-09-270-767-36922
; Sequence 36922, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36922
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-36922

Query Match          9.1%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GLALIFC 46
Db 47 GLALIFC 53

RESULT 5
US-09-270-767-52139
; Sequence 52139, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52139
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
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; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52139

Query Match          9.1%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GLALIFC 46
Db 47 GLALIFC 53

RESULT 6
US-09-489-039A-10661
; Sequence 10661, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10661
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10661

Query Match          9.1%; Score 7; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ILQSLAL 53
Db 16 ILQSLAL 22

RESULT 7
US-09-198-452A-461
; Sequence 461, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 461
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-461

Query Match          9.1%; Score 7; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LCFALTL 30
Db 62 LCFALTL 68

RESULT 8
US-09-438-185A-442
; Sequence 442, Application US/09438185A
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; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 442  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPN0440  
US-09-438-185A-442

Query Match 9.1%; Score 7; DB 4; Length 220;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LCPALTL 30  
Db 62 LCPALTL 68

## RESULT 9

US-08-470-953A-9  
; Sequence 9, Application US/08470953A  
; Patent No. 6346407

; GENERAL INFORMATION:  
; APPLICANT: ANDREE LAHAYE  
; APPLICANT: ERIC DE BUYL  
; APPLICANT: PIERRE LEDOUX  
; APPLICANT: RENE DETROZ  
; TITLE OF INVENTION: Xylanase, microorganisms produced it,  
; TITLE OF INVENTION: DNA molecule, processes for preparation of this xylanase  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WILLIAM BRINKS HOPFER GILSON & LIONE  
; STREET: 2000 K St., N.W., Suite 200  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,953A  
; FILING DATE: 6-OCTOBER-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilhlem F. Gadiano, Esq.  
; REGISTRATION NUMBER: 37,136  
; REFERENCE/DOCKET NUMBER: 4121-40  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-429-0625  
; TELEFAX: (202) 293-1850

; TELEX: 650 383-5605  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-470-953A-9

Query Match 7.8%; Score 6; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CPALTL 30  
Db 15 CPALTL 20

## RESULT 10

US-09-270-767-56935  
; Sequence 56935, Application US/09270767  
; Patent No. 6703491

; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56935  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-56935

Query Match 7.8%; Score 6; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PFARDA 67  
Db 8 PFARDA 13

## RESULT 11

US-09-270-767-34586  
; Sequence 34586, Application US/09270767  
; Patent No. 6703491

; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34586  
; LENGTH: 74  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-34586

Query Match 7.8%; Score 6; DB 4; Length 74;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 RDAVKK 70  
Db 10 RDAVKK 15

## RESULT 12

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US-09-270-767-49803
; Sequence 49803, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49803
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49803

Query Match          7.8%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      65 RDAVKK 70
Db      10 RDAVKK 15

RESULT 13
US-09-248-796A-24206
; Sequence 24206, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24206
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24206

Query Match          7.8%; Score 6; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 FCILQS 50
Db      52 FCILQS 57

RESULT 14
US-09-248-796A-26253
; Sequence 26253, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
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; SEQ ID NO 26253
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26253

Query Match          7.8%; Score 6; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      44 IFCILQ 49
Db      57 IFCILQ 62

RESULT 15
US-09-270-767-41301
; Sequence 41301, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41301
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41301

Query Match          7.8%; Score 6; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 LLCFAL 28
Db      68 LLCFAL 73

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OM protein - protein search, using sw model

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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	77	100.0	77	10	US-09-997-428-283
562	77	100.0	77	14	US-10-174-587-214
626	77	100.0	77	14	US-10-063-742-56
741	77	100.0	77	17	US-10-972-317-56
742	77	100.0	160	9	US-09-799-777-22
743	77	100.0	170	15	US-10-276-774-2357
744	69	89.6	160	11	US-09-978-360A-561
745	8	10.4	65	15	US-10-424-599-156694
746	8	10.4	124	15	US-10-264-232-2023
747	8	10.4	159	9	US-09-731-872-419
748	8	10.4	159	10	US-09-876-997-419
749	8	10.4	178	16	US-10-755-889-34
750	8	10.4	412	15	US-10-282-122A-73517
751	8	10.4	436	15	US-10-282-122A-60321

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438	15	US-10-282-122A-76172	Sequence 76172, A
830	16	US-10-437-963-198121	Sequence 198121, A
840	16	US-10-437-963-198124	Sequence 198124, A
94	16	US-10-767-701-55829	Sequence 55829, A
126	15	US-10-424-599-238797	Sequence 238797, A
197	16	US-10-767-701-35099	Sequence 35099, A
212	15	US-10-312-273-357	Sequence 357, App
220	15	US-10-289-762-461	Sequence 461, App
243	15	US-10-425-114-57246	Sequence 57246, A
304	15	US-10-282-122A-71016	Sequence 71016, A
314	9	US-09-886-055-263	Sequence 263, App
314	10	US-09-804-291-263	Sequence 60, Appl
314	14	US-10-044-643-60	Sequence 44, Appl
314	15	US-10-024-212-44	Sequence 184, App
314	15	US-10-343-650A-184	Sequence 175299, A
337	15	US-10-424-599-175299	Sequence 500, App
448	15	US-10-369-493-500	Sequence 21220, A
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626	16	US-10-437-963-142127	Sequence 10030, A
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1215	15	US-10-282-122A-69475	Sequence 125761, A
3583	16	US-10-437-963-125761	Sequence 37, Appl
11	14	US-10-223-277-37	Sequence 1125, Ap
15	14	US-10-084-813-1125	Sequence 1142, Ap
27	9	US-09-909-207-9	Sequence 9, Appl
35	15	US-10-424-599-270755	Sequence 270755, A
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55	15	US-10-424-599-202813	Sequence 202813, A
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56	14	US-10-091-504-1105	Sequence 1105, Ap
56	15	US-10-227-577-1105	Sequence 1105, Ap
62	9	US-09-864-761-40363	Sequence 40363, A
66	15	US-10-182-243-54	Sequence 54, Appl
70	15	US-10-424-599-179650	Sequence 179650, A
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77	16	US-10-437-963-185844	Sequence 185844, A
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79	16	US-10-437-963-137480	Sequence 282526, A
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86	16	US-10-437-963-131570	Sequence 131570, A
88	16	US-10-767-701-47724	Sequence 47724, A
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94	16	US-10-424-599-192913	Sequence 192913, A
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96	10	US-09-764-891-4819	Sequence 4819, Ap
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98	14	US-10-011-585A-176	Sequence 176, App
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126	15	US-10-276-774-1742	Sequence 1742, Ap
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# SUMMARIES

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7	7	9.1	198	2	hypothetical prote
8	7	9.1	212	2	probable TetR-fami
9	7	9.1	212	2	probable transcrip
10	7	9.1	212	2	tkk protein - Esch
11	7	9.1	212	2	hypothetical prote
12	7	9.1	212	2	hypothetical prote
13	7	9.1	264	2	polysaccharide dea
14	7	9.1	455	2	probable 4-hydroxy
15	7	9.1	458	2	probable 4-hydroxy
16	7	9.1	566	2	hypothetical prote
17	7	9.1	569	2	probable acylamino
18	7	9.1	672	2	Similar to transcr
19	7	9.1	672	2	transcription regu
20	7	9.1	1216	2	spindle assembly c
21	6	7.8	73	2	hypothetical prote
22	6	7.8	78	2	hypothetical prote
23	6	7.8	121	2	hypothetical prote
24	6	7.8	124	1	stage 0 sporulatio
25	6	7.8	126	2	conserved hypotet
26	6	7.8	133	2	botrocetin alpha c
27	6	7.8	133	2	hypothetical prote
28	6	7.8	157	2	16 kD heat shock p
29	6	7.8	160	2	hypothetical prote

30	6	7.8	174	2	A64442	hypothetical prote
31	6	7.8	174	2	C83943	hypothetical prote
32	6	7.8	177	2	B64505	hypothetical prote
33	6	7.8	182	2	AC0749	CDPdiacylglycerol-
34	6	7.8	183	2	D70339	conserved hypotet
35	6	7.8	195	2	D88086	protein Tl1P1.7 [i
36	6	7.8	197	2	T09257	late embryonic abu
37	6	7.8	208	1	B69066	conserved hypotet
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39	6	7.8	220	2	S63051	hypothetical prote
40	6	7.8	234	2	A40710	CD30 ligand - huma
41	6	7.8	240	2	T22850	hypothetical prote
42	6	7.8	241	2	G89925	menaquinone biosyn
43	6	7.8	243	2	AB1191	B. subtilis ynfH p
44	6	7.8	243	2	AB1549	conserved hypotet
45	6	7.8	246	1	NDP57A	type II site-speci
46	6	7.8	246	2	AG2988	competence protein
47	6	7.8	247	2	AD0757	cobalamin (5'-phos
48	6	7.8	247	2	C90977	cobalamin 5'-phosp
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62	6	7.8	277	2	AF3216	ABC transporter, m
63	6	7.8	285	2	AD3175	hypothetical prote
64	6	7.8	286	2	AG0403	anaerobic dimethyl
65	6	7.8	290	2	T39335	probable SURF-fami
66	6	7.8	291	2	JQ0060	hypothetical 32.7K
67	6	7.8	291	2	A99295	competence protein
68	6	7.8	293	2	S58704	probable membrane
69	6	7.8	296	2	S60637	NADH2 dehydrogenas
70	6	7.8	296	2	I52860	smooth muscle myos
71	6	7.8	299	2	AB3191	hypothetical prote
72	6	7.8	300	2	D83487	hypothetical prote
73	6	7.8	305	2	JC4920	2-oxoacid-ferredox
74	6	7.8	306	2	H86695	ABC transporter pe
75	6	7.8	309	2	E84672	hypothetical prote
76	6	7.8	315	2	B83676	hypothetical prote
77	6	7.8	326	2	S73620	hypothetical prote
78	6	7.8	328	2	A70145	prolipoprotein dia
79	6	7.8	330	2	I65768	smooth muscle myos
80	6	7.8	331	2	AF1324	opine catabolism p
81	6	7.8	331	2	AH1695	opine catabolism p
82	6	7.8	332	1	QRECD1	iron(III) dicitrat
83	6	7.8	335	2	AI3063	hypothetical prote
84	6	7.8	335	2	G98222	hypothetical prote
85	6	7.8	340	2	A36988	replication factor
86	6	7.8	345	2	T14053	NADH2 dehydrogenas
87	6	7.8	345	2	T24659	hypothetical prote
88	6	7.8	345	2	T34998	probable transmemb
89	6	7.8	345	2	AB1448	gp18 (Bacteriophag
90	6	7.8	346	2	S22442	probable 3',5'-cyc
91	6	7.8	349	2	D72292	hypothetical prote
92	6	7.8	350	2	S70672	dehydrogenase homo
93	6	7.8	351	2	T04027	hypothetical prote
94	6	7.8	354	2	AF3614	hypothetical prote
95	6	7.8	357	2	S35318	probable undecapre
96	6	7.8	359	2	I50712	MT22 protein - ye
97	6	7.8	365	2	G72306	conserved hypotet
98	6	7.8	378	2	AF1834	citrate synthase [
99	6	7.8	381	2	G83050	L-lactate dehydrog
100	6	7.8	382	2	T48109	hypothetical prote
101	6	7.8	382	2	D86720	transcription term
102	6	7.8	389	2	F86268	aminoalcoholphosph

103	6	7.8	389	2	T14412	ethanolaminephosph	176	6	7.8	765	2	AD0778	beta-glucosidase (
104	6	7.8	395	2	D69312	molybdopterin oxid	177	6	7.8	765	2	C91006	beta-D-glucoside g
105	6	7.8	398	2	S53391	probable membrane	178	6	7.8	765	2	C64981	beta-glucosidase (
106	6	7.8	400	2	T00754	probable integral	179	6	7.8	765	2	D85850	beta-D-glucoside g
107	6	7.8	402	1	S06745	plasmaenogen activa	180	6	7.8	783	2	T18329	icmO protein - leg
108	6	7.8	410	2	S74951	Na+/H+-exchanging	181	6	7.8	823	2	H71300	probable DNA ligase
109	6	7.8	412	2	S07537	myosin heavy chain	182	6	7.8	823	2	B81282	probable integral
110	6	7.8	434	2	C36144	cobyrinic acid a,c	183	6	7.8	872	2	B75073	ATP-dependent RNA
111	6	7.8	434	2	T24952	hypothetical prote	184	6	7.8	873	2	T05189	glutamyl aminopept
112	6	7.8	438	2	A32670	fibronogen gamma c	185	6	7.8	889	1	A44153	aconitate hydratase
113	6	7.8	440	2	G84069	hypothetical prote	186	6	7.8	889	2	A44154	aconitate hydratase
114	6	7.8	440	2	C69545	conserved hypothet	187	6	7.8	889	2	S26403	aconitate hydratase
115	6	7.8	447	2	B98052	probable oxidoredu	188	6	7.8	889	2	S18720	polymorphic outer
116	6	7.8	449	2	T070903	nucleoprotein N -	189	6	7.8	928	2	G81591	excinuclease ABC c
117	6	7.8	450	2	A46104	hypothetical prote	190	6	7.8	953	2	D71645	hypothetical prote
118	6	7.8	452	2	T28094	ABC transporter pe	191	6	7.8	971	2	H97454	conserved hypothet
119	6	7.8	453	2	D86846	drug-export protei	192	6	7.8	971	2	AB2673	probable membrane
120	6	7.8	454	2	D86793	pyruvate dehydroge	193	6	7.8	991	2	S57385	hypothetical prote
121	6	7.8	462	2	T33723	Ca2+/calmodulin-de	194	6	7.8	995	2	C84145	hypothetical prote
122	6	7.8	469	1	S17656	hypothetical prote	195	6	7.8	1070	2	C75506	hypothetical prote
123	6	7.8	474	2	B86221	NADH2 dehydrogenas	196	6	7.8	1098	2	T50364	hypothetical prote
124	6	7.8	478	2	AC3395	NADH ubiquinone ox	197	6	7.8	1114	2	B86423	adenylate cyclase
125	6	7.8	480	2	AC2734	probable MFS trans	198	6	7.8	1144	1	A39833	laminin B1k chain
126	6	7.8	480	2	D83487	NADH dehydrogenase	199	6	7.8	1170	2	AS3612	exopolysaccharona
127	6	7.8	481	2	D87489	NADH-ubiquinone ox	200	6	7.8	1376	2	F83711	hypothetical prote
128	6	7.8	482	2	E97515	alanine transamina	201	6	7.8	1449	2	T20181	hypothetical prote
129	6	7.8	482	2	S28429	probable trna nucl	202	6	7.8	1467	2	T48162	glutathione-conjug
130	6	7.8	484	2	T41527	myosin heavy chain	203	6	7.8	1516	2	F84919	hypothetical prote
131	6	7.8	484	2	B33501	citrate (sl) - synth	204	6	7.8	1584	2	T20180	hypothetical prote
132	6	7.8	486	2	S52814	probable sugar tra	205	6	7.8	1586	2	T20179	hypothetical prote
133	6	7.8	496	2	T52132	NADH2 dehydrogenas	206	6	7.8	1805	2	T02712	similar to late em
134	6	7.8	499	2	A47751	probable replicati	207	6	7.8	1858	2	T18273	1-phosphatidylinos
135	6	7.8	504	2	T12894	cobyrinic acid a,c	208	6	7.8	1938	2	JC5421	smooth muscle myos
136	6	7.8	514	2	AG3297	conserved hypothet	209	6	7.8	1972	1	A41604	myosin heavy chain
137	6	7.8	524	2	H87274	cytochrome P450 4f	210	6	7.8	1972	2	JC5420	smooth muscle myos
138	6	7.8	526	2	JC4533	yfub protein limpo	211	6	7.8	2186	2	H89960	hypothetical prote
139	6	7.8	528	2	T43919	hypothetical prote	212	6	7.8	2672	2	A48126	translation activa
140	6	7.8	535	2	T23419	probable chemotaxi	213	6	7.8	2890	2	B71846	dna-directed RNA p
141	6	7.8	538	2	D83109	probable apolipor	214	6	7.8	2890	2	F64669	DNA-directed RNA p
142	6	7.8	542	2	E71502	protein W03A5.2 [i	215	5	6.5	33	1	Z7BPFI	coat protein C cha
143	6	7.8	547	2	C88456	probable vacuolar	216	5	6.5	33	1	Z7BPFI	coat protein C cha
144	6	7.8	549	2	T50295	lysyl-tRNA synthet	217	5	6.5	33	1	Z7BPFI	coat protein C cha
145	6	7.8	552	2	C87259	pollen-specific pr	218	5	6.5	37	2	C83780	hypothetical prote
146	6	7.8	561	2	T05545	sulfate adenyllylr	219	5	6.5	40	2	F90439	hypothetical prote
147	6	7.8	573	1	A53651	probable glycerol-	220	5	6.5	41	2	B47752	RNA recognition mo
148	6	7.8	577	2	A95902	extracellular solu	221	5	6.5	48	2	S65035	H+-transporting tw
149	6	7.8	582	2	S74819	malate dehydrogena	222	5	6.5	49	2	S77986	cytochrome-c oxida
150	6	7.8	585	2	S43718	malate dehydrogena	223	5	6.5	49	2	T07304	hypothetical prote
151	6	7.8	589	1	S18826	secreted protein M	224	5	6.5	52	2	A37354	sex-specific prote
152	6	7.8	590	2	S77267	malate dehydrogena	225	5	6.5	52	2	G97773	hypothetical prote
153	6	7.8	592	2	JC5967	malate dehydrogena	226	5	6.5	53	2	C97923	degenerate transpo
154	6	7.8	594	2	F98150	probable gamma-glu	227	5	6.5	53	2	WZVZC1	19K truncated Hind
155	6	7.8	594	2	AF3137	gamma-glutamyltran	228	5	6.5	54	4	WZVZC1	ATP synthase F0 ch
156	6	7.8	595	2	T49877	hypothetical prote	229	5	6.5	55	2	E90624	hypothetical prote
157	6	7.8	603	2	C90426	phosphoenolpyruvat	230	5	6.5	55	2	D90972	unknown protein en
158	6	7.8	621	2	S10450	myosin heavy chain	231	5	6.5	56	2	A85820	NADH2 dehydrogenas
159	6	7.8	624	2	T38006	probable lysophosp	232	5	6.5	56	2	G01277	hypothetical prote
160	6	7.8	624	2	B82108	major facilitator	233	5	6.5	57	2	S95052	hypothetical prote
161	6	7.8	630	2	T38110	hypothetical prote	234	5	6.5	61	2	A99931	hypothetical prote
162	6	7.8	631	2	T05103	malate dehydrogena	235	5	6.5	62	2	T08028	ycf9 protein - chl
163	6	7.8	636	1	DEZMMX	NADP-dependent mal	236	5	6.5	62	2	A09926	hypothetical prote
164	6	7.8	638	2	S46499	ABC transport syst	237	5	6.5	62	2	B98853	hypothetical prote
165	6	7.8	643	2	H81361	probable malate ox	238	5	6.5	63	2	C86675	hypothetical prote
166	6	7.8	646	2	E96828	malate dehydrogena	239	5	6.5	64	2	T07218	hypothetical prote
167	6	7.8	647	1	S42939	malate dehydrogena	240	5	6.5	65	2	C81120	hypothetical prote
168	6	7.8	648	1	S12893	probable dna-bindi	241	5	6.5	65	2	T11987	hypothetical prote
169	6	7.8	660	2	T41580	probable lysophosp	242	5	6.5	65	2	T28212	hypothetical prote
170	6	7.8	673	2	T50281	serine/threonine k	243	5	6.5	67	2	F90057	hypothetical prote
171	6	7.8	707	2	AF2277	semaphorin I precu	244	5	6.5	69	2	S58357	pepl protein - Sta
172	6	7.8	711	2	A49423	hypothetical prote	245	5	6.5	70	2	B63223	hypothetical prote
173	6	7.8	714	2	T14080	TonB-dependent rec	246	5	6.5	71	2	B83730	hypothetical prote
174	6	7.8	732	2	F87469	probable sexual cy	247	5	6.5	72	2	T46623	hypothetical prote
175	6	7.8	746	2	T43648		248	5	6.5	72	2	T46623	

249	5	6.5	72	2	E82615	hypothetical prote	322	5	6.5	102	2	E72111	hypothetical prote
250	5	6.5	73	2	T49902	hypothetical prote	323	5	6.5	102	2	G86510	hypothetical prote
251	5	6.5	74	2	E81284	hypothetical prote	324	5	6.5	103	2	F90585	30S ribosomal prot
252	5	6.5	75	2	H81320	small hydrophobic	325	5	6.5	103	2	A69263	conserved hypoteth
253	5	6.5	75	2	AG2371	hypothetical prote	326	5	6.5	104	2	JC5351	2-nitrotoluene dio
254	5	6.5	77	2	JC5052	hypothetical 8.9k	327	5	6.5	104	2	C90958	probable plasmid p
255	5	6.5	77	2	B90781	hypothetical prote	328	5	6.5	104	2	D85806	hypothetical prote
256	5	6.5	78	2	S25619	hypothetical prote	329	5	6.5	105	2	T29918	hypothetical prote
257	5	6.5	78	2	A97974	degenerate transpo	330	5	6.5	105	2	A90560	hypothetical prote
258	5	6.5	81	1	W5WL35	B5 protein - human	331	5	6.5	106	2	T16378	hypothetical prote
259	5	6.5	82	2	S85330	elicitor NIP1 prec	332	5	6.5	106	2	T47814	hypothetical prote
260	5	6.5	82	2	H84046	hypothetical prote	333	5	6.5	107	2	T44493	conserved hypoteth
261	5	6.5	83	2	B97042	hypothetical prote	334	5	6.5	107	2	C72779	hypothetical prote
262	5	6.5	84	2	F64653	hypothetical prote	335	5	6.5	107	2	C97859	hypothetical prote
263	5	6.5	84	2	T14942	hypothetical prote	336	5	6.5	107	4	A60600	hypothetical mutan
264	5	6.5	85	2	T26542	hypothetical prote	337	5	6.5	108	2	C75034	hypothetical-like prot
265	5	6.5	86	2	S63593	acyl-coenzyme A-bi	338	5	6.5	109	2	S54446	prepilin-like prot
266	5	6.5	86	2	S63594	acyl-coenzyme A-bi	339	5	6.5	109	2	C89759	Conserved hypoteth
267	5	6.5	86	2	C71941	hypothetical prote	340	5	6.5	109	2	A71191	hypothetical prote
268	5	6.5	86	2	D97780	hypothetical prote	341	5	6.5	110	2	S04643	glutathione transf
269	5	6.5	86	2	AB3223	conserved hypoteth	342	5	6.5	110	2	S61257	genome polyprotein
270	5	6.5	87	2	B70134	flagellar biosynth	343	5	6.5	110	2	S61254	probable membrane
271	5	6.5	87	2	C81890	hypothetical prote	344	5	6.5	110	2	S45883	hypothetical prote
272	5	6.5	87	2	B97161	probable integral	345	5	6.5	110	2	A90144	hypothetical prote
273	5	6.5	87	2	AF2195	hypothetical prote	346	5	6.5	111	2	T00688	hypothetical prote
274	5	6.5	88	2	A38112	hipB protein - Esc	347	5	6.5	111	2	A81673	conserved hypoteth
275	5	6.5	89	1	C36869	probable export pr	348	5	6.5	111	2	AE0794	probable membrane
276	5	6.5	89	1	D41886	probable export pr	349	5	6.5	112	2	B71211	hypothetical prote
277	5	6.5	89	2	C84939	flagellar biosynth	350	5	6.5	112	2	A71515	hypothetical prote
278	5	6.5	89	2	AE0753	flagellar biosynth	351	5	6.5	112	2	D83730	hypothetical prote
279	5	6.5	89	2	H85812	flagellar biosynth	352	5	6.5	112	2	E97208	probable permease
280	5	6.5	89	2	H90964	probable export pr	353	5	6.5	113	1	S32873	hypA protein - Rhi
281	5	6.5	89	2	S78699	probable export pr	354	5	6.5	113	2	A65047	hypothetical prote
282	5	6.5	89	2	AI0221	flagellar biosynth	355	5	6.5	113	2	H85914	hypothetical prote
283	5	6.5	89	2	S35277	probable export pr	356	5	6.5	113	2	E91070	hypothetical prote
284	5	6.5	89	2	I69150	perC protein - Esc	357	5	6.5	113	2	F71053	hypothetical prote
285	5	6.5	89	2	S75103	hypothetical prote	358	5	6.5	113	2	E82927	hypothetical prote
286	5	6.5	89	2	S51931	cryptogene protein	359	5	6.5	113	2	AE0629	cell invasion prot
287	5	6.5	89	2	G89941	hypothetical prote	360	5	6.5	113	2	A72486	hypothetical prote
288	5	6.5	90	2	A60396	antigen 7H8/5 - ma	361	5	6.5	114	2	S69320	probable membrane
289	5	6.5	90	2	H97228	probable membrane	362	5	6.5	114	2	D71048	hypothetical prote
290	5	6.5	90	2	AE1159	flagellar biosynth	363	5	6.5	114	2	T29992	hypothetical prote
291	5	6.5	90	2	AE1518	flagellar biosynth	364	5	6.5	115	1	JN0318	guanylin precursor
292	5	6.5	92	2	B35392	hypothetical prote	365	5	6.5	115	2	T17090	NADH2 dehydrogenas
293	5	6.5	92	2	T43587	yop secretion and	366	5	6.5	115	2	AD2280	hypothetical prote
294	5	6.5	92	2	S15321	hypothetical prote	367	5	6.5	115	2	S70185	hypothetical prote
295	5	6.5	93	2	S22369	hypothetical prote	368	5	6.5	115	2	F72569	hypothetical prote
296	5	6.5	94	2	H71549	probable trp opero	369	5	6.5	115	2	AI0332	probable membrane
297	5	6.5	96	2	B82311	conserved hypoteth	370	5	6.5	116	2	H58892	NADH2 dehydrogenas
298	5	6.5	96	2	B90831	hypothetical prote	371	5	6.5	116	2	F81796	hypothetical inner
299	5	6.5	96	2	C87024	probable membrane	372	5	6.5	116	2	C70656	hypothetical prote
300	5	6.5	96	2	H84381	hypothetical prote	373	5	6.5	116	2	B85070	hypothetical prote
301	5	6.5	96	2	S66582	hypothetical prote	374	5	6.5	116	2	AE0685	hypothetical prote
302	5	6.5	96	2	F70578	hypothetical prote	375	5	6.5	116	2	T05517	abscisic acid-indu
303	5	6.5	96	2	H69197	hypothetical prote	376	5	6.5	117	2	A69828	hypothetical prote
304	5	6.5	96	2	T26525	hypothetical prote	377	5	6.5	117	2	C98240	hypothetical prote
305	5	6.5	96	2	C64787	ybcO protein - Esc	378	5	6.5	118	1	CCDV3N	cytochrome c3, tet
306	5	6.5	97	2	F83200	conserved hypoteth	379	5	6.5	118	1	PSSNK3	phospholipase A2 (
307	5	6.5	97	2	T16463	hypothetical prote	380	5	6.5	118	2	H34860	phospholipase A2 (
308	5	6.5	98	2	T11188	NADH2 dehydrogenas	381	5	6.5	118	2	C89861	Na+/H+ antiporter
309	5	6.5	98	2	T11397	NADH2 dehydrogenas	382	5	6.5	118	2	D89872	conserved hypoteth
310	5	6.5	98	2	S12189	mobs protein - Thi	383	5	6.5	119	2	G69106	transcription regu
311	5	6.5	99	2	S59145	NADH2 dehydrogenas	384	5	6.5	119	2	S74006	hypothetical prote
312	5	6.5	99	2	T11886	NADH2 dehydrogenas	385	5	6.5	120	2	A81157	hypothetical prote
313	5	6.5	99	2	C90472	NADH2 dehydrogenas	386	5	6.5	120	2	AG3195	conserved hypoteth
314	5	6.5	100	2	A84949	hypothetical prote	387	5	6.5	121	2	A71508	hypothetical prote
315	5	6.5	100	2	C72592	hypothetical prote	388	5	6.5	121	2	F71451	hypothetical prote
316	5	6.5	100	2	A85525	hypothetical prote	389	5	6.5	122	2	F75351	hypothetical prote
317	5	6.5	100	2	F90675	hypothetical prote	390	5	6.5	122	2	F72636	hypothetical prote
318	5	6.5	100	2	P90355	hypothetical prote	391	5	6.5	123	2	AG0283	probable exported
319	5	6.5	101	2	H71178	hypothetical prote	392	5	6.5	123	2	T32704	hypothetical prote
320	5	6.5	101	2	E75487	v-type ATP synthas	393	5	6.5	124	2	D71355	probable ribosomal
321	5	6.5	102	2	S65294	probable membrane	394	5	6.5	124	2	B75040	hypothetical prote

395 124 2 A71122 hypothetical prote  
396 125 2 AE2704 two component resp  
397 125 2 E97486 hypothetical prote  
398 126 2 T47297 hypothetical prote  
399 126 2 F71185 hypothetical prote  
400 126 2 AF1264 hypothetical prote  
401 126 2 G84615 hypothetical prote  
402 126 2 B95415 hypothetical prote  
403 127 2 PC2270 cytochrome P450 pr  
404 127 2 T44119 hypothetical prote  
405 127 2 H82725 hypothetical prote  
406 129 2 A41839 ribosomal protein  
407 129 2 F87468 ubiquinol oxidase  
408 130 2 AD3526 5-carboxymethyl-2-  
409 131 2 G75312 ribosomal protein  
410 132 1 C32057 nitrogenase (EC 1.  
411 132 2 G70314 conserved hypothet  
412 132 2 S30969 gene 24 protein -  
413 132 2 AE2025 hypothetical prote  
414 132 2 A13242 conserved hypothet  
415 132 2 AG3379 molybdopterin-guan  
416 133 2 S70967 bfpG protein - Esc  
417 133 2 A10999 conserved hypothet  
418 133 2 B90260 conserved hypothet  
419 134 2 JC5116 interlukin-5 prec  
420 134 2 C69849 hypothetical prote  
421 134 2 F72802 gp24 protein - Myc  
422 134 2 E88319 protein F54D5.12 [  
423 134 2 E70251 hypothetical prote  
424 134 2 G69802 conserved hypothet  
425 135 2 C82821 NADH2 dehydrogenas  
426 135 2 S78260 ribosomal protein  
427 135 2 A71271 conserved hypothet  
428 135 2 F64034 hypothetical prote  
429 135 2 E75137 hypothetical prote  
430 135 2 F84677 hypothetical prote  
431 135 2 C75465 conserved hypothet  
432 137 2 A58930 succinate dehydrog  
433 137 2 H81452 nucleoside diphosp  
434 137 2 S37870 chromatin-associat  
435 137 2 A75487 nitrogen regulator  
436 137 2 B70123 conserved hypothet  
437 137 2 C69501 conserved hypothet  
438 138 2 T21176 hypothetical prote  
439 138 2 D96841 F23A5.22 (imported  
440 139 2 C83807 hypothetical prote  
441 139 2 F87018 probable membrane  
442 139 2 C97163 hypothetical prote  
443 140 1 D69464 hypothetical prote  
444 140 2 E75518 probable biopolyme  
445 140 2 S73588 MG395 homolog D02  
446 140 2 AC1280 hypothetical prote  
447 140 2 T13643 hypothetical prote  
448 140 2 A19083 hypothetical prote  
449 141 2 A86679 hypothetical prote  
450 141 2 G90762 hypothetical prote  
451 141 2 H85625 hypothetical prote  
452 141 2 G90315 hypothetical prote  
453 142 2 I48552 orf US426 - infect  
454 143 2 S73518 PTS system mannito  
455 143 2 H72616 hypothetical prote  
456 144 2 S78178 succinate dehydrog  
457 144 2 FC1110 riboflavin synthas  
458 144 2 F72556 hypothetical prote  
459 144 2 S69345 oviduct-specific p  
460 145 2 A36569 plastocyanin precu  
461 145 2 T11243 ribosomal protein  
462 145 2 H70022 hypothetical prote  
463 145 2 S30247 Hin-1 protein - nu  
464 145 2 F81338 probable periplasm  
465 146 2 T14667 hypothetical prote  
466 146 2 G70020 hypothetical prote  
467 146 2 S74956 spore protein sp21

468 5 6.5 146 2 H64017 hypothetical prote  
469 5 6.5 147 2 AG0313 phosphotransferase  
470 5 6.5 147 2 AG3578 hypothetical prote  
471 5 6.5 147 2 F87432 hypothetical prote  
472 5 6.5 148 2 G87362 transcribed hypothet  
473 5 6.5 148 2 E81700 conserved hypothet  
474 5 6.5 148 2 H72781 hypothetical prote  
475 5 6.5 148 2 S76922 hypothetical prote  
476 5 6.5 148 2 S21401 homeotic protein -  
477 5 6.5 149 2 B86579 CT667 hypothetical  
478 5 6.5 149 2 E72046 conserved hypothet  
479 5 6.5 149 2 A83045 hypothetical prote  
480 5 6.5 150 2 JH0249 guanine nucleotide  
481 5 6.5 150 2 C86600 hypothetical prote  
482 5 6.5 150 2 C72024 conserved hypothet  
483 5 6.5 150 2 A97536 hypothetical prote  
484 5 6.5 151 1 S73506 pilB homolog K05\_o  
485 5 6.5 151 2 D83290 probable transcrip  
486 5 6.5 151 2 G69014 conserved hypothet  
487 5 6.5 151 2 T42950 hypothetical prote  
488 5 6.5 151 2 T14948 hypothetical prote  
489 5 6.5 152 2 T23449 hypothetical prote  
490 5 6.5 153 2 E95845 conserved hypothet  
491 5 6.5 154 2 S48026 ribosomal protein  
492 5 6.5 154 2 T47667 ribosomal L23a-lik  
493 5 6.5 154 2 T00556 60S ribosomal prot  
494 5 6.5 154 2 T37200 hypothetical prote  
495 5 6.5 155 1 WMBP24 transactivation pr  
496 5 6.5 156 1 R3TW7 ribosomal protein  
497 5 6.5 157 2 A83718 hypothetical prote  
498 5 6.5 157 2 G82080 hypothetical prote  
499 5 6.5 157 2 A11910 hypothetical prote  
500 5 6.5 158 2 C71406 hypothetical prote  
501 5 6.5 160 2 E81919 probable AnC-fami  
502 5 6.5 160 2 B89769 hypothetical prote  
503 5 6.5 160 2 A39061 protein-tyrosine k  
504 5 6.5 161 2 A29557 calcium-binding pr  
505 5 6.5 162 1 LGBUI beta-lactoglobulin  
506 5 6.5 162 2 JC7157 calcium vector pro  
507 5 6.5 162 2 E70195 colicin V producti  
508 5 6.5 162 2 S17806 hypothetical prote  
509 5 6.5 163 2 AF3388 hypothetical prote  
510 5 6.5 164 2 T12408 NADH2 dehydrogenas  
511 5 6.5 164 2 F97897 30S ribosomal prot  
512 5 6.5 164 2 F95026 ribosomal protein  
513 5 6.5 164 2 G87301 transcription regu  
514 5 6.5 164 2 AB0885 hydrogenase-2 comp  
515 5 6.5 164 2 G83606 conserved hypothet  
516 5 6.5 165 2 H64038 hypothetical prote  
517 5 6.5 165 2 E64758 membrane protein y  
518 5 6.5 166 1 R3BS5F ribosomal protein  
519 5 6.5 166 2 JW0031 gp delta - satelll  
520 5 6.5 166 2 H96519 hypothetical prote  
521 5 6.5 166 2 B72607 hypothetical prote  
522 5 6.5 167 2 F70478 hypothetical prote  
523 5 6.5 167 2 D87360 conserved hypothet  
524 5 6.5 167 2 G82892 hypothetical prote  
525 5 6.5 168 1 A37087 pleiotrophin precu  
526 5 6.5 168 2 G81665 GDP-diacylglycerol  
527 5 6.5 168 2 F71503 probable glycerol-  
528 5 6.5 168 2 H01482 pleiotrophin - mou  
529 5 6.5 168 2 I53001 pleiotrophin  
530 5 6.5 168 2 H86866 prophage p3 prote  
531 5 6.5 168 2 T01482 hypothetical prote  
532 5 6.5 169 2 A82099 conserved hypothet  
533 5 6.5 169 2 G89869 outer membrane pro  
534 5 6.5 169 2 A33141 conserved hypothet  
535 5 6.5 170 2 T17914 hypothetical prote  
536 5 6.5 170 2 A82848 16S rRNA processin  
537 5 6.5 170 2 A86638 protein F58F6.3 [i  
538 5 6.5 170 2 A13322 hypothetical prote  
539 5 6.5 170 2 T34588 hypothetical prote  
540 5 6.5 170 2 E81312 probable lipoprote

541	5	6.5	170	2	A12857	probable acetyltra	614	5	6.5	187	2	T51719	hypothetical prote
542	5	6.5	170	2	G97634	hypothetical prote	615	5	6.5	187	2	H86412	protein F1k23.8 [l
543	5	6.5	171	2	T34587	hypothetical prote	616	5	6.5	187	2	B81182	transcription regu
544	5	6.5	171	2	AC1082	hypothetical prote	617	5	6.5	188	2	F75004	hypothetical prote
545	5	6.5	172	2	G87656	conserved hypotet	618	5	6.5	188	2	D70349	conserved hypotet
546	5	6.5	172	2	H84391	hypothetical prote	619	5	6.5	188	2	F82587	dioxygenase XF2210
547	5	6.5	173	2	C82098	riboflavin synthas	620	5	6.5	188	2	AD8945	probable DNA-bindi
548	5	6.5	173	2	T17385	vrlf protein - Dic	621	5	6.5	188	2	G69545	hypothetical prote
549	5	6.5	173	2	F70109	hypothetical prote	622	5	6.5	189	2	T07102	malate dehydrogena
550	5	6.5	173	2	S38231	hypothetical prote	623	5	6.5	189	2	E95418	probable KdpC pota
551	5	6.5	173	2	C84247	hypothetical prote	624	5	6.5	189	2	A71569	hypothetical prote
552	5	6.5	173	2	AB2942	hypothetical prote	625	5	6.5	190	2	T37168	probable tetR-fami
553	5	6.5	174	1	JQ1625	small hydrophobic	626	5	6.5	190	2	A64039	hypothetical prote
554	5	6.5	175	2	T06812	cold acclimation p	627	5	6.5	190	2	F82610	hypothetical prote
555	5	6.5	175	2	B84828	hypothetical prote	628	5	6.5	190	2	B95210	hypothetical prote
556	5	6.5	175	2	F82529	hypothetical prote	629	5	6.5	190	2	E98074	hypothetical prote
557	5	6.5	175	2	T36798	probable transcrip	630	5	6.5	190	2	A87263	hypothetical prote
558	5	6.5	176	2	A90635	probable NAD(P)H o	631	5	6.5	190	2	E89803	conserved hypotet
559	5	6.5	176	2	A85486	probable NAD(P)H o	632	5	6.5	191	2	AE0412	probable 2'-5' RNA
560	5	6.5	176	2	F84110	hypothetical prote	633	5	6.5	191	2	B69462	probable pyruvate
561	5	6.5	177	2	S39710	hypothetical prote	634	5	6.5	191	2	S76838	hypothetical prote
562	5	6.5	177	2	F96739	hypothetical prote	635	5	6.5	191	2	B70788	hypothetical prote
563	5	6.5	177	2	T37723	probable N-termi	636	5	6.5	192	2	G75419	hypothetical prote
564	5	6.5	177	2	E71211	hypothetical prote	637	5	6.5	192	2	E82542	two-component syst
565	5	6.5	178	1	LG80	beta-lactoglobulin	638	5	6.5	192	2	B81911	probable molybdopt
566	5	6.5	178	2	A71730	ubiquinone biosynt	639	5	6.5	193	2	S35630	genome polypeptid
567	5	6.5	178	2	D81400	hypothetical prote	640	5	6.5	193	2	H64174	hypothetical prote
568	5	6.5	178	2	T19064	hypothetical prote	641	5	6.5	193	2	S70279	outer surface prot
569	5	6.5	179	2	G81746	ribosome recycling	642	5	6.5	194	1	S76605	phosphoheptose iso
570	5	6.5	179	2	D71484	ribosome releasing	643	5	6.5	194	2	S19141	beta-coixin, 17K,
571	5	6.5	179	2	A42367	spore coat protein	644	5	6.5	194	2	T19301	hypothetical prote
572	5	6.5	179	2	E88028	protein F46F5.16 [	645	5	6.5	194	2	T14746	hypothetical prote
573	5	6.5	179	2	F18864	hypothetical prote	646	5	6.5	195	2	S46449	hypothetical prote
574	5	6.5	180	1	LG87	beta-lactoglobulin	647	5	6.5	195	2	D64030	hypothetical prote
575	5	6.5	180	2	S39775	alpha-s2-casein fo	648	5	6.5	196	2	AI0270	GTP cyclohydrolase
576	5	6.5	180	2	F75073	pyrazinamide/nic	649	5	6.5	196	2	AD2025	hypothetical prote
577	5	6.5	180	2	C97050	phage related prot	650	5	6.5	196	2	F97786	hypothetical prote
578	5	6.5	180	2	E97355	hypothetical prote	651	5	6.5	196	2	D72554	probable cytochrom
579	5	6.5	180	2	D83812	hypothetical prote	652	5	6.5	197	2	G85521	hypothetical prote
580	5	6.5	180	2	B71092	probable pyrazinam	653	5	6.5	197	2	C90671	hypothetical prote
581	5	6.5	181	2	G81122	N-acetylmuramoyl-L	654	5	6.5	197	2	JC2320	hypothetical 22K p
582	5	6.5	181	2	D81135	N-acetylmuramoyl-L	655	5	6.5	197	2	I39723	ORF13 - Agrobacter
583	5	6.5	181	2	AH2500	peptidase B [impor	656	5	6.5	197	2	C64422	hypothetical prote
584	5	6.5	181	2	T23333	hypothetical prote	657	5	6.5	197	2	H97762	hypothetical prote
585	5	6.5	182	1	XNECPG	CDPdiacylglycerol-	658	5	6.5	197	2	B83561	probable type II s
586	5	6.5	182	2	B90960	CDPdiacylglycerol-	659	5	6.5	197	2	B83768	hypothetical prote
587	5	6.5	182	2	C85808	CDPdiacylglycerol-	660	5	6.5	197	2	S78187	ynf39 protein - Re
588	5	6.5	182	2	S77784	probable phosphogl	661	5	6.5	198	2	T42733	hypothetical prote
589	5	6.5	182	2	B70335	conserved hypotet	662	5	6.5	198	2	I39670	roib protein - Agr
590	5	6.5	182	2	E72630	hypothetical prote	663	5	6.5	199	2	D64770	yaJ1 protein - Esc
591	5	6.5	182	2	C86664	hypothetical prote	664	5	6.5	199	2	E85537	hypothetical prote
592	5	6.5	182	2	D82490	hypothetical prote	665	5	6.5	199	2	A90687	hypothetical prote
593	5	6.5	182	2	T25340	hypothetical prote	666	5	6.5	199	2	T34610	probable periplasm
594	5	6.5	183	2	T44337	hypothetical prote	667	5	6.5	199	2	F81421	dedA protein - Del
595	5	6.5	183	2	T22183	hypothetical prote	668	5	6.5	200	2	E75428	hypothetical prote
596	5	6.5	183	2	T40915	probable RNA-bind	669	5	6.5	200	2	S64905	probable C-P (carb
597	5	6.5	183	2	T11924	hypothetical prote	670	5	6.5	200	2	D96023	probable NADPH-qui
598	5	6.5	183	2	H98340	C4-dicarboxylate t	671	5	6.5	200	2	B71899	hypothetical prote
599	5	6.5	184	2	C64592	hypothetical prote	672	5	6.5	200	2	B6902	probable NADPH-qui
600	5	6.5	184	2	B87501	TPR domain protein	673	5	6.5	201	2	S74841	hypothetical prote
601	5	6.5	185	2	AG0747	conserved hypotet	674	5	6.5	201	2	AH2231	hypothetical prote
602	5	6.5	185	2	S64035	hypothetical prote	675	5	6.5	201	2	F96705	unknown protein, 7
603	5	6.5	185	2	A70075	hypothetical prote	676	5	6.5	201	2	T44594	alcaligin synthesi
604	5	6.5	185	2	H86835	hypothetical prote	677	5	6.5	201	2	T37602	probable excision-
605	5	6.5	185	2	S76991	hypothetical prote	678	5	6.5	201	2	T22543	hypothetical prote
606	5	6.5	186	1	R5D09E	ribosomal protein	679	5	6.5	202	2	A59099	hypothetical prote
607	5	6.5	186	2	S70886	galactosyl transfe	680	5	6.5	202	2	F87697	conserved hypotet
608	5	6.5	186	2	A44968	surface antigen P2	681	5	6.5	202	2	E84135	NAD(P)H oxidoreduc
609	5	6.5	186	2	AE1850	hypothetical prote	682	5	6.5	203	2	S53708	N-methyl-D-asparta
610	5	6.5	186	2	AE1253	hypothetical prote	683	5	6.5	203	2	AH2428	hypothetical prote
611	5	6.5	186	2	AC1616	hypothetical prote	684	5	6.5	203	2	H82327	MSHA pilin protein
612	5	6.5	186	2	G86492	polymorphic outer	685	5	6.5	203	2	T22537	hypothetical prote
613	5	6.5	187	2	B81441	ribosome recycling	686	5	6.5	204	2	H85539	cytochrome o ubiqu

687	5	6.5	204	2	D90689	cytochrome o ubiqu	760	5	6.5	216	2	H72462	hypothetical prote
688	5	6.5	204	2	C42226	bo-type ubiquinol	761	5	6.5	216	2	E83825	hypothetical prote
689	5	6.5	204	2	C84122	thymidine kinase (	762	5	6.5	217	1	GMBPT4	gene 59 protein -
690	5	6.5	204	2	E69764	hypothetical prote	763	5	6.5	217	2	D97529	probable transport
691	5	6.5	204	2	B82166	conserved hypotet	764	5	6.5	217	2	AB2748	hypothetical prote
692	5	6.5	204	2	T36295	probable transcrip	765	5	6.5	217	2	AB1262	O-methyltransferas
693	5	6.5	204	2	S51232	gibberellin-respon	766	5	6.5	217	2	AD1624	O-methyltransferas
694	5	6.5	205	2	E64369	hypothetical prote	767	5	6.5	217	2	D69271	hypothetical prote
695	5	6.5	205	2	T02662	hlni protein homol	768	5	6.5	217	2	D72851	AcOrf-12 protein -
696	5	6.5	205	2	G81354	hypothetical prote	769	5	6.5	217	2	A70123	conserved hypotet
697	5	6.5	205	2	AI1307	conserved hypotet	770	5	6.5	217	2	H70123	hypothetical prote
698	5	6.5	205	2	T14745	hypothetical prote	771	5	6.5	217	2	T33353	hypothetical prote
699	5	6.5	205	2	D95200	conserved hypotet	772	5	6.5	218	1	S14133	DNA endonuclease (
700	5	6.5	205	2	C98067	hypothetical prote	773	5	6.5	218	2	T21221	hypothetical prote
701	5	6.5	206	2	E68669	transport protein	774	5	6.5	218	2	B28946	glutathione transf
702	5	6.5	206	2	TS0439	probable 60S ribos	775	5	6.5	218	2	S33860	glutathione transf
703	5	6.5	207	2	H72550	probable inorganic	776	5	6.5	218	2	B29231	glutathione transf
704	5	6.5	207	2	T02514	hypothetical prote	777	5	6.5	218	2	G86758	DNA-(apurinic or a
705	5	6.5	207	2	D82951	conserved hypotet	778	5	6.5	218	2	F97021	ABC transporter, p
706	5	6.5	207	2	I55145	neud protein - Bsc	779	5	6.5	218	2	E75389	hypothetical prote
707	5	6.5	208	2	JCS638	pH-sensing regulat	780	5	6.5	218	2	C72747	probable endonucle
708	5	6.5	208	2	T47735	hypothetical prote	781	5	6.5	218	2	AC3537	dipeptide transport
709	5	6.5	208	2	T42545	hypothetical prote	782	5	6.5	219	1	A37243	hemopoietic cell s
710	5	6.5	208	2	C83014	hypothetical prote	783	5	6.5	219	1	A39574	leukocyte antigen
711	5	6.5	208	2	T41555	hypothetical prote	784	5	6.5	219	1	RPECYS	tetracycline repre
712	5	6.5	208	2	AC3620	phenylacetic acid	785	5	6.5	219	2	AE3133	hypothetical prote
713	5	6.5	208	2	AC1853	transcriptional regu	786	5	6.5	219	2	G98154	hypothetical prote
714	5	6.5	209	2	S54133	hypothetical 23.7K	787	5	6.5	219	2	S43107	orf2 protein - Yer
715	5	6.5	209	2	AI1679	conserved hypotet	788	5	6.5	219	2	T33332	hypothetical prote
716	5	6.5	209	2	A85557	enterobactin synth	789	5	6.5	219	2	AG2124	hypothetical prote
717	5	6.5	209	2	F90706	enterochelin synth	790	5	6.5	219	2	B72291	hypothetical prote
718	5	6.5	209	2	E64791	enterobactin synth	791	5	6.5	219	2	G84388	hypothetical prote
719	5	6.5	209	2	E84720	hypothetical prote	792	5	6.5	219	2	F70149	hypothetical prote
720	5	6.5	210	1	S74580	hypothetical prote	793	5	6.5	219	2	F87444	dethiobiotin synth
721	5	6.5	210	2	B40203	4-alpha-glucanotra	794	5	6.5	220	2	AE3215	hypothetical prote
722	5	6.5	210	2	E87252	efflux protein, ly	795	5	6.5	220	2	F89823	hypothetical prote
723	5	6.5	210	2	H81360	probable periplasm	796	5	6.5	220	2	A25513	25K silk protein -
724	5	6.5	210	2	A85985	hypothetical prote	797	5	6.5	220	2	E82381	hypothetical prote
725	5	6.5	210	2	F91139	hypothetical prote	798	5	6.5	220	2	H84447	hypothetical prote
726	5	6.5	210	2	A65112	hypothetical prote	799	5	6.5	220	2	AD0938	hypothetical prote
727	5	6.5	210	2	AB2411	probable methyltra	800	5	6.5	220	2	T71946	hypothetical prote
728	5	6.5	211	2	AB3178	glutathione S-tran	801	5	6.5	220	2	T31184	hypothetical prote
729	5	6.5	211	2	E83089	ATP-phosphoribosyl	802	5	6.5	221	2	H97363	amidotransferase h
730	5	6.5	211	2	I40145	outer surface prot	803	5	6.5	221	2	B85688	hypothetical prote
731	5	6.5	211	2	E85091	hypothetical prote	804	5	6.5	221	2	T31863	hypothetical prote
732	5	6.5	211	2	E82070	transcriptional regu	805	5	6.5	222	2	H90746	arginine 3rd trans
733	5	6.5	211	2	T35272	hypothetical prote	806	5	6.5	222	2	D85597	arginine 3rd trans
734	5	6.5	212	2	F64122	phosphoribosylglyc	807	5	6.5	222	2	E64824	arginine transport
735	5	6.5	212	2	D69361	conserved hypotet	808	5	6.5	222	2	F72572	probable TATA-box
736	5	6.5	212	2	G95905	hypothetical prote	809	5	6.5	222	2	C40745	odorant receptor (
737	5	6.5	212	2	AD1958	hypothetical prote	810	5	6.5	222	2	H71408	probable germin ty
738	5	6.5	212	2	H83305	probable radical a	811	5	6.5	222	2	T27916	hypothetical prote
739	5	6.5	212	2	B69493	hypothetical prote	812	5	6.5	222	2	A70165	NH(3)-dependent NA
740	5	6.5	213	2	B83929	NAD(P)H nitroreduc	813	5	6.5	222	2	F64563	hypothetical prote
741	5	6.5	213	2	AH2815	50S ribosomal prot	814	5	6.5	222	2	I39192	gene HOXA1 protein
742	5	6.5	213	2	C97594	SOS ribosomal prot	815	5	6.5	223	2	C81076	ribose 5-phosphate
743	5	6.5	213	2	S35917	capsid protein VP1	816	5	6.5	223	2	B81867	ribose-5-phosphate
744	5	6.5	214	2	T01370	inorganic diphosph	817	5	6.5	223	2	E90795	probable membrane
745	5	6.5	214	2	C69879	hypothetical prote	818	5	6.5	223	2	C86707	ABC transporter At
746	5	6.5	214	2	B86156	hypothetical prote	819	5	6.5	223	2	AB6906	ABC transporter At
747	5	6.5	215	2	T04421	probable inorganic	820	5	6.5	224	2	AB2428	transcription regu
748	5	6.5	215	2	T49657	related to zinc fi	821	5	6.5	225	2	B72202	endonuclease V - T
749	5	6.5	215	2	T09248	heat shock protein	822	5	6.5	225	2	F87528	hypothetical prote
750	5	6.5	215	2	I52523	nucleoporin p62 no	823	5	6.5	225	2	H83750	H+-transporting tw
751	5	6.5	215	2	T22446	hypothetical prote	824	5	6.5	226	2	F59153	smooth muscle myos
752	5	6.5	216	2	AB2582	glutamine amidotra	825	5	6.5	226	2	I65769	probable two-compo
753	5	6.5	216	2	AB1052	probable hexulose-	826	5	6.5	226	2	G83293	probable two-compo
754	5	6.5	216	2	S56421	Probable hexulose-	827	5	6.5	226	2	G83336	hypothetical prote
755	5	6.5	216	2	D91275	probable hexulose-	828	5	6.5	226	2	AC1868	X-linked lymphocyt
756	5	6.5	216	2	D86116	probable hexulose-	829	5	6.5	226	2	I48880	hypothetical prote
757	5	6.5	216	2	S75186	hypothetical prote	830	5	6.5	226	2	I49392	gene xlr3b protein
758	5	6.5	216	2	F84156	hypothetical prote	831	5	6.5	226	2	E70501	probable transmemb
759	5	6.5	216	2	T06289	hypothetical prote	832	5	6.5	227	2	T13783	cytochrome-c oxida

833	5	6.5	227	2	B90738	probable transcrip	906	5	6.5	241	2	H71686	tolQ protein (tolQ
834	5	6.5	227	2	F85433	hypothetical prote	907	5	6.5	241	2	T05040	modulin-26-like pr
835	5	6.5	227	2	E84403	hypothetical prote	908	5	6.5	241	2	B87337	ada regulatory pro
836	5	6.5	227	2	C85588	probable transcrip	909	5	6.5	242	2	D79229	probable pseudouri
837	5	6.5	227	2	D64816	probable transcrip	910	5	6.5	242	2	T27210	hypothetical prote
838	5	6.5	228	2	D70358	hydrogenase (SC 1.	911	5	6.5	243	1	JQ0021	ubiquinol-cytochro
839	5	6.5	228	2	T15325	hypothetical prote	912	5	6.5	243	2	F69553	enoyl-CoA hydratase
840	5	6.5	228	2	F90130	hypothetical prote	913	5	6.5	243	2	A69480	cobalt transport p
841	5	6.5	228	2	AF0462	probable exported	914	5	6.5	243	2	A70670	hypothetical prote
842	5	6.5	228	2	S46673	hypothetical prote	915	5	6.5	243	2	B82390	conserved hypothet
843	5	6.5	229	2	AB1012	peptidase B [impor	916	5	6.5	243	2	C82393	probable amino aci
844	5	6.5	229	2	A86094	peptidase B [impor	917	5	6.5	243	2	B72757	probable phosphate
845	5	6.5	229	2	D65209	peptidase B. - Esch	918	5	6.5	243	2	B95855	probable transcrip
846	5	6.5	229	2	C91246	peptidase B [impor	919	5	6.5	244	2	T12051	3-oxoacyl-facyl-ca
847	5	6.5	229	2	A36867	alpha-aspartyl dip	920	5	6.5	244	2	F69260	nitrate ABC transp
848	5	6.5	229	2	F69096	hypothetical prote	921	5	6.5	244	2	AE1318	hypothetical prote
849	5	6.5	229	2	A69006	triose-phosphate i	922	5	6.5	244	2	AE1690	hypothetical prote
850	5	6.5	229	2	H83503	hypothetical prote	923	5	6.5	244	2	T15647	hypothetical prote
851	5	6.5	229	2	AF3476	methyltransferase	924	5	6.5	244	2	F82838	conserved hypothet
852	5	6.5	230	2	T41660	Glutathione S-tran	925	5	6.5	244	2	F70754	probable lprA prot
853	5	6.5	230	2	T34892	probable IS elemen	926	5	6.5	244	2	D86725	hypothetical prote
854	5	6.5	230	2	T34854	hypothetical prote	927	5	6.5	244	2	E83478	probable ATP-bindi
855	5	6.5	231	2	D69983	conserved hypothet	928	5	6.5	244	2	F69830	conserved hypothet
856	5	6.5	231	2	T27803	hypothetical prote	929	5	6.5	244	2	AB3609	multidrug resistan
857	5	6.5	232	2	AD2542	hypothetical prote	930	5	6.5	244	2	AC2751	transcription regu
858	5	6.5	232	2	E84108	capsular polysacch	931	5	6.5	244	2	C97532	probable transcrip
859	5	6.5	232	2	T25745	hypothetical prote	932	5	6.5	244	2	AG1823	hypothetical prote
860	5	6.5	232	2	AQ0954	probable membrane	933	5	6.5	245	2	AI3412	ribonuclease III (
861	5	6.5	233	1	PQBPL	replication protei	934	5	6.5	245	2	T36127	probable ribonucle
862	5	6.5	233	2	B91002	phage replication	935	5	6.5	245	2	A48598	kalikrein-like se
863	5	6.5	233	2	B85847	hypothetical prote	936	5	6.5	245	2	AG3346	LSU ribosomal prot
864	5	6.5	233	2	F85639	hypothetical prote	937	5	6.5	245	2	I51323	proteolipid protei
865	5	6.5	233	2	D90830	replication protei	938	5	6.5	245	2	D75386	uridylylate kinase -
866	5	6.5	233	2	B75100	glycosyltransferas	939	5	6.5	245	2	G81032	DNA polymerase, ba
867	5	6.5	233	2	S62063	H+-exporting ATPas	940	5	6.5	245	2	D81977	hypothetical prote
868	5	6.5	233	2	D86333	T20H2.22 protein -	941	5	6.5	245	2	A85656	hypothetical prote
869	5	6.5	233	2	AF0110	probable hemolysin	942	5	6.5	246	2	AI0399	tRNA (guanine-N1-)
870	5	6.5	233	2	G70793	hypothetical prote	943	5	6.5	246	2	E89884	hypothetical prote
871	5	6.5	233	2	T22977	hypothetical prote	944	5	6.5	246	2	A81679	conserved hypothet
872	5	6.5	233	2	AI2442	hypothetical prote	945	5	6.5	246	2	B72771	hypothetical prote
873	5	6.5	234	1	G69024	pheromone shutdown	946	5	6.5	246	2	T50987	related to prefold
874	5	6.5	234	2	C83097	InaA protein PA37	947	5	6.5	246	2	H87427	hypothetical prote
875	5	6.5	234	2	T11925	hypothetical prote	948	5	6.5	246	2	T20792	hypothetical prote
876	5	6.5	235	2	AB1570	hypothetical prote	949	5	6.5	246	2	AH3072	transcription regu
877	5	6.5	236	2	F70543	hypothetical prote	950	5	6.5	246	2	A72260	ABC transporter, A
878	5	6.5	237	1	CYRPEE	peptidylprolyl iso	951	5	6.5	247	1	LNRBPS	pulmonary surfacta
879	5	6.5	237	2	AD3474	transporter BME117	952	5	6.5	247	2	T22109	hypothetical prote
880	5	6.5	238	2	T44706	ribonuclease III (	953	5	6.5	247	2	T06721	hypothetical prote
881	5	6.5	238	2	S77699	inner cell wall ma	954	5	6.5	247	2	G64341	hypothetical prote
882	5	6.5	238	2	D83141	probable two-compo	955	5	6.5	247	2	F90510	conserved hypothet
883	5	6.5	238	2	E64416	hypothetical prote	956	5	6.5	247	2	T27205	hypothetical prote
884	5	6.5	238	2	T31218	hypothetical prote	957	5	6.5	247	2	A98009	sortase [imported]
885	5	6.5	238	2	H95105	pilin gene inverti	958	5	6.5	248	2	A86276	F7A19_31 protein -
886	5	6.5	238	2	B95395	protein [imported	959	5	6.5	248	2	B30125	tropomyosin 1, fib
887	5	6.5	238	2	AE2850	peptidyl tRNA hydr	960	5	6.5	248	2	AF0775	probable gntR-fami
888	5	6.5	239	2	I39845	orotidine-5'-phosp	961	5	6.5	248	2	A98143	response regulator
889	5	6.5	239	2	C64188	arginine binding p	962	5	6.5	248	2	AB3145	two component resp
890	5	6.5	239	2	E64961	probable transcrip	963	5	6.5	248	2	F75492	hypothetical prote
891	5	6.5	239	2	B85815	probable 2-compone	964	5	6.5	248	2	AH2339	hypothetical prote
892	5	6.5	239	2	C90967	probable 2-compone	965	5	6.5	248	2	E69505	cytochrome oxidase
893	5	6.5	239	2	C75010	hypothetical prote	966	5	6.5	249	2	G81218	bioH protein, prob
894	5	6.5	239	2	H90516	ABC transporter pe	967	5	6.5	249	2	T20790	hypothetical prote
895	5	6.5	239	2	T36206	hypothetical prote	968	5	6.5	249	2	B84147	ABC transporter (p
896	5	6.5	240	1	Z1ZMD1	19K zein precursor	969	5	6.5	249	2	AG3485	homoserine/homoser
897	5	6.5	240	2	AI2681	oxidoreductase Atu	970	5	6.5	249	4	T41231	wtf protein pseudo
898	5	6.5	240	2	E70748	probable rnc prote	971	5	6.5	250	2	H85577	phosphoglyceromuta
899	5	6.5	240	2	D82288	NADPH-flavin oxido	972	5	6.5	250	2	G90726	phosphoglyceromuta
900	5	6.5	240	2	E70362	UMP kinase - Aquif	973	5	6.5	250	2	AB0594	phosphoglycerate m
901	5	6.5	240	2	S75017	hypothetical prote	974	5	6.5	250	2	C64811	phosphoglycerate m
902	5	6.5	240	2	E87110	ribonuclease HII (	975	5	6.5	250	2	AE0139	phosphoglycerate m
903	5	6.5	240	2	C86194	hypothetical prote	976	5	6.5	250	2	G81365	probable ABC-type
904	5	6.5	240	2	AG1083	hypothetical prote	977	5	6.5	250	2	AD0240	probable IS100 tra
905	5	6.5	241	2	F97752	tolQ protein (impo	978	5	6.5	250	2	H97448	hemolysin (impor

979	5	6.5	250	2	AB2667	hemolysin [importe	1052	5	6.5	260	2	AB0031	insertion sequence
980	5	6.5	250	2	C97812	hypothetical prote	1053	5	6.5	260	2	AH0078	insertion sequence
981	5	6.5	250	2	AB1555	ABC transporter tr	1054	5	6.5	260	2	AI0197	insertion sequence
982	5	6.5	250	2	AD1197	2,3-dihydro-2,3-di	1055	5	6.5	260	2	AF0036	insertion sequence
983	5	6.5	251	2	AH0575	hypothetical prote	1056	5	6.5	260	2	AF0065	insertion sequence
984	5	6.5	251	2	E83885	hypothetical prote	1057	5	6.5	260	2	AC0395	insertion sequence
985	5	6.5	251	2	T15307	hypothetical prote	1058	5	6.5	260	2	AH0047	insertion sequence
986	5	6.5	251	2	C97627	stage v sporulatio	1059	5	6.5	260	2	AC0185	insertion sequence
987	5	6.5	251	2	D69861	RNA polymerase sig	1060	5	6.5	260	2	AD0450	insertion sequence
988	5	6.5	252	2	E81155	conserved hypothet	1061	5	6.5	260	2	AF0254	insertion sequence
989	5	6.5	252	2	F81949	probable RNA-bind	1062	5	6.5	260	2	AE0174	insertion sequence
990	5	6.5	252	2	T17772	hypothetical prote	1063	5	6.5	260	2	AC0070	insertion sequence
991	5	6.5	252	2	B89785	hypothetical prote	1064	5	6.5	260	2	AH0231	insertion sequence
992	5	6.5	252	2	A96549	hypothetical prote	1065	5	6.5	260	2	AH0436	insertion sequence
993	5	6.5	253	2	H65219	pyrrolidine-5-carbox	1066	5	6.5	260	2	AE0124	insertion sequence
994	5	6.5	253	2	C82675	ubiquinone/menaqui	1067	5	6.5	260	2	AC0139	insertion sequence
995	5	6.5	253	2	T50900	photosynthetic rea	1068	5	6.5	260	2	AE0113	insertion sequence
996	5	6.5	253	2	S70170	motA protein - Rho	1069	5	6.5	260	2	AE0459	insertion sequence
997	5	6.5	253	2	AG2920	precorrin-3B C17-m	1070	5	6.5	260	2	AC0206	insertion sequence
998	5	6.5	253	2	H97694	precorrin-3B C17-m	1071	5	6.5	260	2	AE0133	insertion sequence
999	5	6.5	253	2	AH3106	conserved hypothet	1072	5	6.5	260	2	AI0095	insertion sequence
1000	5	6.5	254	1	A72396	L-fucose-phosphat	1073	5	6.5	260	2	AH0389	insertion sequence
1001	5	6.5	254	2	F64583	dihydrodipicolinat	1074	5	6.5	260	2	AF0307	insertion sequence
1002	5	6.5	254	2	B69255	polysaccharide ABC	1075	5	6.5	260	2	AB0332	insertion sequence
1003	5	6.5	254	2	B72549	hypothetical prote	1076	5	6.5	260	2	AD0322	insertion sequence
1004	5	6.5	254	2	T31228	trbC protein homol	1077	5	6.5	260	2	AF0292	insertion sequence
1005	5	6.5	254	2	T04067	hypothetical prote	1078	5	6.5	260	2	AG0004	insertion sequence
1006	5	6.5	254	2	S47698	nkd protein - Esc	1079	5	6.5	260	2	AE0101	insertion sequence
1007	5	6.5	254	2	B91172	ATP-binding protei	1080	5	6.5	260	2	AB0247	insertion sequence
1008	5	6.5	254	2	B86018	hypothetical prote	1081	5	6.5	260	2	AB0211	insertion sequence
1009	5	6.5	255	1	RHRTT	thyloliberin precu	1082	5	6.5	260	2	AD0342	insertion sequence
1010	5	6.5	255	2	T23488	hypothetical prote	1083	5	6.5	260	2	AI0398	insertion sequence
1011	5	6.5	255	2	AB0523	probable transcrip	1084	5	6.5	260	2	AI0487	insertion sequence
1012	5	6.5	255	2	H83464	flagellar biosynth	1085	5	6.5	260	2	AG0213	insertion sequence
1013	5	6.5	255	2	T24364	hypothetical prote	1086	5	6.5	260	2	AE0457	insertion sequence
1014	5	6.5	255	2	B87485	conserved hypothet	1087	5	6.5	260	2	AE0288	insertion sequence
1015	5	6.5	255	2	T03299	expansin 3 - rice	1088	5	6.5	260	2	AH0430	insertion sequence
1016	5	6.5	255	2	A70758	hypothetical prote	1089	5	6.5	260	2	AH0012	insertion sequence
1017	5	6.5	255	2	C75527	conserved hypothet	1090	5	6.5	260	2	AI0021	insertion sequence
1018	5	6.5	255	2	AH2479	transcription regu	1091	5	6.5	260	2	AF0163	insertion sequence
1019	5	6.5	256	1	S20713	alcohol dehydrogen	1092	5	6.5	260	2	AE0265	insertion sequence
1020	5	6.5	256	1	RTWST	thyloliberin precu	1093	5	6.5	260	2	AE0417	insertion sequence
1021	5	6.5	256	2	B32393	T-cell antigen 4-1	1094	5	6.5	260	2	AE0438	hypothetical prote
1022	5	6.5	256	2	B85505	unknown [imported]	1095	5	6.5	260	2	JT0371	Resolvase (protein
1023	5	6.5	256	2	F90654	probable biotin sy	1096	5	6.5	261	2	A82224	cobalamin 5'-phosp
1024	5	6.5	256	2	C90443	hypothetical prote	1097	5	6.5	261	2	I64249	hypothetical prote
1025	5	6.5	256	2	C83474	hypothetical prote	1098	5	6.5	261	2	C69536	hypothetical prote
1026	5	6.5	257	2	T35018	protocatechuate 3,	1099	5	6.5	261	2	T43579	type III secretion
1027	5	6.5	257	2	H97522	hypothetical prote	1100	5	6.5	261	2	T16650	hypothetical prote
1028	5	6.5	257	2	AI2741	conserved hypothet	1101	5	6.5	261	2	G84376	hypothetical prote
1029	5	6.5	257	2	S53365	protein-methionine	1102	5	6.5	261	2	G86880	hypothetical prote
1030	5	6.5	257	2	D95161	hypothetical prote	1103	5	6.5	261	2	T32562	hypothetical prote
1031	5	6.5	257	2	C98027	hypothetical prote	1104	5	6.5	261	2	T95991	probable sugar upt
1032	5	6.5	257	2	C82904	rRNA methylase Uu3	1105	5	6.5	262	2	T24439	hypothetical prote
1033	5	6.5	257	2	B88700	protein K02B2.3 [i	1106	5	6.5	262	2	T11883	cytochrome-c oxida
1034	5	6.5	257	2	C69870	conserved hypothet	1107	5	6.5	262	2	I64139	hypothetical prote
1035	5	6.5	257	2	AF2358	UDP-N-acetyl-D-man	1108	5	6.5	262	2	G82959	hypothetical prote
1036	5	6.5	258	2	A95945	probable oxidoredu	1109	5	6.5	262	2	G02476	lysosomal-associat
1037	5	6.5	258	2	D83190	UDP-N-acetylglucos	1110	5	6.5	262	2	H84152	hypothetical prote
1038	5	6.5	258	2	AF3165	exodeoxyribonuclea	1111	5	6.5	262	2	E97151	ABC transported MD
1039	5	6.5	258	2	T40850	hypothetical wtf p	1112	5	6.5	262	2	H72107	peptide ABC transp
1040	5	6.5	258	2	T08265	conserved hypothet	1113	5	6.5	262	2	G86516	oligopeptide trans
1041	5	6.5	258	2	E87615	ThiJ/PfpI family p	1114	5	6.5	262	2	B71721	probable signal pe
1042	5	6.5	259	1	DEECSP	sorbitol-6-phosphat	1115	5	6.5	264	2	C72080	N-acetylmuramoyl-L
1043	5	6.5	259	2	AF0844	sorbitol-6-phosphat	1116	5	6.5	264	2	G86542	probable ABC-type
1044	5	6.5	259	2	H85918	glucitol (sorbitol	1117	5	6.5	264	2	T36315	probable ABC-type
1045	5	6.5	259	2	A98074	glucitol (sorbitol	1118	5	6.5	264	2	G90695	probable ligase [i
1046	5	6.5	259	2	T08743	probable isocitrat	1119	5	6.5	264	2	C85546	probable ligase yb
1047	5	6.5	259	2	H97708	hypothetical prote	1120	5	6.5	264	2	A64779	yvap protein - Esc
1048	5	6.5	259	2	A70408	phosphatidate_cyt	1121	5	6.5	264	2	B71448	hypothetical prote
1049	5	6.5	259	2	T18151	hypothetical prote	1122	5	6.5	264	2	T13116	proteins gp30 - pha
1050	5	6.5	259	2	C82148	conserved hypothet	1123	5	6.5	264	2	AD0034	probable type III
1051	5	6.5	260	2	T14971	probable transposa	1124	5	6.5	264	2	AG3175	hypothetical prote

1125	5	6.5	264	2	D71037	hypotheical prote	1198	5	6.5	274	2	B89795	hypotheical prote
1126	5	6.5	265	1	BVEG17	1atB protein - Esc	1199	5	6.5	275	2	JC7604	CD86 spliced varia
1127	5	6.5	265	2	A89880	hypotheical prote	1200	5	6.5	275	2	D98180	hypotheical prote
1128	5	6.5	265	2	T23216	hypotheical prote	1201	5	6.5	275	2	D83910	hypotheical prote
1129	5	6.5	265	2	AH0755	conserved hypotet	1202	5	6.5	275	2	C82752	hypotheical prote
1130	5	6.5	265	2	F84071	hypotheical prote	1203	5	6.5	275	2	S03967	intercellular adhe
1131	5	6.5	266	2	H69468	lysophospholipase	1204	5	6.5	276	2	T16765	hypotheical prote
1132	5	6.5	266	2	D97719	signal peptidase I	1205	5	6.5	276	2	E89914	hypotheical prote
1133	5	6.5	266	2	C87367	flagellar biosynth	1206	5	6.5	276	2	A95881	probable trahalose
1134	5	6.5	266	2	T41094	very hypotheical	1207	5	6.5	276	2	C75414	hypotheical prote
1135	5	6.5	266	2	T46533	hypotheical prote	1208	5	6.5	277	2	G75518	probable beta-lact
1136	5	6.5	266	2	T33411	hypotheical prote	1209	5	6.5	277	2	AC2967	hypotheical prote
1137	5	6.5	266	2	C87497	hypotheical prote	1210	5	6.5	277	2	H87213	conserved hypotet
1138	5	6.5	267	2	E81431	ABC transporter in	1211	5	6.5	277	2	E85356	hypotheical prote
1139	5	6.5	267	2	D83313	probable permease	1212	5	6.5	277	2	E82400	hemin ABC transpor
1140	5	6.5	267	2	AE1204	B. subtilis Yoar p	1213	5	6.5	277	2	T39538	probable superoxid
1141	5	6.5	267	2	AD1561	B. subtilis Yoar p	1214	5	6.5	277	2	T27275	hypotheical prote
1142	5	6.5	267	2	D72499	hypotheical prote	1215	5	6.5	277	2	A46510	intercellular adhe
1143	5	6.5	267	2	F97041	hypotheical prote	1216	5	6.5	277	2	C90077	conserved hypotet
1144	5	6.5	267	2	AB2472	hypotheical prote	1217	5	6.5	278	2	IS8150	membrane glycoprot
1145	5	6.5	267	2	S77802	hypotheical prote	1218	5	6.5	278	2	IS1324	proteolipid protei
1146	5	6.5	267	2	B64644	hypotheical prote	1219	5	6.5	278	2	E98118	hypotheical prote
1147	5	6.5	268	2	S07557	cytochrome-c oxida	1220	5	6.5	278	2	D83080	hypotheical prote
1148	5	6.5	268	2	B42424	chitinase [EC 3.2.	1221	5	6.5	278	2	AG0247	probable binding-p
1149	5	6.5	268	2	E71329	probable glutamate	1222	5	6.5	279	2	T04707	L-ascorbate peroxi
1150	5	6.5	268	2	D82888	tryptophan synthas	1223	5	6.5	279	2	B89849	prolipoprotein dia
1151	5	6.5	268	2	S45062	vegetative storage	1224	5	6.5	279	2	F86842	prephenate dehydra
1152	5	6.5	268	2	G90018	conserved hypotet	1225	5	6.5	279	2	S76201	hypotheical prote
1153	5	6.5	268	2	T46755	membrane protein a	1226	5	6.5	279	2	S75552	hypotheical prote
1154	5	6.5	268	2	G95253	zinc ABC transport	1227	5	6.5	279	2	H83504	hypotheical prote
1155	5	6.5	268	2	C90516	esterase/lipase 1	1228	5	6.5	279	2	G72637	hypotheical prote
1156	5	6.5	269	1	WMBE54	UL24 protein - hum	1229	5	6.5	279	2	AC2164	glycosyltransferas
1157	5	6.5	269	2	S32427	prepilin peptidase	1230	5	6.5	280	2	T36066	hypotheical prote
1158	5	6.5	269	2	G87271	triose-phosphate i	1231	5	6.5	280	2	C64471	hypotheical prote
1159	5	6.5	269	2	H70179	spermidine/putresc	1232	5	6.5	280	2	F70805	hypotheical prote
1160	5	6.5	269	2	AH1175	spermidine/putresc	1233	5	6.5	280	2	C70896	probable transport
1161	5	6.5	269	2	AF1532	spermidine/putresc	1234	5	6.5	280	2	F84765	hypotheical prote
1162	5	6.5	269	2	T41611	hypotheical repea	1235	5	6.5	280	2	E98242	hypotheical trans
1163	5	6.5	269	2	G91169	probable acyltrans	1236	5	6.5	281	2	C69588	L-arabinose transp
1164	5	6.5	269	2	C70142	hypotheical prote	1237	5	6.5	281	2	S60477	1-acetylgllycerol-3-p
1165	5	6.5	269	2	T49240	hypotheical prote	1238	5	6.5	281	2	AF2161	cation-efflux syst
1166	5	6.5	270	2	C87068	tryptophan synthas	1239	5	6.5	282	2	B93159	prephenate dehydra
1167	5	6.5	270	2	C70557	probable trpA prot	1240	5	6.5	282	2	B98025	prephenate dehydra
1168	5	6.5	270	2	A03088	triosephosphate is	1241	5	6.5	282	2	B84984	geranyltransferrin
1169	5	6.5	270	2	E72543	probable ABC trans	1242	5	6.5	282	2	D70149	hypotheical prote
1170	5	6.5	270	2	AE3627	maltose transport	1243	5	6.5	282	2	S01072	hypotheical prote
1171	5	6.5	270	2	H83619	hypotheical prote	1244	5	6.5	283	2	F82779	hypotheical prote
1172	5	6.5	270	2	F96675	T23K8.8 [imported]	1245	5	6.5	283	2	AI3027	transcription regu
1173	5	6.5	270	2	AF3088	serine/threonine p	1246	5	6.5	283	2	B98257	lysr-type transcri
1174	5	6.5	271	2	AC2270	hypotheical prote	1247	5	6.5	284	1	RGECH	RNA polymerase sig
1175	5	6.5	271	2	G97463	probable oxidoredu	1248	5	6.5	284	2	F91167	RNA polymerase sig
1176	5	6.5	271	2	A36893	transcription acti	1249	5	6.5	284	2	P86013	RNA polymerase sig
1177	5	6.5	271	2	T36885	probable membrane	1250	5	6.5	284	2	S60166	transcription init
1178	5	6.5	271	2	AG0315	conserved hypotet	1251	5	6.5	284	2	H86515	oligopeptide perme
1179	5	6.5	271	2	H90394	probable cation tr	1252	5	6.5	284	2	F72107	peptide ABC transp
1180	5	6.5	271	2	E80266	conserved hypotet	1253	5	6.5	284	2	AF3531	high-affinity zinc
1181	5	6.5	271	2	T31314	hypotheical prote	1254	5	6.5	285	1	YQEC88	fimbrial adhesin K
1182	5	6.5	272	2	E97451	hypotheical prote	1255	5	6.5	285	2	AE0966	probable PMS syste
1183	5	6.5	272	2	AG2569	enoyl-(acyl)-carrie	1256	5	6.5	285	2	D90500	hypotheical prote
1184	5	6.5	272	2	E64182	cysZ protein - Hae	1257	5	6.5	285	2	S31708	alginate poly(ManA)
1185	5	6.5	272	2	G91202	hypotheical prote	1258	5	6.5	285	2	AB0106	probable lipoprote
1186	5	6.5	272	2	T18915	hypotheical prote	1259	5	6.5	285	2	H85356	hypotheical prote
1187	5	6.5	272	2	B86049	hypotheical prote	1260	5	6.5	285	2	S69312	probable membrane
1188	5	6.5	273	2	H86904	hypotheical prote	1261	5	6.5	286	2	AF2829	hydrolase [importe
1189	5	6.5	273	2	E90516	esterase/lipase 1	1262	5	6.5	286	2	AE2677	ABC transporter, m
1190	5	6.5	273	2	D90516	esterase/lipase 1	1263	5	6.5	286	2	C97459	sulfate ABC transp
1191	5	6.5	273	2	G86015	hypotheical prote	1264	5	6.5	286	2	B70833	carbon-monoxide de
1192	5	6.5	273	2	A83143	probable ethanolam	1265	5	6.5	286	2	B42709	DNA restriction en
1193	5	6.5	273	2	E70742	hypotheical prote	1266	5	6.5	286	2	T33500	hypotheical prote
1194	5	6.5	274	1	DCASOE	orotidine-5'-phosp	1267	5	6.5	286	2	D86163	FltK9.19 protein -
1195	5	6.5	274	2	S22308	type II site-speci	1268	5	6.5	286	2	JS0384	hypotheical 30.5k
1196	5	6.5	274	2	E87456	sterol desaturase	1269	5	6.5	286	2	H89003	protein T24A6.5 [i
1197	5	6.5	274	2	T25783	hypotheical prote	1270	5	6.5	286	2	G90462	ABC transporter, p

1271	287	2	G85859	ferredoxin-type pr	1344	5	6.5	297	2	T40173	probable transcrip
1272	287	2	E91015	ferredoxin-type pr	1345	5	6.5	297	2	G87363	metallo-beta-lacta
1273	287	2	B64990	ferredoxin-type pr	1346	5	6.5	297	2	AC1706	hypothetical prote
1274	287	2	G81662	conserved hypotet	1347	5	6.5	297	2	AD1335	hypothetical prote
1275	287	2	G89766	conserved hypotet	1348	5	6.5	297	2	E97646	ABC transporter (p
1276	287	2	H90674	hypothetical prote	1349	5	6.5	298	2	B83553	probable 3-hydroxy
1277	287	2	D90540	glucokinase (gluco	1350	5	6.5	298	2	A69623	flagellar hook-ass
1278	287	2	G86728	alpha-subuni L-ser	1351	5	6.5	298	2	T33220	hypothetical prote
1279	287	2	A86764	hypothetical prote	1352	5	6.5	298	2	AC0166	probable membrane
1280	287	2	H70923	probable hg transp	1353	5	6.5	298	2	T71024	hypothetical prote
1281	287	2	C85525	hypothetical prote	1354	5	6.5	298	2	E83836	reductase BH1493 [
1282	287	2	G64758	yaHE protein - Esc	1355	5	6.5	298	2	E97032	probable permease
1283	287	2	S58648	hypothetical prote	1356	5	6.5	298	2	G89927	hypothetical prote
1284	288	2	C64450	ATP phosphoribosyl	1357	5	6.5	299	2	F97682	diaminopimelate ep
1285	288	2	T51595	phosphate transpor	1358	5	6.5	299	2	G97980	GTPase/GTP-binding
1286	288	2	D83954	hypothetical prote	1359	5	6.5	299	2	A95112	GTP-binding protei
1287	288	2	T04671	hypothetical prote	1360	5	6.5	299	2	E96012	probable sugar upt
1288	288	2	F71504	hypothetical prote	1361	5	6.5	299	2	AB0609	probable membrane
1289	288	2	D71652	hypothetical prote	1362	5	6.5	299	2	H85599	probable surface p
1290	288	2	T32212	hypothetical prote	1363	5	6.5	299	2	H90748	probable surface p
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1292	289	2	AG3260	exodeoxyribonuclea	1365	5	6.5	299	2	T21685	hypothetical prote
1293	289	2	A43562	homeotic protein H	1366	5	6.5	300	2	A64580	site-specific DNA-
1294	289	2	H98315	thug protein (AF17	1367	5	6.5	300	2	T36768	secreted serine pr
1295	289	2	T48108	hypothetical prote	1368	5	6.5	300	2	A10486	dipeptide transpor
1296	289	2	AC0183	probable LysR-famI	1369	5	6.5	300	2	A84111	sugar transport sy
1297	289	2	A81779	hypothetical lysin	1370	5	6.5	300	2	F81799	hypothetical integ
1298	289	2	C81203	conserved hypotet	1371	5	6.5	300	2	G81069	conserved hypotet
1299	289	2	H69645	myo-inositol catab	1372	5	6.5	300	2	T15690	hypothetical prote
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1301	289	2	G70336	hypothetical prote	1374	5	6.5	300	2	AE0970	probable regulator
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1305	290	2	AD0367	probable sugar kin	1378	5	6.5	301	2	H75470	histone deacetylase
1306	290	2	H97791	hypothetical prote	1379	5	6.5	301	2	T40593	cytoplasmic dynein
1307	290	2	B95926	probable amino aci	1380	5	6.5	301	2	T25741	hypothetical prote
1308	291	2	E69777	transcription regu	1381	5	6.5	301	2	H89927	hypothetical prote
1309	291	2	A82017	lipic acid synthe	1382	5	6.5	301	2	A98214	hypothetical prote
1310	291	2	A96973	probable phosphate	1383	5	6.5	301	2	A70039	ABC transporter (A
1311	291	2	T27534	hypothetical prote	1384	5	6.5	302	2	T36903	probable dihydropi
1312	291	2	AC2870	ABC transporter, m	1385	5	6.5	302	2	G90078	hypothetical prote
1313	292	2	A95163	hypothetical prote	1386	5	6.5	302	2	AB0416	nicotinate-nucleot
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1315	292	2	S76003	hypothetical prote	1388	5	6.5	302	2	AH3108	conserved hypotet
1316	292	2	G97111	uncharacterized st	1389	5	6.5	302	2	G86920	probable integral
1317	292	2	T77525	prolactin receptor	1390	5	6.5	302	2	C96531	hypothetical prote
1318	293	2	C82938	phosphotransacetyl	1391	5	6.5	302	2	B82968	probable transcrip
1319	293	2	S75355	probable [acyl-car	1392	5	6.5	302	2	AC2018	hypothetical prote
1320	293	2	B64339	spermidine synthas	1393	5	6.5	303	1	P3BVAM	3a protein - brome
1321	293	2	H82184	glycerol-3-phospha	1394	5	6.5	303	1	H71246	hypothetical prote
1322	293	2	D69355	hypothetical prote	1395	5	6.5	303	2	C97904	phosphotransferase
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1324	293	2	T51262	hypothetical prote	1397	5	6.5	303	2	T32658	hypothetical prote
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1326	294	1	MUSNM1	lysozyme (BC 3.2.1	1399	5	6.5	303	2	I77524	prolactin receptor
1327	294	2	T11379	NADH2 dehydrogenas	1400	5	6.5	304	2	D86998	probable secreted
1328	294	2	D96542	probable pirin [im	1401	5	6.5	304	2	B86641	hypothetical prote
1329	294	2	D85036	hypothetical prote	1402	5	6.5	305	2	T50474	GTP-binding regula
1330	294	2	T22058	hypothetical prote	1403	5	6.5	305	2	T03558	ribose transport A
1331	294	2	A96707	hypothetical prote	1404	5	6.5	305	2	T36056	hypothetical prote
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1333	295	2	D82170	peptide ABC transp	1406	5	6.5	305	2	H81257	hypothetical prote
1334	295	2	AD3577	sugar transport sy	1407	5	6.5	305	2	D98198	hypothetical prote
1335	295	2	D75010	UDP-N-acetylglucos	1408	5	6.5	306	2	JC1120	sdsB protein - Pse
1336	295	2	F86809	hypothetical prote	1409	5	6.5	306	2	F83348	probable transcrip
1337	295	2	AD0306	probable membrane	1410	5	6.5	306	2	S73876	protein prrB homol
1338	296	2	AB0210	probable ABC sugar	1411	5	6.5	307	2	D86194	hypothetical prote
1339	296	2	H87554	ROK family protein	1412	5	6.5	307	2	B95417	probable ABC trans
1340	296	2	H83157	conserved hypotet	1413	5	6.5	307	2	F83339	probable transcrip
1341	296	2	F87411	hypothetical prote	1414	5	6.5	307	2	G82385	hypothetical prote
1342	296	2	C95961	probable sugar upt	1415	5	6.5	307	2	B86965	probable pyridoxin
1343	297	1	XRBY	ATP phosphoribosyl	1416	5	6.5	307	2	B90303	conserved hypotet

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1490 5 6.5 317 2 T28277  
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 1498 5 6.5 318 2 A32816  
 1499 5 6.5 318 2 H71406  
 1500 5 6.5 318 2 B95883

## ALIGNMENTS

## RESULT 1

## WQSCFP

L-fucose permease - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004

C;Accession: J0184; C33495; S49565; E65062

R;Lu, Z.; Lin, E.C.C.

Nucleic Acids Res. 17, 4883-4884, 1989

A;Title: The nucleotide sequence of Escherichia coli genes for L-fucose dissimilation.

A;Reference number: S04702; MUID:89315234; PMID:2664711

A;Accession: J0184

A;Molecule type: DNA

A;Residues: 1-438 <L>

A;Cross-references: UNIPROT:P11551; EMBL:X15025; NID:g41501; PIDN:CAA33126.1; PID:g41504

X;Chen, Y.M.; Lu, Z.; Lin, E.C.C.

J. Bacteriol. 171, 6097-6105, 1989

A;Title: Constitutive activation of the fucAO operon and silencing of the divergently transcribed genes

A;Reference number: A33495; MUID:90036697; PMID:2553671

A;Accession: C33495

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-31 <CHE>

A;Cross-references: GB:M31059; NID:g146040; PIDN:AAA23822.1; PID:g146041

R;Gunn, P.J.; Tate, C.G.; Henderson, P.J.F.

Mol. Microbiol. 12, 799-809, 1994

A;Title: Identification of a novel sugar-H(+) symport protein, FucP, for transport of L-fucose

A;Reference number: S49564; MUID:94328931; PMID:8052131

A;Accession: S49565

A;Molecule type: protein

A;Residues: 2-21 <GUN>

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: E65062

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-438 <BLAT>

A;Cross-references: GB:AE000364; GB:U00096; NID:G2367162; PIDN:AAC75843.1; PID:g1789166;

A;Experimental source: strain K-12, substrain MGL1655

C;Genetics:

A;Gene: fucP

A;Map position: 60 min

C;Function:

A;Description: this protein is a permease involved in an inducible catabolic pathway for L-fucose  
 C;Superfamily: fucose permease  
 C;Keywords: L-fucose catabolism; L-fucose utilization; transmembrane protein

Query Match 10.4%; Score 8; DB 1; Length 438;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAP 34

DB 353 ALTLCSAF 360

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RESULT 2
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <STO>
A:Cross-references: UNIPROT:Q8X6R7; GB:AE005174; NID:g12517280; PIDN:AAG57915.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Accession: A10862
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: A10862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02801.1; PID:g16504055; GSPDB:GN00176
C:Genetics:
C:Superfamily: fucose permease

Query Match 10.4%; Score 8; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAF 34
Db 353 ALTLCSAF 360

RESULT 3
E91086
fucose permease [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E91086
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Iihii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <HAY>
A:Cross-references: UNIPROT:Q8X6R7; GB:BA000007; PIDN:BA037084.1; PID:g13363133; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
C:Superfamily: fucose permease

Query Match 10.4%; Score 8; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAF 34
Db 353 ALTLCSAF 360

RESULT 4
G85931
fucose permease [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85931
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, U.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001

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A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <STO>
A:Cross-references: UNIPROT:Q8X6R7; GB:AE005174; NID:g12517280; PIDN:AAG57915.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
C:Superfamily: fucose permease

Query Match 10.4%; Score 8; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAF 34
Db 353 ALTLCSAF 360

RESULT 5
A86643
hypothetical protein ybeH [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86643
R:Polotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: A86643
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-183 <STO>
A:Cross-references: UNIPROT:Q9CJ61; GB:AE005176; PID:g12722994; PIDN:AAK04243.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
C:Gene: ybeH

Query Match 9.1%; Score 7; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 IATIMVL 23
Db 17 IATIMVL 23

RESULT 6
D86856
hypothetical protein ytcA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86856
R:Polotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86856
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: UNIPROT:Q9CEI9; GB:AE005176; PID:g12724883; PIDN:AAK05950.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
C:Gene: ytcA

Query Match 9.1%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 IATIMVL 23

```

Db 28 IATIMVL 34  
|||||

RESULT 7  
A:0970  
probable TetR-family transcription regulator STY4062 [imported] - Salmonella enterica subsp. enterica serovar Typhi  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: A10970  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: A10970  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-198 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD03261.1; PID:g16504882; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY4062  
C:Superfamily: hypothetical protein HI0955

Query Match 9.1%; Score 7; DB 2; Length 198;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ILQSLAL 53  
|||||

Db 15 ILQSLAL 21  
|||||

RESULT 8  
D91193  
probable transcription regulator [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
A:Accession: D91193  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands  
A:Reference number: A95629; MUID:21156231; PMID:11258796  
A:Accession: D91193  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-212 <HAY>  
A:Cross-references: UNIPROT:Q8X580; GB:BA000007; PIDN:BA037939.1; PID:g133363991; GSPDB:G  
A:Experimental source: Strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs4516  
C:Superfamily: hypothetical protein HI0955

Query Match 9.1%; Score 7; DB 2; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ILQSLAL 53  
|||||

Db 29 ILQSLAL 35  
|||||

RESULT 9  
E86040  
probable transcription regulator ttk [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
A:Accession: E86040  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisia, K.; Apodaca, Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: E86040  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-212 <STO>  
A:Cross-references: UNIPROT:Q8X580; GB:AE005174; NID:g12518397; PIDN:AGS8785.1; GSPDB:G  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ttk  
C:Superfamily: hypothetical protein HI0955

Query Match 9.1%; Score 7; DB 2; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ILQSLAL 53  
|||||

Db 29 ILQSLAL 35  
|||||

RESULT 10  
C65165  
tkk protein - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
A:Accession: C65165; S07954; B05110  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pefna, N.T.; Burland, V.; Riley, M.; Col A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: C65165  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-212 <BLAT>  
A:Cross-references: UNIPROT:Q8X580; GB:AE000441; GB:U00096; NID:g1790063; PIDN:AAC76665.1  
A:Experimental source: strain K-12, substrain MG1655  
R:Lundberg, L.G.; Thoresson, H.O.; Karlstrom, O.H.; Nyman, P.O.  
EMBO J. 2, 967-971, 1983  
A:Title: Nucleotide sequence of the structural gene for dUTPase of Escherichia coli K-12  
A:Reference number: A30388; MUID:84057777; PMID:6139280  
A:Accession: S07954  
A:Molecule type: DNA  
A:Residues: 15-209, 'SCSNMTPDDFSSGEFL' <LUN>  
A:Cross-references: EMBL:V01578; NID:g41299; PIDN:CAA24898.1; PID:g41301  
R:Poulsen, P.; Jensen, K.P.; Valentini-Hansen, P.; Carlsson, P.; Lundberg, L.G.  
Eur. J. Biochem. 135, 223-229, 1983  
A:Title: Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA in front of  
A:Reference number: A05110; MUID:83287414; PMID:6349999  
A:Accession: B05110  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 199-209, 'SCSNMTPDDFSSGEFL' <POU>  
A:Cross-references: EMBL:V01578  
C:Genetics:  
A:Gene: ttk  
C:Superfamily: hypothetical protein HI0955

Query Match 9.1%; Score 7; DB 2; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ILQSLAL 53  
|||||

Db 29 ILQSLAL 35  
|||||

RESULT 11  
F86545  
hypothetical protein CPJ0440 [imported] - Chlamydomophila pneumoniae (strain J138)



Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 IATIMVL 23  
| | | | |  
Db 103 IATIMVL 109

Search completed: April 7, 2005, 04:48:23  
Job time : 83 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: April 7, 2005, 04:43:34 ; Search time 184 Seconds  
(without alignments)  
214.294 Million cell updates/sec

Title: US-10-063-563-56

Perfect score: 77

Sequence: 1 MGVKQLKMFEPTRLIAT.....LSFIPFARDAVKCFVCLV 77

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	77	2	Q6UWR8
2	77	100.0	160	2	Q95562
3	22	28.6	159	2	Q8VD57
4	20	26.0	161	2	Q7T375
5	9	11.7	113	2	Q86F94
6	8	10.4	136	2	Q922U5
7	8	10.4	159	2	Q8WV19
8	8	10.4	178	2	Q9UIC7
9	8	10.4	438	1	FUCP_ECOLI
10	8	10.4	438	2	Q8Z430
11	8	10.4	438	2	Q8FE8
12	8	10.4	438	2	Q83QC8
13	8	10.4	438	2	Q8XGR7
14	8	10.4	668	2	Q69W11
15	8	10.4	898	2	Q82T85
16	7	9.1	121	2	Q7R543
17	7	9.1	138	1	Y4BI_RHISN
18	7	9.1	141	2	Q64B27
19	7	9.1	163	2	Q9VPD4
20	7	9.1	183	2	Q9CJ61
21	7	9.1	188	2	Q74AN2
22	7	9.1	197	2	Q9CE19
23	7	9.1	198	1	TTK_ECOLI
24	7	9.1	198	2	Q8Z2H4
25	7	9.1	198	2	Q8ZL46
26	7	9.1	211	2	Q93V18
27	7	9.1	212	1	Y440_CHLPN
28	7	9.1	212	2	Q8FC66
29	7	9.1	212	2	Q8X580
30	7	9.1	236	2	Q7WFX7
31	7	9.1	247	2	Q99Y48

32	7	9.1	252	2	Q8NZG8
33	7	9.1	252	2	Q7CMT5
34	7	9.1	258	2	Q823L6
35	7	9.1	264	2	Q9KEF7
36	7	9.1	290	2	Q6N3D2
37	7	9.1	309	2	Q8RCW4
38	7	9.1	312	2	Q7JNP8
39	7	9.1	314	1	OX11_HUMAN
40	7	9.1	322	2	Q8N4F4
41	7	9.1	369	2	Q9ANK6
42	7	9.1	383	2	Q89TQ9
43	7	9.1	393	2	Q9VYR3
44	7	9.1	404	2	Q8P7Q1
45	7	9.1	455	2	Q66BX2
46	7	9.1	455	2	Q8ZFE6
47	7	9.1	458	2	Q46984
48	7	9.1	458	2	Q9RPV1
49	7	9.1	458	2	Q8Z7P8
50	7	9.1	458	2	Q8ZQ46
51	7	9.1	458	2	Q7N7X0
52	7	9.1	501	2	Q72T83
53	7	9.1	501	2	Q8F257
54	7	9.1	516	2	Q82TS0
55	7	9.1	566	2	Q9SCL5
56	7	9.1	569	2	P95915
57	7	9.1	595	2	Q9CA08
58	7	9.1	672	2	Q8Y8M4
59	7	9.1	672	2	Q92DE2
60	7	9.1	672	2	Q721U2
61	7	9.1	760	2	Q8EBB5
62	7	9.1	872	2	Q7SBD4
63	7	9.1	1148	2	Q6SL97
64	7	9.1	1216	2	O59901
65	7	9.1	1229	2	Q881Y1
66	7	9.1	3590	2	Q84MP8
67	6	7.8	30	2	Q6LCD6
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71	6	7.8	68	2	Q6GIS6
72	6	7.8	70	2	Q6UB57
73	6	7.8	71	2	Q8WS64
74	6	7.8	73	2	Q94179
75	6	7.8	77	2	Q8LAD7
76	6	7.8	78	1	YDH2_PLAFA5
77	6	7.8	80	2	Q7WXd5
78	6	7.8	80	2	Q8ERU3
79	6	7.8	82	2	Q7PCA6
80	6	7.8	83	2	Q7PCA8
81	6	7.8	92	2	Q75YW1
82	6	7.8	92	2	Q75YW4
83	6	7.8	92	2	Q75Z57
84	6	7.8	92	2	Q75Z78
85	6	7.8	93	2	Q21343
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87	6	7.8	93	2	Q75YQ1
88	6	7.8	93	2	Q75YQ4
89	6	7.8	93	2	Q75YQ7
90	6	7.8	93	2	Q75YR0
91	6	7.8	93	2	Q75YR3
92	6	7.8	93	2	Q75Y82
93	6	7.8	93	2	Q75Y85
94	6	7.8	93	2	Q75Y88
95	6	7.8	93	2	Q75YT1
96	6	7.8	93	2	Q75YT7
97	6	7.8	93	2	Q75YT0
98	6	7.8	93	2	Q75YU3
99	6	7.8	93	2	Q75YU6
100	6	7.8	93	2	Q75YU9
101	6	7.8	93	2	Q75YV5
102	6	7.8	93	2	Q75YX0
103	6	7.8	93	2	Q75YX3
104	6	7.8	93	2	Q75YX2

Q8nzg8	streptococc
Q8cmt5	streptococc
Q823l6	chlamydophi
Q9kef7	bacillus ha
Q6n3d2	rhodopseudo
Q8rgw4	fusobacteri
Q7jnp8	caenorhabdi
Q9h343	homo sapien
Q8n4f4	homo sapien
Q9ank6	bradyrhizob
Q89tc9	bradyrhizob
Q9vyr3	drosophila
Q8p7q1	xanthomonas
Q66bx2	yersinia ps
Q8zfe6	yersinia pe
Q46984	escherichia
Q9rpv1	salmonella
Q8z7p8	salmonella
Q8zq46	salmonella
Q7n7x0	photorehabdu
Q72t83	leptospira
Q8f257	leptospira
Q82ts0	nitrosomona
Q9sc15	arabidopsis
P95915	sulfolobus
Q9ca08	arabidopsis
Q8y8m4	listeria mo
Q92de2	listeria in
Q721u2	listeria mo
Q8eb5	shewanella
Q7sbd4	neurospora
Q6sl97	botrytis ci
O59901	emericeella
Q881y1	pseudomonas
Q84mp8	oryza sativ
Q6lcd6	xenopus lae
Q97830	human immun
Q8nxx7	staphylococ
Q6gbb4	staphylococ
Q6gis6	staphylococ
Q6ub57	hyaloperono
Q8ws64	glossina mo
Q94179	caenorhabdi
Q8lad7	arabidopsis
P14588	plasmodium
Q7wxd5	alcaligenes
Q8ebu3	shewanella
Q7pca6	lycoperisico
Q7pca8	lycoperisico
Q75yw1	euhadra dec
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Q75z78	euhadra dec
Q21343	euhadra her
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Q75y88	euhadra aom
Q75yt1	euhadra qua
Q75yt7	euhadra aom
Q75yu0	euhadra her
Q75yu3	euhadra san
Q75yu6	euhadra dix
Q75yu9	euhadra dix
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Q75yx3	euhadra nac
Q75yy2	euhadra qua

105	6	7.8	93	2	Q75Y8	Q75Y8	euhadra qua	178	6	7.8	153	2	Q6MAG8	Q6mag8	parachlamyd
106	6	7.8	93	2	Q75Y21	Q75Y21	euhadra aom	179	6	7.8	154	2	Q64S35	Q64s35	bacteroides
107	6	7.8	93	2	Q75Y24	Q75Y24	euhadra qua	180	6	7.8	155	2	Q7YVB3	Q7yvb3	trypanosoma
108	6	7.8	93	2	Q75Y27	Q75Y27	euhadra sig	181	6	7.8	155	2	Q8CR73	Q8cr73	staphylococ
109	6	7.8	93	2	Q75Z00	Q75Z00	euhadra qua	182	6	7.8	157	1	IBP_BUCAI	P57640	buchnera ap
110	6	7.8	93	2	Q75Z06	Q75Z06	euhadra qua	183	6	7.8	159	2	Q8A843	Q8a843	bacteroides
111	6	7.8	93	2	Q75Z12	Q75Z12	euhadra eoa	184	6	7.8	159	2	Q6WAD7	Q6mad7	parachlamyd
112	6	7.8	93	2	Q75Z15	Q75Z15	euhadra lat	185	6	7.8	160	2	Q88KX3	Q88kx3	pseudomonas
113	6	7.8	93	2	Q75Z18	Q75Z18	euhadra her	186	6	7.8	160	2	Q91046	Q91046	pseudomonas
114	6	7.8	93	2	Q75Z21	Q75Z21	euhadra lat	187	6	7.8	161	2	Q96X14	Q96x14	sulfolobus
115	6	7.8	93	2	Q75Z24	Q75Z24	euhadra san	188	6	7.8	161	2	Q884H5	Q884h5	pseudomonas
116	6	7.8	93	2	Q75Z27	Q75Z27	euhadra idz	189	6	7.8	163	2	Q9NEC2	Q9nec2	leishmania
117	6	7.8	93	2	Q75Z30	Q75Z30	euhadra gra	190	6	7.8	164	2	Q98G82	Q98g82	rhizobium 1
118	6	7.8	93	2	Q75Z33	Q75Z33	euhadra con	191	6	7.8	165	2	Q84XV5	Q84xv5	aloe vera (
119	6	7.8	93	2	Q75Z36	Q75Z36	euhadra sen	192	6	7.8	166	1	SSRP_SYNPX	Q7u9w8	synecococc
120	6	7.8	93	2	Q75Z39	Q75Z39	euhadra her	193	6	7.8	166	2	Q148Z7	Q148z7	homo sapien
121	6	7.8	93	2	Q75Z42	Q75Z42	euhadra sen	194	6	7.8	168	2	Q8FT03	Q8ft03	corynebacte
122	6	7.8	93	2	Q75Z45	Q75Z45	euhadra con	195	6	7.8	170	2	Q8IB19	Q8ib19	plasmodium
123	6	7.8	93	2	Q75Z54	Q75Z54	euhadra sen	196	6	7.8	173	2	Q9HEZ6	Q9hez6	neutrospora
124	6	7.8	93	2	Q75Z60	Q75Z60	euhadra eoa	197	6	7.8	174	1	YB38_METJA	Q58538	methanococ
125	6	7.8	93	2	Q75Z66	Q75Z66	euhadra qua	198	6	7.8	174	2	Q9KAE2	Q9kae2	bacillus ha
126	6	7.8	93	2	Q75Z72	Q75Z72	euhadra aom	199	6	7.8	176	1	CK42_THUOB	P80971	thunus obe
127	6	7.8	94	2	Q75Y15	Q75Y15	euhadra bra	200	6	7.8	176	2	Q9XCM8	Q9xcm8	wolinella s
128	6	7.8	94	2	Q7VXQ1	Q7VXQ1	bordetella	201	6	7.8	176	2	Q9XCN3	Q9xcn3	helicobacte
129	6	7.8	94	2	Q7W649	Q7W649	bordetella	202	6	7.8	176	2	Q8EJ7	Q8ej7	shewanella
130	6	7.8	94	2	Q7W115	Q7W115	mokola viru	203	6	7.8	176	2	Q9DAP4	Q9dap4	mus musculu
131	6	7.8	96	2	Q91N51	Q91N51	mokola viru	204	6	7.8	176	2	Q9QUL5	Q9qul5	mus musculu
132	6	7.8	96	2	Q91N52	Q91N52	mokola viru	205	6	7.8	177	1	YG44_METJA	Q59038	methanococ
133	6	7.8	96	2	Q91N53	Q91N53	mokola viru	206	6	7.8	177	2	Q6CDQ8	Q6cdq8	yarrowia li
134	6	7.8	96	2	Q91N54	Q91N54	mokola viru	207	6	7.8	177	2	Q90QJ3	Q90qj3	caprine art
135	6	7.8	96	2	Q9QM94	Q9QM94	mokola viru	208	6	7.8	178	2	Q9XCN1	Q9xcn1	helicobacte
136	6	7.8	96	2	Q9QM95	Q9QM95	mokola viru	209	6	7.8	178	2	Q9XCN7	Q9xcn7	helicobacte
137	6	7.8	96	2	Q9QM96	Q9QM96	mokola viru	210	6	7.8	179	2	Q9XCN0	Q9xcn0	helicobacte
138	6	7.8	96	2	Q9QM97	Q9QM97	mokola viru	211	6	7.8	179	2	Q9XCN5	Q9xcn5	helicobacte
139	6	7.8	96	2	Q9QM98	Q9QM98	mokola viru	212	6	7.8	179	2	Q9F3P0	Q9f3p0	streptomyce
140	6	7.8	96	2	Q9QM99	Q9QM99	mokola viru	213	6	7.8	180	2	Q82IE7	Q82ie7	chlamyidophi
141	6	7.8	106	2	Q7R1F2	Q7R1F2	giardia lam	214	6	7.8	181	2	Q8FIU3	Q8fiu3	escherichia
142	6	7.8	106	2	Q6KYC7	Q6KYC7	oryza sativ	215	6	7.8	181	2	Q8FKW6	Q8fkw6	escherichia
143	6	7.8	109	2	Q6NK95	Q6NK95	corynebacte	216	6	7.8	182	2	Q8XFD0	Q8xf00	salmonella
144	6	7.8	110	2	Q8BS41	Q8BS41	mus musculu	217	6	7.8	182	2	Q7CQB9	Q7cqb9	salmonella
145	6	7.8	110	2	Q8CSD2	Q8CSD2	mus musculu	218	6	7.8	183	2	Q66744	Q66744	aquifex aeo
146	6	7.8	112	2	Q62KN2	Q62KN2	burkholderi	219	6	7.8	185	2	Q7YIM3	Q7yim3	carassius a
147	6	7.8	115	2	Q6GXQ5	Q6GXQ5	human immun	220	6	7.8	188	2	Q8EBK2	Q8ebk2	shewanella
148	6	7.8	121	2	Q8YKX8	Q8YKX8	anabaena sp	221	6	7.8	188	2	Q8CAG5	Q8cag5	mus musculu
149	6	7.8	124	1	SP0F_BACSU	P06628	bacillus su	222	6	7.8	189	2	Q6CUF7	Q6cuf7	kluyveromyc
150	6	7.8	126	2	Q86G62	Q86G62	heterodera	223	6	7.8	189	2	Q6CXY9	Q6cxy9	kluyveromyc
151	6	7.8	126	2	Q9TG20	Q9TG20	phenacobius	224	6	7.8	189	2	Q6AAY6	Q6aay6	propionibac
152	6	7.8	126	2	Q8UC23	Q8UC23	agrobacteri	225	6	7.8	190	2	Q7NOB3	Q7nob3	photornhabu
153	6	7.8	130	2	Q93QX3	Q93QX3	corynebacte	226	6	7.8	197	2	Q40853	Q40853	picea glauc
154	6	7.8	130	2	Q8NSP7	Q8NSP7	corynebacte	227	6	7.8	197	2	Q7MX69	Q7mx69	porphyromon
155	6	7.8	133	1	BOTA_BOTJA	P22029	bothrops ja	228	6	7.8	197	2	Q7NYF4	Q7nyf4	chromobacte
156	6	7.8	133	2	Q6TAR2	Q6tar2	homo sapien	229	6	7.8	198	2	Q6EB39	Q6eb39	campylobact
157	6	7.8	133	2	Q7CW10	Q7cw10	agrobacteri	230	6	7.8	199	2	Q716N8	Q716n8	mycobacteri
158	6	7.8	133	2	Q64SN8	Q64sn8	bacteroides	231	6	7.8	199	2	Q8CWB2	Q8cwb2	escherichia
159	6	7.8	134	2	Q89T51	Q89t51	bradyrhizob	232	6	7.8	201	2	Q6ZSX4	Q6zsx4	homo sapien
160	6	7.8	136	2	Q96MR4	Q96mr4	homo sapien	233	6	7.8	202	2	Q88F43	Q88f43	pseudomonas
161	6	7.8	137	2	Q82J77	Q82j77	streptomyce	234	6	7.8	203	2	Q8WWA1	Q8wwa1	homo sapien
162	6	7.8	137	2	Q90QJ4	Q90qj4	caprine art	235	6	7.8	203	2	Q8NUZ4	Q8nuz4	homo sapien
163	6	7.8	138	2	Q7PYU9	Q7pyu9	anopheles g	236	6	7.8	205	2	Q8ID59	Q8id59	plasmodium
164	6	7.8	142	2	Q6ARU7	Q6aru7	desulfotale	237	6	7.8	205	2	Q6GDT4	Q6gdt4	staphylococ
165	6	7.8	142	2	Q9PSM6	Q9psm6	bothrops ja	238	6	7.8	206	2	Q7QS93	Q7qs93	giardia lam
166	6	7.8	144	2	Q9RHG3	Q9rhg3	mycobacteri	239	6	7.8	206	2	Q820A2	Q820a2	nitrosomona
167	6	7.8	145	2	Q64815	Q64815	uncultured	240	6	7.8	206	2	Q812G3	Q812g3	plasmodium
168	6	7.8	145	2	Q6L166	Q6l166	picophilus	241	6	7.8	207	2	Q7QID5	Q7qid5	anopheles g
169	6	7.8	146	2	Q706N8	Q706n8	pseudomonas	242	6	7.8	207	2	Q7V0B2	Q7v0b2	prochloroco
170	6	7.8	146	2	Q9D546	Q9d546	mus musculu	243	6	7.8	208	1	RHO1_ENTHI	F31021	entamoeba h
171	6	7.8	148	2	Q63CD3	Q63cd3	bacillus ce	244	6	7.8	208	2	O27538	Q27538	methanobact
172	6	7.8	148	2	Q81RL1	Q81rl1	capillus an	245	6	7.8	208	2	Q894K8	Q894k8	clostridium
173	6	7.8	149	2	Q64B21	Q64b21	uncultured	246	6	7.8	208	2	Q8BET3	Q8bet3	shewanella
174	6	7.8	151	2	Q6AQX3	Q6aqx3	desulfotale	247	6	7.8	209	2	Q81Z66	Q81z66	homo sapien
175	6	7.8	152	2	Q8CA26	Q8ca26	mus musculu	248	6	7.8	209	2	Q96196	Q96196	plasmodium
176	6	7.8	153	2	Q6BV00	Q6bv00	debaryomyce	249	6	7.8	209	2	Q6YSX2	Q6ysx2	oryza sativ
177	6	7.8	153	2	Q6WU84	Q6wu84	lactobacill	250	6	7.8	209	2	Q8VCT8	Q8vct8	mus musculu

251	6	7.8	210	2	Q8I890	Q8i890 entamoeba h	324	6	7.8	256	2	Q8EGG3	Q8egg3 shewanella
252	6	7.8	211	2	Q7IDF1	Q7idf1 drosophila	325	6	7.8	257	2	Q8NYX8	Q8nyx8 staphylococ
253	6	7.8	211	2	Q6F9F3	Q6f9f3 acinetobact	326	6	7.8	257	2	Q932K6	Q932k6 staphylococ
254	6	7.8	212	2	Q8I892	Q8i892 entamoeba h	327	6	7.8	257	2	Q99X12	Q99x12 leptospira
255	6	7.8	212	2	Q8I893	Q8i893 entamoeba h	328	6	7.8	257	2	Q75FF8	Q75ff8 leptospira
256	6	7.8	212	2	Q8I894	Q8i894 entamoeba h	329	6	7.8	257	2	Q8EXB2	Q8exb2 leptospira
257	6	7.8	212	2	Q95TD4	Q95td4 entamoeba h	330	6	7.8	257	2	Q9CJX6	Q9cjx6 pasteuralla
258	6	7.8	212	2	Q9VX96	Q9vx96 drosophila	331	6	7.8	257	2	Q6GCR5	Q6gcr5 staphylococ
259	6	7.8	213	2	Q9V8A7	Q9v8a7 drosophila	332	6	7.8	259	2	Q87232	Q87232 lactococcus
260	6	7.8	215	2	Q9H1C6	Q9h1c6 homo sapien	333	6	7.8	259	2	Q837Y4	Q837y4 enterococcu
261	6	7.8	216	2	Q7X242	Q7x242 citrobacter	334	6	7.8	260	2	Q8NT23	Q8nt23 corynebacte
262	6	7.8	218	1	Q7M6_MOUSE	Q7m6 mouse	335	6	7.8	260	2	Q8FS88	Q8fs88 corynebacte
263	6	7.8	220	1	YNL0_YEAST	Ynl0 yeast	336	6	7.8	260	2	Q7TFN5	Q7tfn5 rhesus cyto
264	6	7.8	220	2	Q6G0J1	Q6g0j1 bartonella	337	6	7.8	261	1	COX3_BRARE	Q9miy4 brachydanio
265	6	7.8	220	2	Q6G4P4	Q6g4p4 bartonella	338	6	7.8	261	1	COX3_CARAU	Q9mi13 carassius a
266	6	7.8	221	2	Q8I891	Q8i891 entamoeba h	339	6	7.8	261	1	COX3_CYPCA	PL5952 cyprinus ca
267	6	7.8	222	2	Q9LB02	Q9lb02 mycobacteri	340	6	7.8	261	2	Q94PR1	Q94pr1 crelimugil
268	6	7.8	225	2	Q27013	Q27013 tenebrio mo	341	6	7.8	261	2	Q94Q35	Q94q35 arctocscopus
269	6	7.8	225	2	Q27014	Q27014 tenebrio mo	342	6	7.8	261	2	Q94S84	Q94s84 platichthys
270	6	7.8	225	2	Q8FCY7	Q8fcy7 escherichia	343	6	7.8	261	2	Q94SH5	Q94sh5 gastrosteu
271	6	7.8	225	2	Q8VCR5	Q8vcr5 mus musculu	344	6	7.8	261	2	Q94SR6	Q94sr6 rondeletia
272	6	7.8	227	2	Q7VRW1	Q7vrw1 prochloroco	345	6	7.8	261	2	Q94T27	Q94t27 percopsis t
273	6	7.8	228	2	Q6FFN5	Q6ffn5 acinetobact	346	6	7.8	261	2	Q94T48	Q94t48 zu cristatu
274	6	7.8	228	2	Q748P3	Q748p3 geobacter s	347	6	7.8	261	2	Q94T61	Q94t61 trachipteru
275	6	7.8	231	2	Q7MRJ9	Q7mrj9 wolinnella s	348	6	7.8	261	2	Q94T87	Q94t87 diaphus spl
276	6	7.8	232	2	Q93J82	Q93j82 streptomyce	349	6	7.8	261	2	Q94YN9	Q94yn9 pantodon bu
277	6	7.8	232	2	Q9D5J8	Q9d5j8 mus musculu	350	6	7.8	261	2	Q68GA7	Q68ga7 carassius c
278	6	7.8	233	2	Q8NAL4	Q8nal4 homo sapien	351	6	7.8	261	2	Q69AW8	Q69aw8 acanthogobi
279	6	7.8	234	1	TNFB_HUMAN	Tnfb human	352	6	7.8	261	2	Q6B0M1	Q6b0m1 carassius a
280	6	7.8	234	2	Q96YF6	Q96yf6 sulfolobus	353	6	7.8	261	2	Q6RUI1	Q6ruil1 sebaastes ac
281	6	7.8	234	2	Q7V2Q7	Q7v2q7 prochloroco	354	6	7.8	261	2	Q6Z7Z3	Q6z7z3 elops sauru
282	6	7.8	234	2	Q87BC9	Q87bc9 xylella fas	355	6	7.8	261	2	Q70EC9	Q70ec9 bufo melano
283	6	7.8	236	2	Q67LC3	Q67lc3 symbiobacte	356	6	7.8	261	2	Q70EE2	Q70ee2 ambystoma m
284	6	7.8	238	1	RL3_BRAJA	Q89j84 bradyrhizob	357	6	7.8	261	2	Q75UF4	Q75uf4 carlyodes c
285	6	7.8	238	2	Q8RTN7	Q8rtn7 legionella	358	6	7.8	261	2	Q75VM6	Q75vm6 pagrus auri
286	6	7.8	238	2	Q8S4S9	Q8s4s9 legionella	359	6	7.8	261	2	Q76F99	Q76f99 auxis thaza
287	6	7.8	239	2	Q8ZU23	Q8zu23 pyrobaculum	360	6	7.8	261	2	Q76G43	Q76g43 auxis roche
288	6	7.8	240	2	Q9XXT4	Q9xxt4 caenorhabdi	361	6	7.8	261	2	Q76HG7	Q76hg7 thunnus ala
289	6	7.8	240	2	Q6MIL1	Q6mil1 bdellovibri	362	6	7.8	261	2	Q76H10	Q76h10 katsuonus
290	6	7.8	240	2	Q73H87	Q73h87 wolbachia p	363	6	7.8	261	2	Q76MD4	Q76md4 elops hawai
291	6	7.8	240	2	Q800J1	Q800j1 gallus gall	364	6	7.8	261	2	Q76ML3	Q76ml3 mugil cepha
292	6	7.8	241	1	RL3_RHOFA	P60456 rhodopsudo	365	6	7.8	261	2	Q7HJL3	Q7hj17 thunnus thy
293	6	7.8	241	1	UBIE_STAAM	P67061 staphylococ	366	6	7.8	261	2	Q7YC36	Q7yc36 atheostoma
294	6	7.8	241	1	UBIE_STAAM	P67062 staphylococ	367	6	7.8	261	2	Q7YC36	Q7yc36 galaxias ma
295	6	7.8	241	1	UBIE_STAAM	P67063 staphylococ	368	6	7.8	261	2	Q85D40	Q85d40 pseudobagru
296	6	7.8	241	2	Q6G952	Q6g992 staphylococ	369	6	7.8	261	2	Q85E41	Q85e41 pseudobagru
297	6	7.8	241	2	Q6GGU0	Q6gg00 staphylococ	370	6	7.8	261	2	Q85E67	Q85e67 cobitis str
298	6	7.8	243	2	Q9LVH9	Q9lvh9 arabidopsis	371	6	7.8	261	2	Q85E80	Q85e80 sarcocelli
299	6	7.8	243	2	Q8Y8H4	Q8y8h4 listeria mo	372	6	7.8	261	2	Q85E85	Q85e85 eucyprinus a
300	6	7.8	243	2	Q92D87	Q92d87 listeria in	373	6	7.8	261	2	Q8HL09	Q8hl09 caraux mela
301	6	7.8	244	2	Q82Z39	Q82z39 enterococcu	374	6	7.8	261	2	Q8HL22	Q8hl22 carangoides
302	6	7.8	245	1	T2P7_PSEAE	P05104 pseudomonas	375	6	7.8	261	2	Q8HL48	Q8hl48 cottus rein
303	6	7.8	245	2	Q8NCL8	Q8ncl8 homo sapien	376	6	7.8	261	2	Q8HL61	Q8hl61 satyrichthy
304	6	7.8	245	2	Q6NSH5	Q6nsh5 homo sapien	377	6	7.8	261	2	Q8HLB2	Q8hlb2 hypoptychus
305	6	7.8	246	2	Q7WT43	Q7wt43 streptococc	378	6	7.8	261	2	Q8HLR8	Q8hlr8 anoplogaste
306	6	7.8	246	2	Q8UA62	Q8ua62 agrobacteri	379	6	7.8	261	2	Q8HLZ5	Q8hlz5 melanoaeni
307	6	7.8	246	2	Q8CM62	Q8cm62 streptococc	380	6	7.8	261	2	Q8HMD7	Q8hmd7 diplacantho
308	6	7.8	247	1	COBS_ECOL57	Q8x8u9 escherichia	381	6	7.8	261	2	Q8HMF0	Q8hmf0 cataetx ru
309	6	7.8	247	1	COBS_ECOL6	Q8fga4 escherichia	382	6	7.8	261	2	Q8HMH6	Q8hnh6 bassozetus
310	6	7.8	247	1	COBS_ECOL1	P36561 escherichia	383	6	7.8	261	2	Q9BG14	Q9bg14 carassius c
311	6	7.8	247	1	COBS_SALTI	Q8z5n8 salmonella	384	6	7.8	261	2	Q9G6Q7	Q9g6q7 diplophos t
312	6	7.8	247	1	COBS_SALTY	Q05602 salmonella	385	6	7.8	261	2	Q644X8	Q644x8 ambystoma l
313	6	7.8	247	1	COBS_SHIFL	Q83r13 shigella fl	386	6	7.8	262	2	Q6ZLZ2	Q6z1z2 albulu glos
314	6	7.8	247	2	P78834	P78834 schizosacch	387	6	7.8	264	2	Q7RLZ2	Q7rlz2 plasmodium
315	6	7.8	247	2	Q9MX51	Q9mx51 oryzias lat	388	6	7.8	265	2	Q6MA31	Q6ma31 parachlamyd
316	6	7.8	247	2	Q8LIR7	Q8lir7 oryza sativ	389	6	7.8	270	1	COX3_CVACA	P48873 cyanidium c
317	6	7.8	247	2	Q8ECC5	Q8ecc5 shewanella	390	6	7.8	270	2	Q8KZ99	Q8kz99 desulfovibr
318	6	7.8	253	1	Y116_METTH	Q27844 methanobact	391	6	7.8	271	1	LPXA_RALSO	Q8xzh9 ralstonia s
319	6	7.8	253	2	Q84EO6	Q84eo6 wautersia o	392	6	7.8	271	2	Q9AL46	Q9al46 shigella fl
320	6	7.8	253	2	Q6NX94	Q6nx94 brachydanio	393	6	7.8	271	2	Q6GIJ1	Q6gij1 bartonella
321	6	7.8	255	1	RLJ3_CAUCR	Q9a8v3 caulobacter	394	6	7.8	271	2	Q6G5C5	Q6g5c5 bartonella
322	6	7.8	255	2	Q76BT0	Q76bt0 vibrio mimi	395	6	7.8	272	1	UPPB_PHOLL	Q6955 bartonella
323	6	7.8	256	2	Q96122	Q96i22 homo sapien	396	6	7.8	272	2	Q8VQP9	Q8vqp9 escherichia

397	6	7.8	272	2	Q8VQR4	O8vqr4	escherichia	470	6	7.8	316	2	Q6UYB9	O6uyb9	bovine herp
398	6	7.8	272	2	Q93R10	O93fj0	citrobacter	471	6	7.8	316	2	Q6JWV9	O6jwv9	brachydanio
399	6	7.8	272	2	Q7D3V0	O7d3v0	agrobacteri	472	6	7.8	317	2	O8GXR5	O8gxr5	arabidopsis
400	6	7.8	272	2	Q9AJ35	O9aj35	escherichia	473	6	7.8	317	2	Q68EV0	O68ev0	xenopus lae
401	6	7.8	272	2	Q6D159	O6d159	erwinia car	474	6	7.8	318	2	Q7D3I4	O7d3i4	agrobacteri
402	6	7.8	273	1	UPPP_ECO57	P60933	escherichia	475	6	7.8	318	2	Q82MD4	O82md4	streptomyce
403	6	7.8	273	1	UPPP_ECOL6	P67386	escherichia	476	6	7.8	319	2	Q740U3	O740u3	mycobacteri
404	6	7.8	273	1	UPPP_ECOLI	P69322	escherichia	477	6	7.8	320	2	Q704X6	O704x6	anopheles g
405	6	7.8	273	1	UPPP_SALTI	P67389	salmonella	478	6	7.8	320	2	Q64VQ7	O64vq7	bacteroides
406	6	7.8	273	1	UPPP_SALTY	P67388	salmonella	479	6	7.8	321	2	Q9VMP1	O9vmp1	drosophila
407	6	7.8	273	1	UPPP_SHIFL	P67387	shigella fl	480	6	7.8	321	2	Q966M0	O966m0	caenorhabdi
408	6	7.8	273	2	Q7TFX5	O7tfx5	rhesus cyto	481	6	7.8	325	2	Q7Q728	O7q728	anopheles g
409	6	7.8	274	2	Q6D760	O6d760	erwinia car	482	6	7.8	325	2	Q93F20	O93f20	shigella fl
410	6	7.8	276	2	Q95NZ4	O95nz4	sarcocystis	483	6	7.8	326	1	Y370_MYCPN	P75230	mycoplaema
411	6	7.8	276	2	Q7YSU2	O7ysu2	sarcocystis	484	6	7.8	326	2	O8XYG0	O8xyg0	ralstonia s
412	6	7.8	276	2	Q6LX38	O6lx38	photobacter	485	6	7.8	326	2	Q98UW4	O98uw4	hepatitis c
413	6	7.8	276	2	Q82BB4	O82bb4	streptomyce	486	6	7.8	328	1	LGT_BORBU	O51337	borrelia bu
414	6	7.8	277	2	Q6N902	O6n902	rhodospheudo	487	6	7.8	328	2	Q63HP2	O63hp2	homo sapien
415	6	7.8	277	2	Q8UJL5	O8ujl5	agrobacteri	488	6	7.8	328	2	Q661Q7	O661q7	borrelia ga
416	6	7.8	279	2	Q758X7	O758x7	ashbya goss	489	6	7.8	328	2	Q8XU53	O8xu53	ralstonia s
417	6	7.8	279	2	Q7Z0V1	O7z0v1	sarcocystis	490	6	7.8	329	2	O6CNE4	O6cne4	kluveromyce
418	6	7.8	279	2	Q86M54	O86m54	sarcocystis	491	6	7.8	329	2	O65MR6	O65mr6	bacillus li
419	6	7.8	283	2	Q702E8	O702e8	uncultured	492	6	7.8	329	2	Q7NQ17	O7nd17	chromobacte
420	6	7.8	283	2	Q8XNP7	O8xnp7	clostridium	493	6	7.8	330	2	Q16086	O16086	homo sapien
421	6	7.8	284	2	Q83JP0	O83jp0	shigella fl	494	6	7.8	330	2	Q8Y5Q8	O8y5q8	listeria mo
422	6	7.8	285	2	Q32731	O32731	agrobacteri	495	6	7.8	331	2	Q92A16	O92a16	listeria in
423	6	7.8	285	2	Q7CP39	O7cp39	agrobacteri	496	6	7.8	331	2	Q71V24	O71v24	listeria mo
424	6	7.8	286	2	Q66E86	O66e86	yersinia ps	497	6	7.8	332	1	FECC_ECOLI	P15030	escherichia
425	6	7.8	286	2	Q82HK5	O82hk5	streptomyce	498	6	7.8	332	2	Q8EU33	O8ej33	shewanella
426	6	7.8	286	2	Q9X6B4	O9x6b4	yersinia pe	499	6	7.8	333	2	Q7R4X8	O7r4x8	giardia lam
427	6	7.8	288	2	Q65TR7	O65tr7	manheimia	500	6	7.8	333	2	Q9MNJ4	O9mnj4	helobdella
428	6	7.8	288	2	Q9DG22	O9dg22	gallus gall	501	6	7.8	334	2	Q752L0	O752l0	ashbya goss
429	6	7.8	289	2	Q9KZ73	O9kz73	streptomyce	502	6	7.8	335	2	O8MXL9	O8mxl9	dictyosteli
430	6	7.8	290	1	SHY1_SCHPO	O9y810	schizosacch	503	6	7.8	335	2	O8U8G5	O8u8g5	agrobacteri
431	6	7.8	290	1	Y32K_MCMV	P11641	maize chlor	504	6	7.8	336	2	Q943X2	O943x2	oryza sativ
432	6	7.8	290	2	Q70JY7	O70jy7	bacillus an	505	6	7.8	337	2	Q6BNF0	O6bnf0	debaryomyce
433	6	7.8	291	2	Q7CSN3	O7csn3	agrobacteri	506	6	7.8	338	2	Q6RWH1	O6rwh1	uncultured
434	6	7.8	293	1	YIA3_YEAST	P40558	saccharomyc	507	6	7.8	340	1	RF33_YEAST	P38629	saccharomyc
435	6	7.8	296	1	NU2M_ARTSF	Q37704	artemia san	508	6	7.8	344	2	O8PFH6	O8pfh6	xanthomonas
436	6	7.8	296	2	Q16085	O16085	homo sapien	509	6	7.8	345	1	DDL_WOLSU	O7ma71	wolinella s
437	6	7.8	298	2	Q7YSV4	O7ysv4	bacterioph	510	6	7.8	345	1	P2A6_ARATH	O9asu7	arabidopsis
438	6	7.8	299	2	Q8SB85	O8sb85	oryza sativ	511	6	7.8	345	1	P92653	P92653	euprepis au
439	6	7.8	299	2	Q8UX68	O8ux68	agrobacteri	512	6	7.8	345	2	Q92F14	O92f14	listeria in
440	6	7.8	300	2	Q9I479	O9i479	pseudomonas	513	6	7.8	345	2	Q92BW2	O92bw2	streptomyce
441	6	7.8	301	2	Q89P49	O89p49	bradyrhizob	514	6	7.8	346	1	CNA1_SCHPO	P36599	schizosacch
442	6	7.8	301	2	Q6UBL6	O6ubl6	psittacid h	515	6	7.8	346	2	O6CDZ0	O6cdz0	yarrowia li
443	6	7.8	302	2	Q84W69	O84w69	arabidopsis	516	6	7.8	346	2	Q644Z6	O644z6	eurycea bis
444	6	7.8	302	2	Q9FN16	O9fn16	arabidopsis	517	6	7.8	346	2	Q82M16	O82m16	streptomyce
445	6	7.8	302	2	Q65P02	O65p02	bacillus li	518	6	7.8	347	2	Q94RK1	O94rk1	chimaera mo
446	6	7.8	302	2	Q9I8S9	O9i8s9	oncorhynch	519	6	7.8	348	2	Q8HM26	O8hm26	caulophryne
447	6	7.8	303	2	Q9IB66	O9ib66	xenopus lae	520	6	7.8	348	2	O8VNZ6	O8vnz6	bordetella
448	6	7.8	304	2	Q8LHB6	O8lhb6	oryza sativ	521	6	7.8	348	2	O8EKB4	O8ekb4	shewanella
449	6	7.8	305	2	P72579	P72579	sulfolobus	522	6	7.8	349	2	Q9XOK3	O9xok3	thermotoga
450	6	7.8	305	2	Q96Y68	O96y68	sulfolobus	523	6	7.8	350	2	Q9VQ77	O9vq77	drosophila
451	6	7.8	306	2	Q9CI00	O9ci00	lactococcus	524	6	7.8	350	2	Q6HW78	O6hw78	bacillus an
452	6	7.8	307	2	Q8D190	O8d190	versinia pe	525	6	7.8	350	2	Q638N3	O638n3	bacillus ce
453	6	7.8	309	2	Q9XIP5	O9xip5	arabidopsis	526	6	7.8	350	2	Q45376	O45376	bordetella
454	6	7.8	310	1	PANC_ARATH	O9fxb3	arabidopsis	527	6	7.8	350	2	Q734N1	O734n1	bacillus ce
455	6	7.8	310	2	Q8LEA6	O8lea6	arabidopsis	528	6	7.8	350	2	Q79H45	O79h45	bordetella
456	6	7.8	310	2	Q7WXS3	O7wx3	alcaligenes	529	6	7.8	350	2	Q8IN18	O8in18	bacillus th
457	6	7.8	311	2	Q7RA93	O7ra93	plasmodium	530	6	7.8	350	2	Q6HG64	O6hg64	bacillus th
458	6	7.8	312	1	NU1M_DROME	P18929	drosophila	531	6	7.8	351	2	Q9SE295	O9se295	arabidopsis
459	6	7.8	312	2	Q9MI09	O9mi09	drosophila	532	6	7.8	351	2	Q9SE51	O9se51	arabidopsis
460	6	7.8	312	2	Q9M111	O9m111	drosophila	533	6	7.8	351	2	Q9SE51	O9se51	arabidopsis
461	6	7.8	312	2	Q9KXH3	O9kxh3	yersinia en	534	6	7.8	354	2	O8XKQ3	O8xkq3	clostridium
462	6	7.8	314	2	Q662B0	O662b0	borrelia ga	535	6	7.8	354	2	O8YBQ5	O8ybq5	bruceella me
463	6	7.8	315	2	Q6BJA0	O6bjao	debaryomyce	536	6	7.8	355	2	O8RON5	O8ron5	mus musculus
464	6	7.8	315	2	Q6IGT5	O6igt5	drosophila	537	6	7.8	357	1	HAL2_YEAST	P32179	saccharomyc
465	6	7.8	315	2	Q72ST8	O6igt5	leptospiro	538	6	7.8	357	2	Q6RFY5	O6rfy5	saccharomyc
466	6	7.8	315	2	Q8F2F2	O72st8	leptospiro	539	6	7.8	357	2	Q69XT6	O69xt6	oryza sativ
467	6	7.8	315	2	Q9KGA2	O8f2p2	leptospiro	540	6	7.8	357	2	Q9DG23	O9dg23	gallus gall
468	6	7.8	316	2	Q72UZ0	O9kga2	bacillus ha	541	6	7.8	359	2	Q9BWF8	O9bwf8	homo sapien
469	6	7.8	316	2	Q8EZY3	O72uz0	leptospiro	542	6	7.8	359	2	Q90634	O90634	gallus gall
						O8ezy3	leptospiro	543	6	7.8	360	1	MRAY_SHEON	O8e9p5	shewanella

543	6	7.8	360	1	MRAY_SHEVI	Q9fln3 shewanella	616	6	7.8	429	2	Q8YOK6	Q8yOk6 ralstonia s
544	6	7.8	361	1	PZY4_MOUSE	Q6jij7 mus musculus	617	6	7.8	431	2	Q8D500	Q6d500 erwinia car
545	6	7.8	362	1	Q6C1O8	Q6ciq8 kluyveromyc	618	6	7.8	433	1	COBB_PSEDE	P21632 pseudomonas
546	6	7.8	363	2	Q68573	Q68573 streptococc	619	6	7.8	434	2	Q8XUP8	Q9xup8 caenorhabdi
547	6	7.8	364	2	Q9X092	Q9x092 thermotoga	620	6	7.8	434	2	Q87N91	Q87n91 vibrio para
548	6	7.8	365	2	Q6BNJ1	Q6bnj1 debaryomyc	621	6	7.8	435	2	Q64VY8	Q64vy8 bacteroides
549	6	7.8	366	2	Q7NVB3	Q7nvb3 chromobacte	622	6	7.8	436	2	Q86285	Q86285 diadromus p
550	6	7.8	366	2	Q7TUW1	Q7tuvw1 prochloroco	623	6	7.8	437	2	Q75S57	Q75s57 rabies viru
551	6	7.8	368	2	Q9H841	Q9h841 homo sapien	624	6	7.8	438	1	FIBG_XENLA	FI7634 xenopus lae
552	6	7.8	368	2	Q93285	Q93285 staphylococ	625	6	7.8	439	2	Q8A1L2	Q8a1l2 bacteroides
553	6	7.8	369	2	Q6QH15	Q6qhi5 thiobacillu	626	6	7.8	439	2	Q9F2N1	Q9f2n1 streptomyce
554	6	7.8	371	2	Q8XLI0	Q8xli0 staphylococ	627	6	7.8	439	2	Q7SZ13	Q7sz13 xenopus lae
555	6	7.8	373	2	Q937R1	Q937r1 brucella me	628	6	7.8	440	2	Q30307	Q30307 archaeoglob
556	6	7.8	374	2	Q7MAT1	Q7mat1 wolinnella s	629	6	7.8	440	2	Q9K7K2	Q9k7k2 bacillus ha
557	6	7.8	375	2	Q8FMW3	Q8fmw3 brucella su	630	6	7.8	444	2	Q73NC8	Q73nc8 treponema d
558	6	7.8	376	2	Q87XJ3	Q87xj3 pseudomonas	631	6	7.8	444	2	Q6D8P7	Q6d8p7 erwinia car
559	6	7.8	378	2	Q9ZER5	Q9zer5 anabaena sp	632	6	7.8	445	2	Q72WJ6	Q72wj6 desulfovibr
560	6	7.8	378	2	Q9RGV4	Q9rgv4 anabaena sp	633	6	7.8	447	2	Q8GQX0	Q8gqx0 selenomonas
561	6	7.8	380	1	ARGE_MYXXA	Q68873 myxococcus	634	6	7.8	447	2	Q8DNZ9	Q8dnz9 streptococc
562	6	7.8	381	2	Q88DT3	Q88dt3 pseudomonas	635	6	7.8	447	2	Q8EKI3	Q8eki3 shewanella
563	6	7.8	381	2	Q9HV37	Q9hv37 pseudomonas	636	6	7.8	448	2	Q83CC1	Q83cc1 coxiella bu
564	6	7.8	382	2	Q9MLW9	Q9mlw9 arabadopsis	637	6	7.8	449	2	O07406	O07406 mycobacteri
565	6	7.8	382	2	Q9CHG7	Q9chg7 lactococcus	638	6	7.8	449	2	Q7U2P7	Q7u2p7 mycobacteri
566	6	7.8	383	2	Q72SZ8	Q72sz8 leptospira	639	6	7.8	450	2	Q82994	Q82994 lagos bat v
567	6	7.8	383	2	Q8FZH1	Q8fzh1 leptospira	640	6	7.8	450	2	Q83544	Q83544 mokola viru
568	6	7.8	384	2	Q93ZQ3	Q93zq3 arabadopsis	641	6	7.8	450	2	Q86593	Q86593 mokoia viru
569	6	7.8	386	1	ICEA_XENLA	P58665 xenopus lae	642	6	7.8	450	2	Q9WJY5	Q9wjy5 rabies viru
570	6	7.8	386	2	Q6H7L8	Q6h7l8 oryza sativ	643	6	7.8	451	2	Q7NGW2	Q7ngw2 gloeobacter
571	6	7.8	386	2	Q8A2B6	Q8a2b6 bacteroides	644	6	7.8	451	2	Q66453	Q66453 duvenhage v
572	6	7.8	387	2	Q65Y10	Q65y10 butyrivibri	645	6	7.8	451	2	Q66532	Q66532 european ba
573	6	7.8	389	2	O04178	O04178 brassica ca	646	6	7.8	451	2	Q66533	Q66533 european ba
574	6	7.8	389	2	O82567	O82567 arabadopsis	647	6	7.8	451	2	Q66534	Q66534 european ba
575	6	7.8	389	2	Q74IF5	Q74if5 lactobacill	648	6	7.8	451	2	Q66535	Q66535 european ba
576	6	7.8	390	2	Q64Y28	Q64y28 bacteroides	649	6	7.8	451	2	Q6X1D4	Q6x1d4 khujand lys
577	6	7.8	392	2	Q6CPH2	Q6cph2 kluyveromyc	650	6	7.8	451	2	Q6X1D8	Q6x1d8 aravan lys
578	6	7.8	393	2	Q22305	Q22305 caenorhabdi	651	6	7.8	451	2	Q76K69	Q76k69 aravan lys
579	6	7.8	393	2	Q8LBE8	Q8lee8 arabadopsis	652	6	7.8	452	2	Q23660	Q23660 caenorhabdi
580	6	7.8	394	2	O6C2Q9	O6c2q9 yarrowia li	653	6	7.8	453	2	Q9CER2	Q9cer2 lactococcus
581	6	7.8	394	2	Q8LSZ8	Q8lsz8 arabadopsis	654	6	7.8	454	2	Q9CFW6	Q9cfw6 lactococcus
582	6	7.8	395	1	HMEB_ARCFU	O29750 archaeoglob	655	6	7.8	455	2	Q9LNB1	Q9lnb1 arabadopsis
583	6	7.8	395	2	O8L571	O8l571 lycopersico	656	6	7.8	455	2	Q7VBQ7	Q7vbq7 prochloroco
584	6	7.8	395	2	Q8RVL3	Q8rvl3 lycopersico	657	6	7.8	456	2	Q8KQJ0	Q8kqj0 haemophilus
585	6	7.8	397	1	PGK_BORBR	Q7wmk9 bordetella	658	6	7.8	458	2	Q74CL4	Q74cl4 geobacter s
586	6	7.8	397	1	PGK_BORPA	Q7vzb8 bordetella	659	6	7.8	461	2	Q6Z625	Q6z625 oryza sativ
587	6	7.8	397	1	PGK_BORPE	Q7vzb8 bordetella	660	6	7.8	461	2	Q8GFB5	Q8gfb5 photorhabdu
588	6	7.8	398	2	O6E159	O6e159 saccharomyc	661	6	7.8	461	2	Q90Z63	Q90z63 oncorhynch
589	6	7.8	400	2	O22204	Q22204 arabadopsis	662	6	7.8	462	1	ODPB_ZYMMO	O66113 zymomonas m
590	6	7.8	400	2	Q8FL54	Q8fl54 escherichia	663	6	7.8	462	2	Q64YD7	Q64yd7 oryza sativ
591	6	7.8	401	2	Q7X5N8	Q7y5n8 bacterioph	664	6	7.8	462	2	Q64Y27	Q64y27 bacteroides
592	6	7.8	401	2	Q69Y51	Q69y51 oryza sativ	665	6	7.8	463	2	Q8TNH6	Q8tnh6 methanosarc
593	6	7.8	402	1	PAI1_BOVIN	PI3909 bos taurus	666	6	7.8	463	2	Q9CLQ0	Q9clq0 pasteurella
594	6	7.8	402	2	Q7X6V4	Q7x6v4 oryza sativ	667	6	7.8	465	2	Q7P902	Q7p902 rickettsia
595	6	7.8	402	2	Q886K0	Q886k0 pseudomonas	668	6	7.8	465	2	Q8ECK2	Q8eck2 shewanella
596	6	7.8	403	2	Q9L3V2	Q9l3v2 streptomyce	669	6	7.8	469	1	KCCA_MOUSE	P08414 mus musculu
597	6	7.8	403	2	Q7W236	Q7w236 bordetella	670	6	7.8	470	2	Q6SR88	Q6sr88 mannheimia
598	6	7.8	408	2	Q85454	Q85454 pasteurella	671	6	7.8	470	2	Q88F87	Q88f87 pseudomonas
599	6	7.8	408	2	Q83AP2	Q83ap2 coxiella bu	672	6	7.8	472	2	Q6VUH0	Q6vuh0 paenibacill
600	6	7.8	408	2	Q9CWP3	Q9cmp3 pasteurella	673	6	7.8	474	2	O04036	O04036 arabadopsis
601	6	7.8	409	2	Q8CDW9	Q8cdw9 mus musculu	674	6	7.8	474	2	Q8LOV5	Q8lov5 oryza sativ
602	6	7.8	409	2	Q9D408	Q9d408 mus musculu	675	6	7.8	476	2	Q7B9Y7	Q7b9y7 lactobacill
603	6	7.8	410	2	P72973	P72973 synecocyst	676	6	7.8	476	2	Q6DRJ6	Q6drj6 brachydanio
604	6	7.8	411	2	Q6BYS9	Q6bys9 debaryomyc	677	6	7.8	477	2	Q8MS56	Q8ms56 drosophila
605	6	7.8	411	2	Q62KL3	Q62kl3 burkholderi	678	6	7.8	477	2	Q9FT94	Q9ft94 arabadopsis
606	6	7.8	411	2	Q63TQ2	Q63tq2 burkholderi	679	6	7.8	478	1	NUON_RHOCA	P50973 rhodobacter
607	6	7.8	411	2	Q73ZB4	Q73zb4 mycobacteri	680	6	7.8	478	2	Q69Y52	Q69y52 oryza sativ
608	6	7.8	412	2	Q7Z630	Q7z630 homo sapien	681	6	7.8	478	2	Q84UT9	Q84uy9 oryza sativ
609	6	7.8	414	2	Q8SR58	Q8sr58 encephalito	682	6	7.8	478	2	Q8YGL3	Q8ygl3 brucella me
610	6	7.8	414	2	Q8XNH5	Q8xnh5 clostridium	683	6	7.8	478	2	Q8G1A4	Q8g1a4 brucella su
611	6	7.8	417	2	Q96VU7	Q96vu7 neurospora	684	6	7.8	480	2	Q8UFW4	Q8ufw4 agrobacteri
612	6	7.8	420	2	Q69PG3	Q69fg3 debaryomyc	685	6	7.8	480	2	Q92QN9	Q92qn9 rhizobium m
613	6	7.8	422	2	Q21298	Q21298 caenorhabdi	686	6	7.8	480	2	Q6MIS6	Q6mis6 bdellovibri
614	6	7.8	422	2	Q6MUG5	Q6mug5 mycoplasma	687	6	7.8	480	2	Q91482	Q91482 pseudomonas
615	6	7.8	423	2	Q9P417	Q9p417 cephalospor	688	6	7.8	480	2	Q6AJ25	Q6aj25 desulfotale

689	6	7.8	481	2	Q6FUZ8	Q6fuz8 candida gla	762	6	7.8	558	2	Q7QGW6	Q7qgw6 anopheles g
690	6	7.8	481	2	Q9AC59	Q9acy9 caulobacter	763	6	7.8	558	2	Q6MF08	Q6mf08 parachlamyid
691	6	7.8	482	1	ALA2 PANMI	P34106 panicum mil	764	6	7.8	560	2	Q7WZL7	Q7wzl7 xanthomonas
692	6	7.8	482	2	Q7C2K9	Q7czk9 agrobacteri	765	6	7.8	568	2	Q8YOH0	Q8yoh0 ralstonia s
693	6	7.8	482	2	Q8GAU6	Q8gau6 bifidobacte	766	6	7.8	570	1	GLT2 MOUSE	Q6pb93 m polypepti
694	6	7.8	483	2	Q9BW35	Q9bw35 homo sapien	767	6	7.8	570	2	Q6T5D1	Q6tsd1 oryza sativ
695	6	7.8	483	2	Q9S768	Q9s768 oryza sativ	768	6	7.8	572	2	Q8SDL2	Q8sdl2 apium grave
696	6	7.8	483	2	Q7U8T7	Q7uet7 rhodopirell	769	6	7.8	572	1	MET3_PENCH	Q12650 penicillium
697	6	7.8	484	2	Q9Y7U9	Q9y7u9 schizosacch	770	6	7.8	574	2	Q8JWN1	Q8jwn1 human respi
698	6	7.8	484	2	Q28713	Q28713 oryctolagus	771	6	7.8	575	2	Q6PMI1	Q6pmi1 hydrilla ve
699	6	7.8	484	2	Q94HC5	Q94hc5 oryza sativ	772	6	7.8	575	2	Q85221	Q85221 human parai
700	6	7.8	484	2	Q7XF06	Q7xf06 oryza sativ	773	6	7.8	575	2	Q85222	Q85222 human parai
701	6	7.8	484	2	Q6FZX8	Q6fzx8 bartonella	774	6	7.8	577	2	Q8HOE8	Q8hoe8 lithospermu
702	6	7.8	484	2	Q6G3A1	Q6g3a1 bartonella	775	6	7.8	577	2	Q92W64	Q92w64 rhizobium m
703	6	7.8	485	2	Q8SC10	Q8sci0 propionibac	776	6	7.8	579	2	Q8NHH8	Q8nhh8 homo sapien
704	6	7.8	485	2	Q9PWC0	Q9pwc0 gallus gall	777	6	7.8	581	2	Q7PXR2	Q7pxr2 anopheles g
705	6	7.8	486	1	CISX YEAST	P43635 saccharomyc	778	6	7.8	582	2	P73732	P73732 synechocyst
706	6	7.8	491	2	Q960S7	Q960s7 drosophila	779	6	7.8	583	2	Q8NHH9	Q8nhh9 homo sapien
707	6	7.8	494	2	Q8PYS7	Q8py87 methanosarc	780	6	7.8	585	1	MAOX_MESCR	P37223 mesembryant
708	6	7.8	495	2	Q7X740	Q7x740 oryza sativ	781	6	7.8	585	2	Q92WJ4	Q92wj4 alooe arbore
709	6	7.8	496	2	Q65799	Q65799 arabidopsis	782	6	7.8	586	2	Q943H8	Q943h8 oryza sativ
710	6	7.8	498	2	Q66K75	Q66k75 homo sapien	783	6	7.8	588	2	Q75CO4	Q75cq4 ashbya goss
711	6	7.8	499	1	NQOE_PARDE	P29926 paracoccus	784	6	7.8	588	2	O14729	O14729 homo sapien
712	6	7.8	500	2	Q8T9D2	Q8t9d2 drosophila	785	6	7.8	588	2	Q9PVX4	Q9pvx4 cynops pyrr
713	6	7.8	502	2	Q7WBN8	Q7wbn8 bordetella	786	6	7.8	589	1	SKS1_ARATH	Q8vxx5 arabidopsis
714	6	7.8	502	2	Q7WPM7	Q7wpm7 bordetella	787	6	7.8	589	2	Q94G02	Q94g02 flaveria pr
715	6	7.8	504	2	Q64143	Q64143 bacterioph	788	6	7.8	589	2	Q94G03	Q94g03 flaveria pr
716	6	7.8	504	2	Q31905	Q31905 bacillus su	789	6	7.8	590	2	Q7O8B5	Q7q8b5 anopheles g
717	6	7.8	504	2	Q6DRB2	Q6drb2 brachydanto	790	6	7.8	590	2	P73561	P73561 synechocyst
718	6	7.8	505	1	LNT_HAEDU	Q7vm56 haemophilus	791	6	7.8	591	1	MAOX_POPTR	P34105 populus tri
719	6	7.8	505	2	Q6C654	Q6c654 yarrowia li	792	6	7.8	591	1	MAOX_VITVI	P51615 vitis vinif
720	6	7.8	506	2	Q89G09	Q89g09 bradyrhizob	793	6	7.8	592	2	O48656	O48656 alooe arbore
721	6	7.8	507	2	Q6GPJ1	Q6gpj1 xenopus lae	794	6	7.8	593	2	Q71S51	Q71s51 ophiopholis
722	6	7.8	509	2	Q9VTH6	Q9vth6 drosophila	795	6	7.8	594	2	Q9ZXM5	Q9zxm5 bacterioph
723	6	7.8	509	2	Q8XIG3	Q8xig3 clostridium	796	6	7.8	594	2	Q6YZH8	Q6yzh8 oryza sativ
724	6	7.8	510	2	Q7S6W6	Q7s6w6 neurospora	797	6	7.8	594	2	Q8DKN0	Q8dkn0 synechococ
725	6	7.8	510	2	Q9GCM9	Q9gcm9 pieris napi	798	6	7.8	594	2	Q8U6T4	Q8uet4 agrobacteri
726	6	7.8	511	2	Q7QJZ4	Q7qjz4 anopheles g	799	6	7.8	595	2	Q7S925	Q7s925 neurospora
727	6	7.8	514	2	Q8YQ99	Q8yq99 anabaena sp	800	6	7.8	595	2	Q9LY22	Q9ly22 arabidopsis
728	6	7.8	518	2	Q6LEJ5	Q6lej5 oryctolagus	801	6	7.8	596	2	Q7WJL1	Q7wj11 vibrio vuln
729	6	7.8	520	2	Q9Y7C0	Q9y7c0 neurospora	802	6	7.8	596	2	Q8DAJ1	Q8daj1 vibrio vuln
730	6	7.8	520	2	Q81YS4	Q81ys4 homo sapien	803	6	7.8	600	1	VIN3_ARATH	Q9f1e3 arabidopsis
731	6	7.8	520	2	Q8NCV0	Q8ncv0 homo sapien	804	6	7.8	602	2	Q6C6Y8	Q6c6y8 yarrowia li
732	6	7.8	522	1	PME_PRUPE	Q43062 prunus pers	805	6	7.8	603	1	PPCK_SULSO	Q97v85 sulfolobus
733	6	7.8	523	2	Q8MNX4	Q8mux4 caenorhabdi	806	6	7.8	604	2	Q644W1	Q644w1 rhyacocrito
734	6	7.8	524	2	Q9ABL8	Q9abl8 caulobacter	807	6	7.8	607	2	Q7R3S2	Q7r3s2 giardia lam
735	6	7.8	525	2	Q9WOL9	Q9wol9 drosophila	808	6	7.8	608	2	Q9PVX3	Q9px3 cynops pyrr
736	6	7.8	526	1	CPF5_RAT	P51870 rattus norv	809	6	7.8	611	2	Q8SCV8	Q8scv8 opisthoproc
737	6	7.8	526	2	Q755C0	Q755c0 ashbya goss	810	6	7.8	612	2	Q69MX4	Q69mx4 oryza sativ
738	6	7.8	526	2	Q52405	Q52405 pseudomonas	811	6	7.8	613	2	Q8IBE6	Q8ibe6 plasmodium
739	6	7.8	526	2	Q7BG55	Q7bg55 bacillus st	812	6	7.8	615	2	Q85D10	Q85d10 nansenia ar
740	6	7.8	526	2	Q9EQ70	Q9eq70 rattus norv	813	6	7.8	615	2	Q85D23	Q85d23 glossanodon
741	6	7.8	528	2	Q56926	Q56926 yersinia en	814	6	7.8	615	2	Q85D75	Q85d75 bathylagus
742	6	7.8	533	2	Q7SA99	Q7sa99 neurospora	815	6	7.8	617	2	Q8EF90	Q8ef90 shewanella
743	6	7.8	535	2	Q6NXG4	Q6nxg4 homo sapien	816	6	7.8	618	2	Q8RZA4	Q8rza4 oryza sativ
744	6	7.8	535	2	Q95JW1	Q95jw1 macaca fasc	817	6	7.8	619	2	Q6BXU2	Q6bxu2 debaryomyce
745	6	7.8	537	2	Q7Q135	Q7q135 anopheles g	818	6	7.8	619	2	Q6LFR9	Q6lfr9 photobacter
746	6	7.8	538	2	Q9HWB0	Q9hwb0 pseudomonas	819	6	7.8	620	2	Q93F38	Q93f38 shigella fl
747	6	7.8	539	2	Q7S413	Q7s413 neurospora	820	6	7.8	621	2	Q6BVV1	Q6bv1 debaryomyce
748	6	7.8	541	2	Q65LN3	Q65ln3 oryza sativ	821	6	7.8	622	2	O14794	O14794 homo sapien
749	6	7.8	541	2	Q6FBD3	Q6fbd3 acinetobact	822	6	7.8	623	2	Q6A4K8	Q6a4k8 mus musculu
750	6	7.8	542	1	LNT_CHLTR	Q84539 chlamydia t	823	6	7.8	624	1	PLB2_SCHPO	O13857 schizosacch
751	6	7.8	543	2	Q8PXV0	Q8pxv0 methanosarc	824	6	7.8	624	2	Q8G5P3	Q8g5p3 bifidobacte
752	6	7.8	543	2	Q876L1	Q876l1 saccharomyc	825	6	7.8	624	2	Q9KQ16	Q9kq16 vibrio chol
753	6	7.8	544	2	Q7RRP5	Q7rrp5 plasmodium	826	6	7.8	628	2	Q94GB3	Q94gb3 oryza sativ
754	6	7.8	545	2	Q9H882	Q9h882 homo sapien	827	6	7.8	628	2	Q7XGT5	Q7xgt5 oryza sativ
755	6	7.8	545	2	Q9VM14	Q9vm14 drosophila	828	6	7.8	629	2	Q6J1Y6	Q6j1y6 bacterioph
756	6	7.8	546	2	Q7QA61	Q7qa61 anopheles g	829	6	7.8	630	1	STR3_SCHPO	Q92341 schizosacch
757	6	7.8	549	2	Q9UEW7	Q9uew7 schizosacch	830	6	7.8	631	2	O81780	O81780 arabidopsis
758	6	7.8	551	2	Q6BFF2	Q6bff2 paramecium	831	6	7.8	631	2	O67XW5	O67xw5 arabidopsis
759	6	7.8	552	1	SYK_CAUCR	Q9aby6 caulobacter	832	6	7.8	632	2	Q682A0	Q682a0 arabidopsis
760	6	7.8	553	2	Q81KQ4	Q81kq4 plasmodium	833	6	7.8	632	2	Q8J0D5	Q8j0d5 microsporim
761	6	7.8	554	2	Q62FW3	Q62fw3 oryza sativ	834	6	7.8	632	2	Q6WIH7	Q6wih7 microsporim

835	6	7.8	633	2	Q8J0D6	Q8j0d6 microsporium	908	6	7.8	765	2	Q8Z5B5	Q8z5b5 salmonella
836	6	7.8	634	2	Q9UWV4	Q9uvv4 aspergillus	909	6	7.8	765	2	Q8CVX0	Q8cvx0 escherichia
837	6	7.8	634	2	Q7RRP9	Q7rrp9 plasmodium	910	6	7.8	765	2	Q83KF8	Q83kf8 shigella fl
838	6	7.8	635	2	Q8NIB6	Q8nib6 trichophyto	911	6	7.8	777	1	CUL3 CAEEL	Q17391 caenorhabdi
839	6	7.8	635	2	Q6WIH5	Q6wih5 arthroderma	912	6	7.8	783	2	O545Z4	O54524 legionella
840	6	7.8	636	1	MAOC MAIZE	E16243 zea mays (m	913	6	7.8	785	2	O6SLA6	O6sls6 gibberella
841	6	7.8	636	2	Q84LF6	Q84lf6 zea mays (m	914	6	7.8	790	2	Q9HBB2	Q9hb2 homo sapien
842	6	7.8	636	2	Q84LQ5	Q84lq5 sorghum bic	915	6	7.8	796	2	Q7ROA3	Q7rq3 plasmodium
843	6	7.8	638	1	MAOC ORYSA	P43279 oryza sativ	916	6	7.8	798	2	Q9VVM8	Q9vv8 drosophila
844	6	7.8	639	2	Q9LDH7	Q9ldh7 oryza sativ	917	6	7.8	804	2	Q65GD3	Q65gd3 bacillus li
845	6	7.8	640	2	Q24550	Q24550 vitis vinif	918	6	7.8	813	2	Q6ZPM4	Q6zpm4 mus musculu
846	6	7.8	640	2	Q8M348	Q8w348 oryza sativ	919	6	7.8	816	2	Q8D3K7	Q8d3k7 vibrio vuln
847	6	7.8	640	2	Q7XGZ1	Q7xgz1 oryza sativ	920	6	7.8	822	2	Q6BGJ1	Q6bgj1 paramecium
848	6	7.8	641	2	Q9M4Q9	Q9m4q9 ricinus com	921	6	7.8	823	1	DNLJ TREPA	Q83642 treponema p
849	6	7.8	643	2	Q9PP43	Q9pp43 campylobact	922	6	7.8	823	2	Q9PMS7	Q9pms7 campylobact
850	6	7.8	644	2	Q8W000	Q8w000 zea mays (m	923	6	7.8	825	2	Q6CLZ8	Q6clz8 kluyveromyc
851	6	7.8	646	2	Q7Q813	Q7q813 giardia lam	924	6	7.8	825	2	Q7UU73	Q7uu73 rhodopirell
852	6	7.8	646	2	Q7Q813	Q7q813 giardia lam	924	6	7.8	825	2	Q7UU73	Q7uu73 rhodopirell
853	6	7.8	646	2	Q9CA83	Q9ca83 arabisdopsis	925	6	7.8	827	2	Q7ME19	Q7mf19 vibrio vuln
854	6	7.8	647	1	MAOC FLAPR	P36444 flaveria pr	926	6	7.8	832	2	Q23136	Q23136 caenorhabdi
855	6	7.8	647	2	Q7QDZ1	Q7qdz1 anopheles g	927	6	7.8	841	2	Q8X0X9	Q8x0x9 neurospora
856	6	7.8	648	1	MAOC FLATR	P22178 flaveria tr	928	6	7.8	841	2	Q8RWY4	Q8rwy4 arabisdopsis
857	6	7.8	657	2	Q871Q7	Q871q7 neurospora	929	6	7.8	841	2	Q8H105	Q8h105 arabisdopsis
858	6	7.8	658	2	Q8XVA3	Q8xva3 ralsstonia s	930	6	7.8	844	2	Q9XZS7	Q9xzs7 drosophila
859	6	7.8	660	2	Q94Z47	Q94z47 schizosacch	931	6	7.8	847	2	Q9SGW2	Q9sgw2 arabisdopsis
860	6	7.8	662	2	Q9ZRH5	Q9zrh5 zea mays (m	932	6	7.8	849	2	Q9DKV4	Q9dkv4 caprine art
861	6	7.8	663	2	Q9MA03	Q9ma03 arabisdopsis	933	6	7.8	850	2	Q82SY1	Q82sy1 nitrosomona
862	6	7.8	666	2	Q6BFC0	Q6bfc0 paramecium	934	6	7.8	851	2	Q8TMG3	Q8tmg3 methanosarc
863	6	7.8	671	2	Q9C547	Q9c547 arabisdopsis	935	6	7.8	857	2	Q6CVG2	Q6cvg2 kluyveromyc
864	6	7.8	672	2	Q9W7B7	Q9w7b7 brachydanio	936	6	7.8	864	2	Q8BDF7	Q8bdf7 jamestown c
865	6	7.8	673	1	FLB4_SCHPO	Q9p327 schizosacch	937	6	7.8	866	2	Q6PFZ0	Q6pfz0 mus musculu
866	6	7.8	676	2	Q6NV02	Q6nv02 brachydanio	938	6	7.8	869	2	Q752E8	Q752e8 ahybya goss
867	6	7.8	677	2	Q7ZTU9	Q7ztu9 brachydanio	939	6	7.8	872	2	Q9V019	Q9v019 pyrococcus
868	6	7.8	678	2	Q8MT15	Q8mt15 leishmania	940	6	7.8	873	2	Q9SN00	Q9sn00 arabisdopsis
869	6	7.8	679	2	Q6N925	Q6n925 rhodopseudo	941	6	7.8	879	2	Q8ILP6	Q8ilp6 plasmodium
870	6	7.8	681	2	Q9H7M4	Q9h7m4 homo sapien	942	6	7.8	879	2	Q8VZH2	Q8vzh2 arabisdopsis
871	6	7.8	684	2	Q8IUH8	Q8iuh8 kluyveromyc	943	6	7.8	884	2	Q8H8H0	Q8h8h0 oryza sativ
872	6	7.8	684	2	Q8TC67	Q8tc67 homo sapien	944	6	7.8	886	2	Q6GNK8	Q6gnk8 xenopus lae
873	6	7.8	684	2	Q7R173	Q7r173 giardia lam	945	6	7.8	886	2	Q7ZX16	Q7zx16 xenopus lae
874	6	7.8	685	2	Q8GUH6	Q8guh6 arabisdopsis	946	6	7.8	886	2	Q804C7	Q804c7 xenopus lae
875	6	7.8	687	2	Q84ZD7	Q84zd7 oryza sativ	947	6	7.8	889	1	IRE1_HUMAN	P21399 homo sapien
876	6	7.8	687	2	Q9IAL0	Q9ial0 brachydanio	948	6	7.8	889	1	IRE1_MOUSE	P28271 mus musculu
877	6	7.8	688	2	Q9IB08	Q9ibc8 xenopus lae	949	6	7.8	889	1	IRE1_RABIT	Q01059 oryctolagus
878	6	7.8	688	2	Q9W7R7	Q9w7r7 xenopus lae	950	6	7.8	889	1	IRE1_RAT	Q63270 rattus norv
879	6	7.8	690	2	Q8WVZ6	Q8wvz6 homo sapien	951	6	7.8	889	1	IREB_CHICK	Q90875 gallus gall
880	6	7.8	693	2	Q8WG20	Q8wg20 gallus gall	952	6	7.8	889	2	Q875Q5	Q875q5 saccharomyc
881	6	7.8	696	2	Q8GVW4	Q8gvw4 oryza sativ	953	6	7.8	893	2	Q9FLX6	Q9flx6 arabisdopsis
882	6	7.8	698	2	Q96078	Q96078 ephydatia f	954	6	7.8	899	2	Q8VDC3	Q8vdc3 mus musculu
883	6	7.8	704	2	Q7VGG3	Q7vgs3 helicobacte	955	6	7.8	900	2	Q6CUN9	Q6cun9 kluyveromyc
884	6	7.8	707	2	Q8YQP7	Q8yqp7 anabaena sp	956	6	7.8	913	2	Q7NLM6	Q7nlm6 gloeobacter
885	6	7.8	712	1	SM1A_TRICF	Q26972 tribolium c	957	6	7.8	928	1	PM10_CHLPN	Q9rb65 chlamydia p
886	6	7.8	713	2	Q81JF1	Q81jf1 plasmodium	958	6	7.8	931	1	CDG5_HUMAN	Q9y5g8 homo sapien
887	6	7.8	714	2	Q9SUM4	Q9sum4 arabisdopsis	959	6	7.8	935	2	Q7NUJ4	Q7nuj4 chromobacte
888	6	7.8	718	2	Q92614	Q92614 ophiostoma	960	6	7.8	939	2	Q8CGH5	Q8cgh5 mus musculu
889	6	7.8	719	2	Q838H7	Q838h7 enterococcu	961	6	7.8	939	2	Q8CGH5	Q8cgh5 mus musculu
890	6	7.8	720	2	Q80R01	Q80r01 sclerotinia	962	6	7.8	953	2	Q68Y12	Q68y12 rickettsia
891	6	7.8	731	2	Q6YX11	Q6yx11 oryza sativ	963	6	7.8	953	2	Q6BKM3	Q6bkm3 debaryomyc
892	6	7.8	731	2	Q7UOK4	Q7uok4 rhodopirell	964	6	7.8	971	2	Q8UH99	Q8uh99 agrobacteri
893	6	7.8	732	2	Q8VQM5	Q8vqm5 klebsiella	965	6	7.8	978	2	Q7Z3P2	Q7z3p2 homo sapien
894	6	7.8	732	2	Q8VQM5	Q8vqm5 klebsiella	966	6	7.8	978	2	Q95KE0	Q95ke0 macaca fasc
895	6	7.8	732	2	Q9LVDT	Q9lvdt caulobacter	967	6	7.8	991	2	Q12252	Q12252 saccharomyc
896	6	7.8	737	2	Q9LAQ3	Q9laq3 tt virus. o	968	6	7.8	995	2	Q9K5K4	Q9k5k4 bacillus ha
897	6	7.8	739	2	Q99AQ3	Q99aq3 tt virus. o	969	6	7.8	1002	2	Q6AXB1	Q6axb1 oryza sativ
898	6	7.8	741	2	Q658T4	Q658t4 homo sapien	970	6	7.8	1005	2	Q6PG12	Q6pg12 mus musculu
899	6	7.8	741	2	Q9C6V7	Q9c6v7 arabisdopsis	971	6	7.8	1030	2	Q9P8F2	Q9p8f2 zygoacchar
900	6	7.8	746	1	RNG3_SCHPO	Q74994 schizosacch	972	6	7.8	1032	2	Q8X0X6	Q8x0x6 neurospora
901	6	7.8	747	2	Q6SGI1	Q6sg11 uncultured	973	6	7.8	1035	2	Q6FDB1	Q6fdb1 acinetobact
902	6	7.8	748	2	Q6A6C2	Q6a6c2 propionibac	974	6	7.8	1040	2	Q7P0T4	Q7p0t4 chromobacte
903	6	7.8	749	2	Q67IU4	Q67iu4 oryza sativ	975	6	7.8	1052	2	Q7Z7R0	Q7z7r0 homo sapien
904	6	7.8	753	2	Q7PVN0	Q7pvn0 anopheles g	976	6	7.8	1070	2	Q7PT99	Q7pt99 anopheles g
905	6	7.8	765	1	EGLX_ECOLI	P33363 escherichia	977	6	7.8	1070	2	Q9RWX7	Q9rwx7 deinococcus
906	6	7.8	765	1	EGLX_SALTY	Q56078 salmonella	978	6	7.8	1078	2	Q8MLA4	Q8mla4 drosophila
907	6	7.8	765	2	Q7ACAB	Q7aca8 escherichia	979	6	7.8	1084	2	Q7QTS9	Q7qts9 giardia lam
	6	7.8	765	2	Q8X668	Q8x668 escherichia	980	6	7.8	1098	2	Q9P7K5	Q9p7k5 schizosacch

981	6	7.8	1098	2	Q64719	Q64719 bos taurus	1054	6	7.8	1972	1	MYHB_HUMAN	P35749 homo sapien
982	6	7.8	1102	2	Q75AR3	Q75ar3 ashbya goss	1055	6	7.8	1972	1	MYHB_MOUSE	O08638 mus musculus
983	6	7.8	1104	2	Q6Z8S8	Q6z8s8 oryza sativ	1056	6	7.8	1972	1	MYHB_RABIT	P35748 oryctolagus
984	6	7.8	1114	2	Q9C8S4	Q9c8s4 arabidopsis	1057	6	7.8	1972	2	Q9LUD7	Q9lud7 arabidopsis
985	6	7.8	1120	2	Q6B8R8	Q6b8r8 gracilaria	1058	6	7.8	1972	2	Q7WY92	Q7wy92 staphylococ
986	6	7.8	1120	2	Q6SES8	Q6ses8 uncultured	1059	6	7.8	1972	2	Q8R384	Q8r384 mus musculus
987	6	7.8	1131	2	Q9V7A5	Q9v7a5 drosophila	1060	6	7.8	1983	2	Q931N9	Q931n9 staphylococ
988	6	7.8	1134	2	Q8P378	Q8p378 xanthomonas	1061	6	7.8	1984	2	Q69ZX3	Q69zx3 mus musculus
989	6	7.8	1134	2	Q8PEL2	Q8pel2 xanthomonas	1062	6	7.8	1995	2	Q724O6	Q724o6 homo sapien
990	6	7.8	1136	2	Q7SHY6	Q7shy6 oryza sativ	1063	6	7.8	2030	2	Q9VXV3	Q9vxy3 drosophila
991	6	7.8	1144	1	CYA3_HUMAN	Q60266 homo sapien	1064	6	7.8	2043	2	Q8WQ87	Q8wq87 chironomus
992	6	7.8	1144	1	CYA3_RAT	P21932 rattus norv	1065	6	7.8	2124	2	Q7WRR9	Q7wrr9 staphylococ
993	6	7.8	1144	2	Q6PGC0	Q6pgc0 mus musculus	1066	6	7.8	2126	1	WNK1_RAT	Q9fjfh7 rattus norv
994	6	7.8	1145	1	CYA3_MOUSE	Q8vhh7 mus musculus	1067	6	7.8	2131	2	Q6SLK2	Q6slk2 mus musculus
995	6	7.8	1150	2	Q80TY9	Q80ty9 mus musculus	1068	6	7.8	2133	2	Q7WRQ2	Q7wrq2 staphylococ
996	6	7.8	1159	2	Q6SLC9	Q6slc9 cochllobolu	1069	6	7.8	2152	2	Q9ALM5	Q9alm5 saccharopol
997	6	7.8	1160	2	Q7SBL3	Q7sbl3 neurospora	1070	6	7.8	2186	2	Q7WS91	Q7ws91 staphylococ
998	6	7.8	1162	2	Q9LFPQ7	Q9lfpq7 arabidopsis	1071	6	7.8	2186	2	Q8NW19	Q8nw19 staphylococ
999	6	7.8	1168	2	Q7SDF3	Q7sdf3 neurospora	1072	6	7.8	2186	2	Q99TB0	Q99tb0 staphylococ
1000	6	7.8	1172	1	LMB3_HUMAN	Q13751 homo sapien	1073	6	7.8	2186	2	Q6G8H1	Q6g8h1 staphylococ
1001	6	7.8	1185	2	Q9HCJ9	Q9hcj9 homo sapien	1074	6	7.8	2189	2	Q6GFU5	Q6gfu5 staphylococ
1002	6	7.8	1189	2	Q7UPG0	Q7upg0 rhodopirell	1075	6	7.8	2241	2	Q7XRJ2	Q7xrj2 oryza sativ
1003	6	7.8	1196	2	Q6FIK1	Q6fik1 candida gla	1076	6	7.8	2253	2	Q7QW26	Q7qw26 giardia lam
1004	6	7.8	1213	2	Q9SPH2	Q9sph2 dictyosteli	1077	6	7.8	2375	2	Q9FR96	Q9fr96 arabidopsis
1005	6	7.8	1213	2	Q86CZ2	Q86cz2 dictyosteli	1078	6	7.8	2375	2	WNK1_MOUSE	P83741 mus musculus
1006	6	7.8	1223	2	Q9FXG4	Q9fxg4 arabidopsis	1079	6	7.8	2382	1	WNK1_HUMAN	Q86b02 dictyosteli
1007	6	7.8	1234	1	RPOB_THETN	Q8r7u6 thermosnaer	1080	6	7.8	2454	2	Q86B02	Q86b02 caenorhabdi
1008	6	7.8	1246	2	Q6BZU0	Q6bzu0 yarrowia li	1081	6	7.8	2581	2	Q9N4C8	Q9nac8 caenorhabdi
1009	6	7.8	1250	2	Q67JT3	Q67jt3 symbiobacte	1082	6	7.8	2672	1	GCN1_YEAST	P33992 saccharomyc
1010	6	7.8	1260	2	Q9XZC5	Q9xzc5 cryptospori	1083	6	7.8	2883	1	RPBC_WOLSU	P73556 w bifunctio
1011	6	7.8	1269	2	Q6C740	Q6c740 yarrowia li	1084	6	7.8	2890	1	RPBC_HELPJ	Q92k23 h bifunctio
1012	6	7.8	1271	2	Q75B800	Q75b00 ashbya goss	1085	6	7.8	2890	1	RPBC_HELPJ	Q25806 h bifunctio
1013	6	7.8	1288	2	Q6PBJ1	Q6pdj1 mus musculus	1086	6	7.8	2894	2	RPBC_HELHP	Q7v182 h bifunctio
1014	6	7.8	1297	2	Q9V604	Q9v604 drosophila	1087	6	7.8	2898	2	Q872P1	Q872p1 neurospora
1015	6	7.8	1304	2	Q9U3L2	Q9u3l2 caenorhabdi	1088	6	7.8	3099	2	Q7R5I4	Q7r5i4 giardia lam
1016	6	7.8	1327	1	MYHB_RAT	Q83862 rattus norv	1089	6	7.8	3218	2	Q8ILX0	Q8ilx0 plasmodium
1017	6	7.8	1329	2	Q8N3P4	Q8n3p4 homo sapien	1090	6	7.8	3379	2	Q9JAD5	Q9jad5 rio bravo v
1018	6	7.8	1348	2	Q9VCM6	Q9vcm6 drosophila	1091	6	7.8	4335	2	Q6NA45	Q6na45 rhodopseudo
1019	6	7.8	1376	2	Q9KFI5	Q9kfi5 bacillus ha	1092	6	7.8	6473	2	Q81KH9	Q8ikh9 rhodopseud
1020	6	7.8	1394	2	Q86UX3	Q86ux3 homo sapien	1093	5	6.5	14	2	Q7SCJ3	Q7scj3 neurospora
1021	6	7.8	1399	2	Q6APK0	Q6apk0 desulfotale	1094	5	6.5	14	2	Q6SEH0	Q6seho umbra limi
1022	6	7.8	1406	2	Q80TR5	Q80tr5 mus musculus	1095	5	6.5	14	2	Q6SEH1	Q6seho numvbra hu
1023	6	7.8	1422	2	Q6MJ09	Q6mj09 bdellovibri	1096	5	6.5	18	2	Q9WUQ6	Q9wuq6 mus musculu
1024	6	7.8	1425	2	Q7S802	Q7s802 neurospora	1097	5	6.5	24	2	Q788Q0	Q788q0 xenopus lae
1025	6	7.8	1436	1	MRP5_MOUSE	Q9kix5 mus musculus	1098	5	6.5	25	2	Q64FD9	Q64fd9 toxoplasma
1026	6	7.8	1436	1	MRP5_RAT	Q9qym0 rattus norv	1099	5	6.5	26	2	Q64FE3	Q64fe3 toxoplasma
1027	6	7.8	1437	1	MRP5_HUMAN	Q15440 homo sapien	1100	5	6.5	27	2	Q94448	Q94448 chaetopteru
1028	6	7.8	1443	2	Q57106	Q57106 inkoo virus	1101	5	6.5	29	2	Q71U28	Q71uz8 sus scrofa
1029	6	7.8	1443	2	Q57107	Q57107 inkoo virus	1102	5	6.5	29	2	Q93IG2	Q93ig2 thibacillu
1030	6	7.8	1444	2	Q9QKE5	Q9qke5 south river	1103	5	6.5	30	2	Q86SJ1	Q86sj1 homo sapien
1031	6	7.8	1449	2	Q8LSR0	Q8lsr0 oryza sativ	1104	5	6.5	31	2	Q6NJM4	Q6njm4 corynebacte
1032	6	7.8	1457	2	Q9M033	Q9m033 arabidopsis	1105	5	6.5	32	2	Q65W75	Q65w75 mannheimia
1033	6	7.8	1500	2	Q8IH00	Q8ihh0 drosophila	1106	5	6.5	33	1	COAL_BPFD	P03675 bacterioph
1034	6	7.8	1503	2	Q9V6P4	Q9v6p4 drosophila	1107	5	6.5	33	2	Q67B72	Q67b72 dehalococco
1035	6	7.8	1516	2	Q24525	Q24525 arabidopsis	1108	5	6.5	33	2	Q7VCT4	Q7vet4 prochloroco
1036	6	7.8	1521	2	Q6BUY8	Q6buy8 debaryomyce	1109	5	6.5	33	2	Q83EB8	Q83eb8 coxiella bu
1037	6	7.8	1527	2	Q8GUG4	Q8gug4 oryza sativ	1110	5	6.5	34	2	Q6UJ39	Q6ujj9 carphodacty
1038	6	7.8	1571	2	Q76B62	Q76b62 homo sapien	1111	5	6.5	35	2	Q87904	Q87904 coxiella bu
1039	6	7.8	1584	2	Q7JM28	Q7j28 caenorhabdi	1112	5	6.5	36	2	Q696V2	Q696v2 rissa trida
1040	6	7.8	1586	2	Q18798	Q18798 caenorhabdi	1113	5	6.5	37	2	Q8EIQ2	Q8eiq2 shewanella
1041	6	7.8	1599	2	Q854N0	Q854n0 mycobacteri	1114	5	6.5	37	2	Q8F5H3	Q8f5h3 leptospira
1042	6	7.8	1657	1	IQG1_MOUSE	Q9jfk1 mus musculus	1115	5	6.5	37	2	Q9KBL5	Q9kel5 bacillus ha
1043	6	7.8	1657	2	Q80UW7	Q80uw7 mus musculus	1116	5	6.5	37	2	Q6DNC6	Q6dnc6 rattus norv
1044	6	7.8	1681	2	Q6ZQK2	Q6zqk2 mus musculus	1117	5	6.5	37	2	Q9PVL3	Q9pvl3 triakis sp.
1045	6	7.8	1726	2	Q6C012	Q6c012 yarrowia li	1118	5	6.5	38	2	Q8HKI7	Q8hki7 amblyomma v
1046	6	7.8	1765	2	Q9JMD4	Q9jmd4 mus musculus	1119	5	6.5	38	2	Q6M3Y2	Q6m3y2 corynebacte
1047	6	7.8	1765	2	Q9R053	Q9r053 mus musculus	1120	5	6.5	38	2	Q90X31	Q90x31 typhlonecte
1048	6	7.8	1768	2	Q9N8K7	Q9n8k7 trypanosoma	1121	5	6.5	38	2	Q90XL9	Q90xl9 latimeria m
1049	6	7.8	1774	2	Q754J8	Q754j8 ashbya goss	1122	5	6.5	38	2	Q9PVL2	Q9pvl2 lepisosteus
1050	6	7.8	1784	2	Q7UPX3	Q7upx3 rhodopirell	1123	5	6.5	40	2	Q97VH1	Q97vh1 sulfolobus
1051	6	7.8	1805	2	Q81060	Q81060 arabidopsis	1124	5	6.5	40	2	Q73PJ4	Q73pj4 treponema d
1052	6	7.8	1858	1	P3K2_DICDI	P54674 dictyosteli	1125	5	6.5	41	2	Q26281	Q26281 drosophila
1053	6	7.8	1924	2	Q67654	Q67654 garlic late	1126	5	6.5	42	2	Q86YY8	Q86yy8 homo sapien

1127	5	6.5	42	2	Q8BM1	Q8bm1 asphondylia	1200	5	6.5	55	2	Q8JUI7	Q8ju17 foot-and-mo
1128	5	6.5	42	2	Q8VIR6	Q8vir6 mycobacteri	1201	5	6.5	55	2	Q8JUI8	Q8ju18 foot-and-mo
1129	5	6.5	42	2	Q7VJU8	Q7vju8 helicobacte	1202	5	6.5	55	2	Q8JUJ1	Q8juj1 foot-and-mo
1130	5	6.5	44	2	Q8EX68	Q8ex68 leptospira	1203	5	6.5	55	2	Q8JN4	Q8jn4 foot-and-mo
1131	5	6.5	44	2	Q8ZV9	Q8zzv9 pyrobaculum	1204	5	6.5	55	2	Q913N5	Q913n5 foot-and-mo
1132	5	6.5	44	2	Q8T954	Q8t954 drosophila	1205	5	6.5	55	2	Q913N6	Q913n6 foot-and-mo
1133	5	6.5	44	2	Q8T273	Q8t273 brassica na	1206	5	6.5	55	2	Q913N7	Q913n7 foot-and-mo
1134	5	6.5	45	2	Q7PB27	Q7pb27 rickettsia	1207	5	6.5	55	2	Q913N8	Q913n8 foot-and-mo
1135	5	6.5	46	2	Q8NNU6	Q8nnu6 corynebacte	1208	5	6.5	55	2	Q913P0	Q913p0 foot-and-mo
1136	5	6.5	46	2	Q8FBK6	Q8fbk6 escherichia	1209	5	6.5	55	2	Q913P1	Q913p1 foot-and-mo
1137	5	6.5	46	2	Q42535	Q42535 brachydanio	1210	5	6.5	55	2	Q913P2	Q913p2 foot-and-mo
1138	5	6.5	47	2	Q69YT9	Q69yt9 homo sapien	1211	5	6.5	55	2	Q913P6	Q913p6 foot-and-mo
1139	5	6.5	47	2	Q77777	Q77777 bos taurus	1212	5	6.5	55	2	Q913P7	Q913p7 foot-and-mo
1140	5	6.5	47	2	Q853T3	Q853t3 mycobacteri	1213	5	6.5	55	2	Q913P9	Q913p9 foot-and-mo
1141	5	6.5	47	2	Q7MP32	Q7mp32 vibrio vuln	1214	5	6.5	55	2	Q913Q0	Q913q0 foot-and-mo
1142	5	6.5	48	1	ATP8_TRIRU	Q36838 trichophyto	1215	5	6.5	55	2	Q913Q1	Q913q1 foot-and-mo
1143	5	6.5	48	1	Q7UAC6	Q7uac6 shigella fl	1216	5	6.5	55	2	Q913Q3	Q913q3 foot-and-mo
1144	5	6.5	48	2	Q8F357	Q8f357 leptospira	1217	5	6.5	55	2	Q913Q5	Q913q5 foot-and-mo
1145	5	6.5	48	2	Q8FEQ8	Q8feq8 escherichia	1218	5	6.5	55	2	Q913Q7	Q913q7 foot-and-mo
1146	5	6.5	49	1	COXH_THUOB	P80977 thunnus obe	1219	5	6.5	55	2	Q913Q8	Q913q8 foot-and-mo
1147	5	6.5	49	2	Q8EZK6	Q8ezk6 leptospira	1220	5	6.5	55	2	Q913Q9	Q913q9 foot-and-mo
1148	5	6.5	50	2	Q9XLF4	Q9xlf4 crax globul	1221	5	6.5	55	2	Q913R0	Q913r0 foot-and-mo
1149	5	6.5	50	2	Q8KMU5	Q8kmu5 enterococcu	1222	5	6.5	55	2	Q913R1	Q913r1 foot-and-mo
1150	5	6.5	51	2	Q8KGD9	Q8kgd9 bacterioph	1223	5	6.5	55	2	Q913R2	Q913r2 foot-and-mo
1151	5	6.5	52	1	A95E_DROME	P16548 drosophila	1224	5	6.5	55	2	Q913R3	Q913r3 foot-and-mo
1152	5	6.5	52	2	Q6T0Y8	Q6t0y8 ducula bico	1225	5	6.5	55	2	Q913R5	Q913r5 foot-and-mo
1153	5	6.5	53	2	Q6T0W6	Q6t0w6 metriopelia	1226	5	6.5	55	2	Q913R7	Q913r7 foot-and-mo
1154	5	6.5	53	2	Q6T0W7	Q6t0w7 metriopelia	1227	5	6.5	55	2	Q913R8	Q913r8 foot-and-mo
1155	5	6.5	53	2	Q6T0Y2	Q6t0y2 chalcochaps	1228	5	6.5	55	2	Q913R9	Q913r9 foot-and-mo
1156	5	6.5	53	2	Q6T0Y4	Q6t0y4 turtur chal	1229	5	6.5	55	2	Q913S0	Q913s0 foot-and-mo
1157	5	6.5	53	2	Q6T0Y6	Q6t0y6 phapitreron	1230	5	6.5	55	2	Q913S2	Q913s2 foot-and-mo
1158	5	6.5	53	2	Q6T0Y9	Q6t0y9 ducula pist	1231	5	6.5	55	2	Q913S4	Q913s4 foot-and-mo
1159	5	6.5	53	2	Q6T0Z0	Q6t0z0 ducula rubr	1232	5	6.5	55	2	Q913S9	Q913s9 foot-and-mo
1160	5	6.5	53	2	Q6T0Z1	Q6t0z1 ducula paci	1233	5	6.5	55	2	Q913T1	Q913t1 foot-and-mo
1161	5	6.5	53	2	Q6T0Z7	Q6t0z7 prtilinopus	1234	5	6.5	55	2	Q913T4	Q913t4 foot-and-mo
1162	5	6.5	53	2	Q6T102	Q6t102 leptotilia m	1235	5	6.5	55	2	Q913T7	Q913t7 foot-and-mo
1163	5	6.5	53	2	Q6T103	Q6t103 leptotilia r	1236	5	6.5	55	2	Q913T9	Q913t9 foot-and-mo
1164	5	6.5	53	2	Q6T104	Q6t104 leptotilia p	1237	5	6.5	55	2	Q913U0	Q913u0 foot-and-mo
1165	5	6.5	53	2	Q6T105	Q6t105 leptotilia c	1238	5	6.5	55	2	Q913U1	Q913u1 foot-and-mo
1166	5	6.5	53	2	Q6T106	Q6t106 zenaida aur	1239	5	6.5	55	2	Q913U2	Q913u2 foot-and-mo
1167	5	6.5	53	2	Q6T107	Q6t107 zenaida aur	1240	5	6.5	55	2	Q913U3	Q913u3 foot-and-mo
1168	5	6.5	53	2	Q6T108	Q6t108 zenaida mac	1241	5	6.5	55	2	Q913U8	Q913u8 foot-and-mo
1169	5	6.5	53	2	Q6T109	Q6t109 zenaida gal	1242	5	6.5	55	2	Q913U9	Q913u9 foot-and-mo
1170	5	6.5	53	2	Q6T110	Q6t110 zenaida mel	1243	5	6.5	55	2	Q91H71	Q91h71 foot-and-mo
1171	5	6.5	53	2	Q6T111	Q6t111 zenaida asi	1244	5	6.5	55	2	Q9DJ54	Q9dj54 foot-and-mo
1172	5	6.5	53	2	Q6T112	Q6t112 geotrygon c	1245	5	6.5	55	2	Q9DJ62	Q9dj62 foot-and-mo
1173	5	6.5	53	2	Q6T113	Q6t113 geotrygon c	1246	5	6.5	55	2	Q9DJ84	Q9dj84 foot-and-mo
1174	5	6.5	53	2	Q6T115	Q6t115 reinwardtoe	1247	5	6.5	55	2	Q9DJ85	Q9dj85 foot-and-mo
1175	5	6.5	53	2	Q6T117	Q6t117 macropygia	1248	5	6.5	55	2	Q9DJ87	Q9dj87 foot-and-mo
1176	5	6.5	53	2	Q6T118	Q6t118 columba fas	1249	5	6.5	55	2	Q9DJ88	Q9dj88 foot-and-mo
1177	5	6.5	53	2	Q6T121	Q6t121 columba sub	1250	5	6.5	55	2	Q9DJ90	Q9dj90 foot-and-mo
1178	5	6.5	53	2	Q6T123	Q6t123 columba spe	1251	5	6.5	55	2	Q9DJA0	Q9dja0 foot-and-mo
1179	5	6.5	53	2	Q6T124	Q6t124 columba oen	1252	5	6.5	55	2	Q9DSB7	Q9dsb7 foot-and-mo
1180	5	6.5	53	2	Q6T125	Q6t125 columba fla	1253	5	6.5	55	2	Q9DSN7	Q9dsn7 foot-and-mo
1181	5	6.5	53	2	Q6T134	Q6t134 streptopeli	1254	5	6.5	56	2	Q34398	Q34398 drosophila
1182	5	6.5	53	2	Q6T135	Q6t135 nesoenas ma	1255	5	6.5	56	2	Q6PU88	Q6pu88 vibrio harv
1183	5	6.5	53	2	Q6QX02	Q6qx02 oryza sativ	1256	5	6.5	56	2	Q97SC9	Q97sc9 streptococc
1184	5	6.5	53	2	Q8K749	Q8k749 streptococc	1257	5	6.5	56	2	Q73D06	Q73d06 bacillus ce
1185	5	6.5	53	2	Q92129	Q92129 rickettsia	1258	5	6.5	56	2	Q8LHHS	Q8lhs bacillus ce
1186	5	6.5	53	2	Q8DQ29	Q8dq29 streptococc	1259	5	6.5	56	2	Q8IUP6	Q8iup6 bacillus an
1187	5	6.5	53	2	Q8E102	Q8e102 streptococc	1260	5	6.5	56	2	Q9DJ46	Q9dj46 foot-and-mo
1188	5	6.5	54	2	Q85332	Q85332 vaccinia vi	1261	5	6.5	56	2	Q9DJ80	Q9dj80 foot-and-mo
1189	5	6.5	55	1	SECG_SULSO	P60465 sulfolobus	1262	5	6.5	57	2	Q9HQV4	Q9hqv4 halobacteri
1190	5	6.5	55	1	SKK4_MESMA	Q95nj8 mesobuthus	1263	5	6.5	57	2	Q9BDG3	Q9bdg3 bos taurus
1191	5	6.5	55	2	Q957Z3	Q957z3 casuarinus c	1264	5	6.5	57	2	Q6JLY5	Q6jly5 bacterioph
1192	5	6.5	55	2	Q6Y0F6	Q6y0f6 amazona far	1265	5	6.5	57	2	Q7X1Q4	Q7x1q4 pseudomonas
1193	5	6.5	55	2	Q9TBJ0	Q9tbj0 neomorphus	1266	5	6.5	57	2	Q7X1R0	Q7x1r0 pseudomonas
1194	5	6.5	55	2	Q64U35	Q64u35 bacteroides	1267	5	6.5	57	2	Q7X1T1	Q7x1t1 pseudomonas
1195	5	6.5	55	2	Q8PJ07	Q8pj07 xanthomonas	1268	5	6.5	57	2	Q64TR7	Q64tr7 bacteroides
1196	5	6.5	55	2	Q98E41	Q98e41 rhizobium l	1269	5	6.5	57	2	Q879H2	Q879h2 streptococc
1197	5	6.5	55	2	Q7V1Y0	Q7v1y0 prochloroco	1270	5	6.5	57	2	Q913Q4	Q913q4 foot-and-mo
1198	5	6.5	55	2	Q8X283	Q8x283 escherichia	1271	5	6.5	57	2	Q913T8	Q913t8 foot-and-mo
1199	5	6.5	55	2	Q8JUH9	Q8juh9 foot-and-mo	1272	5	6.5	57	2	Q671I1	Q671i1 chlorella v

1273	5	6.5	58	2	Q651J9	Q651j9	oryza sativ	1346	5	6.5	67	2	Q792Z2	Q792z2	staphylococ
1274	5	6.5	58	2	Q7X1S3	Q7x1s3	pseudomonas	1347	5	6.5	67	2	Q7A3G9	Q7a3g9	staphylococ
1275	5	6.5	58	2	Q7USQ5	Q7usq5	rhodopirell	1348	5	6.5	67	2	Q6G6E1	Q6g6e1	staphylococ
1276	5	6.5	58	2	Q9DJ47	Q9dj47	foot-and-mo	1349	5	6.5	67	2	Q6GDR5	Q6gdr5	staphylococ
1277	5	6.5	58	2	Q9PV03	Q9pv03	mugil cepha	1350	5	6.5	67	2	Q9PTZ0	Q9ptz0	polyterus
1278	5	6.5	59	1	Y9G1_PSEPK	Q88ea5	pseudomonas	1351	5	6.5	67	2	Q9PTZ3	Q9ptz3	dicertrarch
1279	5	6.5	59	2	Q9VUJ6	Q9vuj6	drosohilla	1352	5	6.5	67	2	Q9PTZ4	Q9ptz4	chirocentru
1280	5	6.5	59	2	Q466G3	Q466g3	enterobacte	1353	5	6.5	67	2	Q9PTZ6	Q9ptz6	amia calva
1281	5	6.5	59	2	Q39847	Q39847	foot-and-mo	1354	5	6.5	67	2	Q9PUT8	Q9put8	salarias sp
1282	5	6.5	59	2	Q671H4	Q671h4	chlorella v	1355	5	6.5	67	2	Q9PV02	Q9pv02	psettodes s
1283	5	6.5	60	2	Q8VSN6	Q8vsn6	shigella fl	1356	5	6.5	67	2	Q9PV04	Q9pv04	gadu morhu
1284	5	6.5	60	2	Q7MBP0	Q7mbp0	vibrio vuln	1357	5	6.5	67	2	Q9PV05	Q9pv05	harpadon sp
1285	5	6.5	61	2	Q7Z2R6	Q7z2r6	homo sapien	1358	5	6.5	68	2	Q9TP06	Q9tp06	brachydanio
1286	5	6.5	61	2	Q967U2	Q967u2	branchiosto	1359	5	6.5	68	2	Q6CTH7	Q6cth7	staphylococ
1287	5	6.5	61	2	Q7QVC1	Q7qvc1	giardia lam	1360	5	6.5	68	2	Q6DB23	Q6db23	erwinia car
1288	5	6.5	61	2	Q8SC27	Q8sc27	stx2 conver	1361	5	6.5	68	2	Q913P8	Q913p8	foot-and-mo
1289	5	6.5	61	2	Q94CK6	Q94ck6	oryza sativ	1362	5	6.5	69	2	Q8L822	Q8l822	linum usita
1290	5	6.5	61	2	Q7WS68	Q7ws68	pseudomonas	1363	5	6.5	69	2	Q57052	Q57052	staphylococ
1291	5	6.5	61	2	Q7X1R5	Q7x1r5	pseudomonas	1364	5	6.5	69	2	Q72WH5	Q72wh5	desulfovibr
1292	5	6.5	61	2	Q99RV5	Q99rv5	staphylococ	1365	5	6.5	69	2	Q7MZJ2	Q7mzj2	photohabdu
1293	5	6.5	61	2	Q7A405	Q7a405	staphylococ	1366	5	6.5	69	2	Q6MCF8	Q6mcf8	parachlamyd
1294	5	6.5	61	2	Q6GEB5	Q6geb5	staphylococ	1367	5	6.5	69	2	Q913U7	Q913u7	foot-and-mo
1295	5	6.5	61	2	Q8JUH6	Q8juh6	foot-and-mo	1368	5	6.5	69	2	Q6B4E5	Q6b4e5	clostera an
1296	5	6.5	61	2	Q84148	Q84148	orf virus	1369	5	6.5	69	2	Q6TVF7	Q6tvf7	bovine papu
1297	5	6.5	62	1	PSBZ_CHLRE	P92276	chlamydomon	1370	5	6.5	70	2	O26195	O26195	methanobact
1298	5	6.5	62	1	Y100_XANAC	Q8br66	xanthomonas	1371	5	6.5	70	2	P77081	P77081	escherichia
1299	5	6.5	62	2	Q8Z364	Q8z364	salmonella	1372	5	6.5	70	2	Q8EGV4	Q8egv4	shewanella
1300	5	6.5	62	2	Q8ZMS5	Q8zms5	salmonella	1373	5	6.5	70	2	Q8JUH7	Q8juh7	foot-and-mo
1301	5	6.5	62	2	Q99VI6	Q99vi6	staphylococ	1374	5	6.5	70	2	Q8JUH7	Q8juh7	foot-and-mo
1302	5	6.5	62	2	Q7A1F0	Q7a1f0	staphylococ	1375	5	6.5	70	2	Q913T0	Q913t0	foot-and-mo
1303	5	6.5	62	2	Q7A6N7	Q7a6n7	staphylococ	1376	5	6.5	70	2	Q913U6	Q913u6	foot-and-mo
1304	5	6.5	62	2	Q8B6X8	Q8b6x8	pseudomonas	1377	5	6.5	70	2	Q6TVT9	Q6tv9	orf virus
1305	5	6.5	62	2	Q6AKV1	Q6akv1	desulfotale	1378	5	6.5	70	2	Q9DJ93	Q9dj93	foot-and-mo
1306	5	6.5	62	2	Q6GB36	Q6gb36	staphylococ	1379	5	6.5	71	2	Q6I1I1	Q6i1i1	drosohilla
1307	5	6.5	62	2	Q6GIJ6	Q6gi6	staphylococ	1380	5	6.5	71	2	Q8D776	Q8d776	vibrio vuln
1308	5	6.5	63	1	YF96_PSESM	Q88613	pseudomonas	1381	5	6.5	71	2	Q9KP44	Q9kp44	bacillus ha
1309	5	6.5	63	2	Q8ESN6	Q8esn6	pseudomonas	1382	5	6.5	71	2	Q6AQB2	Q6aqb2	desulfotale
1310	5	6.5	63	2	Q8F6F8	Q8f6f8	leptosira	1383	5	6.5	72	2	Q09137	Q09137	rattus sp.
1311	5	6.5	63	2	Q8FCIF9	Q8fcif9	lactococcus	1384	5	6.5	72	2	Q6XQF3	Q6xqf3	enterobacte
1312	5	6.5	63	2	Q9L5F0	Q9l5f0	salmonella	1385	5	6.5	72	2	Q8XU54	Q8xu54	raletonia s
1313	5	6.5	63	2	Q671I3	Q671i3	chlorella v	1386	5	6.5	72	2	Q9PC18	Q9pcl8	xylella fas
1314	5	6.5	64	1	V07K_LSV	P27333	lily sympto	1387	5	6.5	73	2	Q9LXV1	Q9lxx1	arabidopsis
1315	5	6.5	64	2	Q42196	Q42196	arabidopsis	1388	5	6.5	73	2	Q7UUV7	Q7uuv7	white spot
1316	5	6.5	64	2	Q8FKX7	Q8fkx7	escherichia	1389	5	6.5	73	2	Q8VAN0	Q8van0	rhodopirell
1317	5	6.5	64	2	Q913S3	Q913s3	foot-and-mo	1390	5	6.5	74	1	YD97_CAMJE	YD97	campylobact
1318	5	6.5	64	2	Q70WL4	Q70wl4	lily sympto	1391	5	6.5	74	2	Q9HC47	Q9hc47	homo sapien
1319	5	6.5	64	2	Q83088	Q83088	lily sympto	1392	5	6.5	74	2	Q6V9D7	Q6v9d7	penicillium
1320	5	6.5	64	2	Q9PV06	Q9pv06	plecoglossu	1393	5	6.5	74	2	Q83YP6	Q83yp6	pseudomonas
1321	5	6.5	65	2	Q9C4Y1	Q9c4y1	sulfolobus	1394	5	6.5	74	2	Q746V9	Q746v9	geobacter s
1322	5	6.5	65	2	Q19919	Q19919	cyanidium c	1395	5	6.5	74	2	Q822T0	Q822t0	enterococcu
1323	5	6.5	65	2	Q6U9J9	Q6u9j9	bacterioph	1396	5	6.5	74	2	Q9ERA4	Q9era4	microtus ar
1324	5	6.5	65	2	Q707K3	Q707k3	escherichia	1397	5	6.5	74	2	Q913P4	Q913p4	foot-and-mo
1325	5	6.5	65	2	Q63EJ8	Q63ej8	bacillus ce	1398	5	6.5	74	2	Q6XM30	Q6xm30	feldmannia
1326	5	6.5	65	2	Q64UL0	Q64ul0	bacteroides	1399	5	6.5	74	2	Q9DU22	Q9du22	foot-and-mo
1327	5	6.5	65	2	Q73BY5	Q73by5	bacillus ce	1400	5	6.5	74	2	Q9DJ92	Q9dj92	foot-and-mo
1328	5	6.5	65	2	Q7NTW2	Q7niw2	gloeobacter	1401	5	6.5	75	2	Q611Q3	Q611q3	drosohilla
1329	5	6.5	65	2	Q81GN8	Q81gm8	bacillus ce	1402	5	6.5	75	2	Q95LM4	Q95lm4	macaca fasc
1330	5	6.5	65	2	Q81T78	Q81tt8	bacillus an	1403	5	6.5	75	2	Q9BF34	Q9bf34	erinaeac c
1331	5	6.5	65	2	Q9J868	Q9j868	neisseria m	1404	5	6.5	75	2	Q85FK0	Q85fk0	adiantum ca
1332	5	6.5	65	2	Q6HM16	Q6hm16	bacillus th	1405	5	6.5	75	2	Q76YJ9	Q76yj9	bacterioph
1333	5	6.5	65	2	Q9YW41	Q9yw41	melanoplus	1406	5	6.5	75	2	Q8VNN7	Q8vnn7	anabaena sp
1334	5	6.5	66	2	Q9PT45	Q9pt45	pantodon bu	1407	5	6.5	75	2	Q9PND7	Q9pnd7	campylobact
1335	5	6.5	66	2	Q9PTZ5	Q9ptz5	anguilla sp	1408	5	6.5	75	2	Q8JUI3	Q8ju13	foot-and-mo
1336	5	6.5	66	2	Q9PV01	Q9pv01	mola mola	1409	5	6.5	75	2	Q6ZVH5	Q6zv5	pyrobaculum
1337	5	6.5	66	2	Q9PV07	Q9pv07	esox lucius	1410	5	6.5	76	2	Q8PY85	Q8py85	methanosarc
1338	5	6.5	66	2	Q9PV08	Q9pv08	barbus tetr	1411	5	6.5	76	2	Q8GVZ5	Q8gvz5	oryza sativ
1339	5	6.5	66	2	Q9PV09	Q9pv09	chano chan	1412	5	6.5	76	2	Q83YN2	Q83yn2	pseudomonas
1340	5	6.5	66	2	Q9PV10	Q9pv10	notopterus	1413	5	6.5	76	2	Q83YP3	Q83yp3	pseudomonas
1341	5	6.5	66	2	Q9PV11	Q9pv11	ostecoglossu	1414	5	6.5	76	2	Q83YP7	Q83yp7	pseudomonas
1342	5	6.5	67	2	Q7Z4F1	Q7z4f1	homo sapien	1415	5	6.5	76	2	Q833E6	Q833e6	enterococcu
1343	5	6.5	67	2	Q7R5Y3	Q7r5y3	giardia lam	1416	5	6.5	76	2	Q889K4	Q889k4	pseudomonas
1344	5	6.5	67	2	Q8GA62	Q8ga62	escherichia	1417	5	6.5	76	2	Q913U5	Q913u5	foot-and-mo
1345	5	6.5	67	2	Q99RA2	Q99ra2	staphylococ	1418	5	6.5	77	2	Q8LEC6	Q8lec6	arabidopsis

1419 5 6.5 77 2 Q54148 Q54148 shigella fl  
1420 5 6.5 77 2 Q83YP0 Q83YP0 pseudomonas  
1421 5 6.5 77 2 Q9AH74 Q9AH74 salmonella  
1422 5 6.5 77 2 Q9AH76 Q9AH76 escherichia  
1423 5 6.5 77 2 Q9EZG8 Q9EZG8 streptococ  
1424 5 6.5 77 2 Q62YB4 Q62YB4 bacillus li  
1425 5 6.5 77 2 Q635B7 Q635B7 bacillus ce  
1426 5 6.5 77 2 Q8R9R8 Q8R9R8 thermoanaer  
1427 5 6.5 77 2 Q8VSD1 Q8VSD1 shigella fl  
1428 5 6.5 77 2 Q8X2Q7 Q8X2Q7 escherichia  
1429 5 6.5 77 2 Q81M63 Q81M63 bacillus an  
1430 5 6.5 77 2 Q89N23 Q89N23 bradyrhizob  
1431 5 6.5 77 2 Q6HDZ6 Q6HDZ6 bacillus th  
1432 5 6.5 77 2 Q913Q6 Q913Q6 foot-and-mo  
1433 5 6.5 78 1 VES\_HPV70 Q73MI3 treponema d  
1434 5 6.5 78 2 Q8D072 Q8D072 streptococ  
1435 5 6.5 78 2 Q6D620 Q6D620 erwinia car  
1436 5 6.5 78 2 Q913S5 Q913S5 foot-and-mo  
1437 5 6.5 78 2 Q91P99 Q91P99 canine herp  
1438 5 6.5 79 2 Q8LH71 Q8LH71 oryza sativ  
1439 5 6.5 79 2 Q42006 Q42006 arabidopsis  
1440 5 6.5 79 2 Q8QRX9 Q8QRX9 pongine her  
1441 5 6.5 79 2 Q913T6 Q913T6 foot-and-mo  
1442 5 6.5 79 2 Q6GZM3 Q6GZM3 frog virus  
1443 5 6.5 79 2 Q9DW04 Q9DW04 plutella xy  
1444 5 6.5 80 2 Q6IGM8 Q6IGM8 drosophila  
1445 5 6.5 80 2 Q64V26 Q64V26 bacteroides  
1446 5 6.5 80 2 Q8XVX1 Q8XVX1 ralstonia s  
1447 5 6.5 80 2 Q734N3 Q734N3 bacillus ce  
1448 5 6.5 80 2 Q83JZ8 Q83JZ8 shigella fl  
1449 5 6.5 81 1 VES\_HPV35 P27226 human papil  
1450 5 6.5 81 2 Q68DQ1 Q68DQ1 homo sapien  
1451 5 6.5 81 2 Q8SC26 Q8SC26 stx2 conver  
1452 5 6.5 81 2 Q7Y2H0 Q7Y2H0 stx1 conver  
1453 5 6.5 81 2 Q7I2J3 Q7I2J3 salmonella  
1454 5 6.5 81 2 Q8KLJ7 Q8KLJ7 foot-and-mo  
1455 5 6.5 81 2 Q91H50 Q91H50 rhynchospo  
1456 5 6.5 82 2 Q02039 Q02039 rhynchospo  
1457 5 6.5 82 2 Q30603 Q30603 macaca mula  
1458 5 6.5 82 2 Q7X9E4 Q7X9E4 hordeum vul  
1459 5 6.5 82 2 Q851F7 Q851F7 oryza sativ  
1460 5 6.5 82 2 Q7N7R3 Q7N7R3 photorhabdu  
1461 5 6.5 82 2 Q7NEN6 Q7NEN6 gloeobacter  
1462 5 6.5 82 2 Q9K831 Q9K831 bacillus ha  
1463 5 6.5 83 2 Q94ML7 Q94ML7 bacterioph  
1464 5 6.5 83 2 Q6QG5 Q6QG5 bacterioph  
1465 5 6.5 83 2 Q97JX0 Q97JX0 clostridium  
1466 5 6.5 83 2 Q6LQ25 Q6LQ25 photobacter  
1467 5 6.5 83 2 Q7U620 Q7U620 synecococ  
1468 5 6.5 83 2 Q89DP8 Q89DP8 bradyrhizob  
1469 5 6.5 83 2 Q72007 Q72007 murine hepa  
1470 5 6.5 83 2 Q8JU12 Q8JU12 foot-and-mo  
1471 5 6.5 83 2 Q91G36 Q91G36 chilo iride  
1472 5 6.5 83 2 Q66193 Q66193 murine hepa  
1473 5 6.5 84 1 YA70\_HELPY Q612N8 helicobact  
1474 5 6.5 84 2 Q6J2N8 Q6J2N8 acinetobact  
1475 5 6.5 84 2 Q54681 Q54681 lactococci  
1476 5 6.5 84 2 Q74YN9 Q74YN9 versinia pe  
1477 5 6.5 84 2 Q934Z3 Q934Z3 salmonella  
1478 5 6.5 84 2 Q72RS3 Q72RS3 leptospira  
1479 5 6.5 84 2 Q7ARA5 Q7ARA5 versinia pe  
1480 5 6.5 84 2 Q81N20 Q81N20 bacillus an  
1481 5 6.5 84 2 Q9ZH06 Q9ZH06 versinia pe  
1482 5 6.5 84 2 Q919H0 Q919H0 culex nigrl  
1483 5 6.5 84 2 Q91E08 Q91E08 cydia pomon  
1484 5 6.5 85 2 Q7YVK0 Q7YVK0 trypanosoma  
1485 5 6.5 85 2 Q9XXH2 Q9XXH2 caenorhabdi  
1486 5 6.5 85 2 Q7P2Z5 Q7P2Z5 fusobacteri  
1487 5 6.5 85 2 Q6GND4 Q6GND4 xenopus lae  
1488 5 6.5 85 2 P89731 P89731 human immun  
1489 5 6.5 86 1 YA70\_HELPJ Q9ZM67 helicobact  
1490 5 6.5 86 2 Q9T1L1 Q9T1L1 bacterioph  
1491 5 6.5 86 2 Q9T1L1 Q9T1L1 bacterioph

1492 5 6.5 86 2 P94863 P94863 lactobacill  
1493 5 6.5 86 2 Q92HX6 Q92HX6 rickettsia  
1494 5 6.5 86 2 Q6MBB6 Q6MBB6 parachlamyd  
1495 5 6.5 86 2 Q8UJG0 Q8UJG0 agrobacteri  
1496 5 6.5 87 1 FLIQ\_BORBU Q44906 borrelia bu  
1497 5 6.5 87 2 Q75YV6 Q75YV6 euhadra bra  
1498 5 6.5 87 2 Q71T70 Q71T70 bacterioph  
1499 5 6.5 87 2 Q661Z1 Q661Z1 borrelia ga  
1500 5 6.5 87 2 Q8YS68 Q8YS68 anabaena sp

## ALIGNMENTS

## RESULT 1

Q6UWR8 PRELIMINARY; PRT; 77 AA.  
AC Q6UWR8;  
DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE GPK512.  
GN ORFNames=UNO512;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2287296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
Vandien R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,  
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR ENBL; AY358675; AAQ89038.1; -.  
SQ SEQUENCE 77 AA; 8772 MW; 110CBCF87CCC4B86 CRC64;

Query Match 100.0%; Score 77; DB 2; Length 77;  
Best Local Similarity 100.0%; Pred. No. 1e-71;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPVKQLKRMFEPTRIATIMVLLCSAFWVHNGKGLALIFCIQLSALTWYLSLF 60  
DB 1 MGPVKQLKRMFEPTRIATIMVLLCSAFWVHNGKGLALIFCIQLSALTWYLSLF 60  
QY 61 IPFADAVKKCFVAVCLA 77  
DB 61 IPFADAVKKCFVAVCLA 77

## RESULT 2

Q95562 PRELIMINARY; PRT; 160 AA.  
AC Q95562;  
DT 01-MAY-1999 (T-EMBLrel. 10, Created)  
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Rhodes S.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL035297; CAA22897.1; -;  
 DR EMBL: BC068098; AAH68098.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 160 AA; 17779 MW; F05C57532B7593BD CRC64;

Query Match 100.0%; Score 77; DB 2; Length 160;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-71;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPVKQLKRMFETRIATIMVLLCFALTCSAFWHNGKGLALIFCILOSALTWTYSLSF 60  
 DB 84 MGPVKQLKRMFETRIATIMVLLCFALTCSAFWHNGKGLALIFCILOSALTWTYSLSF 143

QY 61 IPPARDVKKCFVCLIA 77  
 DB 144 IPPARDVKKCFVCLIA 160

RESULT 3  
 Q8VD57 PRELIMINARY; PRT; 159 AA.  
 AC Q8VD57;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE RIKEN cDNA 201005Q13 (Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:983013K19 product:hypothetical protein, full insert sequence).  
 DE protein, full insert sequence).  
 GN Name=201005Q13Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RA The RIKEN Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu M., Hayashizaki Y.;  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takahashi A., Takada Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017549; AAH17549.1; -;  
DR EMBL; AK036578; BAC29488.1; -;  
DR MGD; MGI:1917362; 2010005013Rik.  
KW Hypothetical protein.  
SQ SEQUENCE 159 AA; 17499 MW; B30B7E5FE92A0E6 CRC64;  
Query Match 28.6%; Score 22; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 1.7e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 NKGLALIFCQLSLATWYSL 59  
DB 120 NKGLALIFCQLSLATWYSL 141  
RESULT 4  
Q77375 PRELIMINARY; PRT; 161 AA.  
AC Q77375  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein zgc:64053.  
GN ORFNames=zgc:64053;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins L., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053226; AAH53226.1; -;  
DR ZFIN; ZDB-GENE-040426-1350; zgc:64053.  
KW Hypothetical protein.  
SQ SEQUENCE 161 AA; 18025 MW; 5BACAB7DDACDE634 CRC64;  
Query Match 26.0%; Score 20; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.1e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPVKOLKRMFEPTRLIATI 20  
DB 85 MGPVKOLKRMFEPTRLIATI 104  
RESULT 5  
Q86F94 PRELIMINARY; PRT; 113 AA.  
AC Q86F94  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Clone ZZZ409 mRNA sequence.  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;  
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,  
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,  
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,  
RA Xue C.L., Feng Z., Chen Z., Han Z.G.;  
RT "Evolutionary and biomedical implications of a Schistosoma japonicum  
complementary DNA resource."  
RL Nat. Genet. 35:139-147(2003).  
DR EMBL; AY222969; AAP05981.1; -;  
SQ SEQUENCE 113 AA; 12524 MW; 2FF26F707A512D73 CRC64;  
Query Match 11.7%; Score 9; DB 2; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 43 LIFCQLSL 51  
DB 79 LIFCQLSL 87  
RESULT 6  
Q922U5 PRELIMINARY; PRT; 136 AA.  
AC Q922U5  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE RIKEN cDNA 563040J11 (Similar to CGS104).  
GN Name=563040J11Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053226; AAH53226.1; -;  
DR ZFIN; ZDB-GENE-040426-1350; zgc:64053.  
KW Hypothetical protein.  
SQ SEQUENCE 161 AA; 18025 MW; 5BACAB7DDACDE634 CRC64;  
Query Match 26.0%; Score 20; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.1e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129S6/SVEVtac;  
 RA Brathwaite M., Waelitz P., Qian Y., Dudekula D., Schlessinger D.,  
 RA Nagaraja R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006777; AAH07777.1; -  
 DR EMBL; AF466883; AA021003.1; -  
 DR MGD; MG1:1918689; 563040J11.rik.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 SQ SEQUENCE 136 AA; 15085 MW; 3FEAF412B5E9840C CRC64;  
 Query Match 10.4%; Score 8; DB 2; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 4.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGPVKQLK 8  
 DB 83 MGPVKQLK 90  
 RESULT 7  
 Q8WV19 PRELIMINARY; PRT; 159 AA.  
 AC Q8WV19;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Chromosome 6 open reading frame 83.  
 GN Name=C6orf83;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalka U., Smaluk D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018969; AAH18969.1; -

SQ SEQUENCE 159 AA; 17804 MW; 0EC8A9CED7EF27E0 CRC64;  
 Query Match 10.4%; Score 8; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGPVKQLK 8  
 DB 83 MGPVKQLK 90  
 RESULT 8  
 Q9UIC7 PRELIMINARY; PRT; 178 AA.  
 AC Q9UIC7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE PRGRI (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hu Y.F., Mao X.H., Zhuang M., Lu C.D.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF041429; AAF18564.1; -  
 DR Genew; HGNC:21102; C6orf83.  
 FT NON TER 1  
 SQ SEQUENCE 178 AA; 19879 MW; 72C1E2BA35F3C6EA CRC64;  
 Query Match 10.4%; Score 8; DB 2; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 6.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGPVKQLK 8  
 DB 102 MGPVKQLK 109  
 RESULT 9  
 FUCP\_ECOLI STANDARD; PRT; 438 AA.  
 ID FUCP\_ECOLI  
 AC P11551;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE L-fucose permease.  
 GN Name=fucP; OrderedLocusNames=b2801;  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KL2;  
 RX MEDLINE=89315234; PubMed=2664711;  
 RA Lu Z., Lin E.C.C.;  
 RT "The nucleotide sequence of Escherichia coli genes for L-fucose  
 RT dissimilation.";  
 RL Nucleic Acids Res. 17:4883-4884(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KL2 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [3]

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RP SEQUENCE OF 1-31 FROM N.A.
RX MEDLINE=9003697; PubMed=2553671;
RA Chen Y.M., Lu Z., Lin E.C.C.;
RT "Constitutive activation of the fucAO operon and silencing of the
RT "Constitutively transcribed fucPK operon by an IS element in Escherichia
RL coli mutants selected for growth on L-1,2-propanediol.";
RN J. Bacteriol. 171:6097-6105(1989).
RN [4]
RN TOPOLOGY.
RX MEDLINE=95302988; PubMed=7783647;
RA Gunn F.J., Tate C.G., Sansom C.E., Henderson P.J.;
RT "Topological analyses of the L-fucose-H+ symport protein, FucP, from
RT Escherichia coli.";
RL Mol. Microbiol. 15:771-783(1995).
CC -|- FUNCTION: Transport of L-fucose into the cell.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -|- SIMILARITY: Belongs to the FHS transporter (TC 2.A.1.7) family.
CC -----
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CC -----
DR EMBL; X15025; CAA33126.1; -
DR EMBL; U29581; AAB40451.1; -
DR EMBL; U00096; AAC75843.1; -
DR EMBL; M31059; AAA23822.2; -
DR PIR; JS0184; WQECFF.
DR ECHOBASE; EB0348; -
DR EcoGene; EG10352; fucP.
DR InterPro; IPR005275; Lfuc_permease.
DR InterPro; IPR007114; MFS.
DR TIGRFAMS; TIGR00885; fucP; 1.
DR PROSITE; PS00850; MFS; 1.
KW Complete proteome; Fucose metabolism; Inner membrane; Sugar transport;
KW Transmembrane.
FT DOMAIN 1 24 Cytoplasmic (Probable).
FT TRANSMEM 25 45 Probable.
FT TRANSMEM 46 55 Periplasmic (Probable).
FT TRANSMEM 56 76 Probable.
FT TRANSMEM 77 95 Cytoplasmic (Probable).
FT TRANSMEM 96 115 Probable.
FT TRANSMEM 116 118 Periplasmic (Probable).
FT TRANSMEM 119 139 Probable.
FT TRANSMEM 140 166 Cytoplasmic (Probable).
FT TRANSMEM 167 187 Probable.
FT TRANSMEM 188 206 Periplasmic (Probable).
FT TRANSMEM 207 227 Probable.
FT TRANSMEM 228 265 Cytoplasmic (Probable).
FT TRANSMEM 266 286 Probable.
FT TRANSMEM 287 295 Periplasmic (Probable).
FT TRANSMEM 296 316 Probable.
FT TRANSMEM 317 326 Cytoplasmic (Probable).
FT TRANSMEM 327 347 Probable.
FT TRANSMEM 348 352 Periplasmic (Probable).
FT TRANSMEM 353 373 Probable.
FT TRANSMEM 374 381 Cytoplasmic (Probable).
FT TRANSMEM 382 402 Probable.
FT TRANSMEM 403 413 Periplasmic (Probable).
FT TRANSMEM 414 434 Probable.
FT TRANSMEM 435 438 Cytoplasmic (Probable).
SQ SEQUENCE 438 AA; 47544 MW; DBAA3785274A0085 CRC64;

Query Match 10.4%; Score 8; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAF 34
Db 353 ALTLCSAF 360

RESULT 11
Q8FEES Q8FEES PRELIMINARY; PRT; 438 AA.
AC Q8FEES;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE L-fucose permease.
GN Name=fucP; OrderedLocusNames=c3370;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]

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RESULT 10
Q8Z430 Q8Z430 PRELIMINARY; PRT; 438 AA.
AC Q8Z430; Q7C7H5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE L-fucose permease.
GN Name=fucP; OrderedLocusNames=STV3115, t2883;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=126444504;
DOI=10.1128/JB.185.7.2330-2337-2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanlani V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627277; CAD02801.1; -
DR EMBL; AE016843; AAO70439.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR TIGRFAMS; TIGR00885; fucP; 1.
DR PROSITE; PS00850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 47773 MW; AFDED4C0C344994E CRC64;

Query Match 10.4%; Score 8; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAF 34
Db 353 ALTLCSAF 360

RESULT 11
Q8FEES Q8FEES PRELIMINARY; PRT; 438 AA.
AC Q8FEES;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE L-fucose permease.
GN Name=fucP; OrderedLocusNames=c3370;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]

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SEQUENCE FROM N.A.
RC STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=2238234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR ENBL; AE016765; AAN81817.1; -.
DR InterPro; IPR005275; Lfuc_permease.
DR TIGRFAMs; TIGR00885; fucP; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 47536 MW; C919EBA3A4378CEC CRC64;

Query Match 10.4%; Score 8; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCASF 34
DB 353 ALTLCASF 360
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RESULT 12
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DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Fucose permease.
GN Names=fucP; OrderedLocusNames=S3010, SP2815;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding X., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR ENBL; AE015295; AAN43303.1; -.
DR ENBL; AE016987; AAP18128.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005275; Lfuc_permease.
DR InterPro; IPR007114; MFS.
DR TIGRFAMs; TIGR00885; fucP; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 47590 MW; AFB09C88BE0E4C81 CRC64;

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SEQUENCE FROM N.A.
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RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR ENBL; AE016765; AAN81817.1; -.
DR InterPro; IPR005275; Lfuc_permease.
DR TIGRFAMs; TIGR00885; fucP; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 47536 MW; C919EBA3A4378CEC CRC64;

Query Match 10.4%; Score 8; DB 2; Length 438;
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QY 27 ALTLCASF 34
DB 353 ALTLCASF 360
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AC Q8X6R7; Q7AB68;
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DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Fucose permease.
GN Names=fucP; OrderedLocusNames=ECs3661, z4118;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:111-22(2001).
DR ENBL; AE005508; AAG57915.1; -.
DR ENBL; AP002563; BAB37084.1; -.
DR PIR; E91086; E91086.
DR PIR; G85931; G85931.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005275; Lfuc_permease.
DR InterPro; IPR007114; MFS.
DR TIGRFAMs; TIGR00885; fucP; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
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Query Match 10.4%; Score 8; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCASF 34
DB 353 ALTLCASF 360
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RESULT 14
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ID Q69W11
AC Q69W11

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Search completed: April 7, 2005, 04:52:11  
Job time : 262 secs

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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative aluminum-activated malate transporter.
GN Names=P0531C01.9; Synonyms=P0577H07.17;
OS Oryza sativa (japonica cultivar-group)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone:P0531C01."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone:P0577H07."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003763; BAD32958.1; -.
DR EMBL; AP003619; BAD32889.1; -.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
SQ SEQUENCE 668 AA; 71022 MW; E0C236AFB248362B CRC64;

Query Match 10.4%; Score 8; DB 2; Length 668;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ALTLCSAF 34
DB 90 ALTLCSAF 97
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RESULT 15
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AC Q82T85;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=NE2033;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RX DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Savavedra-Soto L.A.,
RA Arciero B.M., Holmes N.G., Whitaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321863; CAB85944.1; -.
DR InterPro; IPR008928; Glyco trans 6hp.
KW Complete proteome; Hypothetical Protein.
SQ SEQUENCE 898 AA; 103602 MW; 2CA7DCBE9F5D9198 CRC64;

Query Match 10.4%; Score 8; DB 2; Length 898;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LLCFALT 30
DB 73 LLCFALT 80
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 7, 2005, 03:13:17 ; Search time 43 Seconds  
(without alignments)  
133.674 Million cell updates/sec

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Perfect score: 410

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*

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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep:\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	94	22.9	235	4	US-09-248-796A-20672
4	75	18.3	215	4	US-09-538-092-22
5	66.5	16.2	404	4	US-09-489-039A-11699
6	66	16.1	289	4	US-09-489-039A-12390
7	64	15.6	416	4	US-09-252-991A-24117
8	64	15.6	685	4	US-08-937-067-14
9	63	15.4	74	3	US-09-134-001C-3503
10	61.5	15.0	464	4	US-09-252-991A-24883
11	61.5	15.0	2396	1	US-08-157-005-2
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13	61.5	15.0	2396	4	US-09-565-864-2
14	61.5	15.0	2396	4	US-10-226-065-2
15	61	14.9	386	4	US-09-248-796A-17451
16	60.5	14.8	441	4	US-09-489-039A-10091
17	60	14.6	521	4	US-09-902-540-11865
18	60	14.6	585	4	US-08-937-067-9
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23	59	14.4	244	3	US-08-772-440-2
24	59	14.4	328	3	US-08-513-974B-56
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52	57	13.9	328	4	US-09-102-710B-2
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54	57	13.9	761	4	US-09-949-016-9802
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57	56.5	13.8	161	4	US-09-270-767-49330
58	56.5	13.8	170	4	US-10-000-489-68
59	56.5	13.8	246	4	US-09-107-532A-4119
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97	55.5	13.5	883	4	US-09-543-681A-6947
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Sequence 4119, Ap  
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Sequence 51834, A  
Sequence 23, Appl

101	55	13.4	218	4	US-09-270-767-42904	Sequence 42904, A	174	53	12.9	350	1	US-08-076-093A-2	Sequence 2, Appli
102	55	13.4	272	4	US-09-270-767-46084	Sequence 46084, A	175	53	12.9	350	1	US-08-450-393A-7	Sequence 7, Appli
103	55	13.4	289	3	US-09-134-001C-2917	Sequence 2917, Ap	176	53	12.9	350	1	US-08-410-453A-1	Sequence 1, Appli
104	55	13.4	327	4	US-09-107-532A-4522	Sequence 4522, Ap	177	53	12.9	350	1	US-08-701-265-2	Sequence 2, Appli
105	55	13.4	354	1	US-07-759-568-2	Sequence 2, Appli	178	53	12.9	350	1	US-08-410-454A-1	Sequence 1, Appli
106	55	13.4	355	1	US-07-759-568-1	Sequence 1, Appli	179	53	12.9	350	2	US-08-284-586-2	Sequence 2, Appli
107	55	13.4	355	1	US-08-450-393A-8	Sequence 8, Appli	180	53	12.9	350	2	US-08-410-456A-1	Sequence 1, Appli
108	55	13.4	355	2	US-08-390-000A-5	Sequence 5, Appli	181	53	12.9	350	2	US-08-805-478-2	Sequence 2, Appli
109	55	13.4	355	3	US-08-446-669-8	Sequence 8, Appli	182	53	12.9	350	2	US-08-802-627A-2	Sequence 2, Appli
110	55	13.4	355	4	US-09-625-573-8	Sequence 8, Appli	183	53	12.9	350	2	US-08-801-238-2	Sequence 2, Appli
111	55	13.4	355	5	PCT-US95-00476-8	Sequence 8, Appli	184	53	12.9	350	2	US-08-801-228-2	Sequence 2, Appli
112	55	13.4	360	1	US-08-202-056-7	Sequence 7, Appli	185	53	12.9	350	3	US-09-104-296-2	Sequence 2, Appli
113	55	13.4	360	4	US-09-409-778-4	Sequence 4, Appli	186	53	12.9	350	3	US-08-446-669-7	Sequence 7, Appli
114	54.5	13.3	100	4	US-09-543-681A-4791	Sequence 4791, Ap	187	53	12.9	350	5	PCT-US95-00476-7	Sequence 7, Appli
115	54.5	13.3	109	4	US-09-489-039A-13816	Sequence 13816, A	188	53	12.9	375	4	US-09-540-236-3290	Sequence 3290, Ap
116	54.5	13.3	175	4	US-09-479-313B-3	Sequence 3, Appli	189	53	12.9	386	4	US-09-543-681A-8033	Sequence 8033, Ap
117	54.5	13.3	267	4	US-09-949-016-9088	Sequence 9088, Ap	190	53	12.9	405	4	US-09-134-000C-5472	Sequence 5472, Ap
118	54.5	13.3	275	4	US-09-949-016-8346	Sequence 8346, Ap	191	53	12.9	474	4	US-09-252-991A-26872	Sequence 26872, A
119	54.5	13.3	398	4	US-09-830-428A-5	Sequence 5, Appli	192	53	12.9	534	4	US-09-252-991A-30725	Sequence 30725, A
120	54.5	13.3	483	4	US-09-905-999-20	Sequence 20, Appl	193	53	12.9	537	4	US-08-937-067-11	Sequence 11, Appl
121	54.5	13.3	509	4	US-09-328-352-5785	Sequence 5785, Ap	194	53	12.9	547	4	US-09-489-039A-13843	Sequence 13843, A
122	54.5	13.3	2763	3	US-08-496-944-1	Sequence 2, Appli	195	53	12.9	555	4	US-09-328-352-5873	Sequence 5873, Ap
123	54.5	13.3	2818	1	US-08-510-284-1	Sequence 1, Appli	196	53	12.9	589	2	US-08-937-540-6	Sequence 6, Appli
124	54.5	13.3	2818	1	US-08-411-389-2	Sequence 2, Appli	197	53	12.9	590	4	US-09-398-395A-54	Sequence 54, Appl
125	54.5	13.3	2818	2	US-08-449-933-2	Sequence 2, Appli	198	53	12.9	590	4	US-09-887-586A-54	Sequence 54, Appl
126	54.5	13.3	2818	3	US-07-966-049A-2	Sequence 2, Appli	199	53	12.9	590	4	US-09-895-752-54	Sequence 54, Appl
127	54.5	13.3	2818	3	US-09-542-331-2	Sequence 2, Appli	200	53	12.9	590	4	US-09-903-012B-54	Sequence 54, Appl
128	54.5	13.3	2818	3	US-09-510-791-2	Sequence 2, Appli	201	53	12.9	590	4	US-09-900-797-54	Sequence 54, Appl
129	54	13.2	98	4	US-09-540-236-3312	Sequence 3312, Ap	202	53	12.9	768	4	US-09-489-039A-12897	Sequence 12897, A
130	54	13.2	182	4	US-09-107-532A-4456	Sequence 4456, Ap	203	53	12.9	1077	4	US-09-397-550-24	Sequence 24, Appl
131	54	13.2	242	3	US-08-980-832-32	Sequence 32, Appl	204	53	12.9	1091	4	US-10-162-012-18	Sequence 18, Appl
132	54	13.2	242	4	US-09-920-923B-32	Sequence 32, Appl	205	53	12.9	1371	4	US-09-902-540-16024	Sequence 16024, A
133	54	13.2	279	2	US-08-326-286-7	Sequence 7, Appli	206	53	12.9	60	4	US-09-621-976-5232	Sequence 5232, Ap
134	54	13.2	332	4	US-09-248-796A-15840	Sequence 15840, A	207	52.5	12.8	82	4	US-09-248-796A-22737	Sequence 22737, A
135	54	13.2	360	3	US-09-116-498-12	Sequence 12, Appl	208	52.5	12.8	82	4	US-09-248-796A-25141	Sequence 25141, A
136	54	13.2	360	4	US-09-852-156-12	Sequence 12, Appl	209	52.5	12.8	113	4	US-09-710-279-452	Sequence 452, App
137	54	13.2	394	4	US-09-252-991A-27511	Sequence 27511, A	210	52.5	12.8	113	4	US-09-710-279-1206	Sequence 1206, A
138	54	13.2	400	4	US-09-252-991A-22821	Sequence 22821, A	211	52.5	12.8	113	4	US-09-949-016-11441	Sequence 11441, A
139	54	13.2	418	4	US-09-248-796A-18870	Sequence 18870, A	212	52.5	12.8	175	1	US-08-010-099-83	Sequence 83, Appl
140	54	13.2	434	4	US-09-543-681A-7154	Sequence 7154, Ap	213	52.5	12.8	175	1	US-08-010-099-87	Sequence 87, Appl
141	54	13.2	542	4	US-09-693-746-18	Sequence 18, Appl	214	52.5	12.8	175	1	US-08-448-716-83	Sequence 83, Appl
142	54	13.2	543	4	US-09-938-956-7	Sequence 7, Appli	215	52.5	12.8	175	1	US-08-448-716-87	Sequence 87, Appl
143	54	13.2	572	4	US-08-937-067-13	Sequence 13, Appl	216	52.5	12.8	175	1	US-09-304-186-83	Sequence 83, Appl
144	54	13.2	592	2	US-08-846-526-11	Sequence 11, Appl	217	52.5	12.8	175	3	US-09-304-186-87	Sequence 87, Appl
145	54	13.2	599	3	US-09-172-339-2	Sequence 2, Appli	218	52.5	12.8	175	4	US-09-754-532-83	Sequence 83, Appl
146	54	13.2	599	4	US-09-398-395A-22	Sequence 22, Appl	219	52.5	12.8	175	4	US-09-754-532-87	Sequence 87, Appl
147	54	13.2	599	4	US-09-887-586A-22	Sequence 22, Appl	220	52.5	12.8	190	4	US-09-543-681A-5070	Sequence 5070, Ap
148	54	13.2	599	4	US-09-895-752-22	Sequence 22, Appl	221	52.5	12.8	228	4	US-09-248-796A-20444	Sequence 20444, A
149	54	13.2	599	4	US-09-303-012B-22	Sequence 22, Appl	222	52.5	12.8	228	4	US-09-489-039A-14250	Sequence 14250, A
150	54	13.2	599	4	US-09-300-797-22	Sequence 22, Appl	223	52.5	12.8	230	4	US-09-489-039A-13302	Sequence 13302, A
151	54	13.2	776	4	US-09-489-039A-7465	Sequence 7465, Ap	224	52.5	12.8	289	4	US-09-489-039A-10785	Sequence 10785, A
152	53.5	13.0	147	4	US-09-489-039A-13728	Sequence 13728, A	225	52.5	12.8	302	4	US-09-583-110-4512	Sequence 4512, Ap
153	53.5	13.0	175	1	US-08-010-099-85	Sequence 85, Appl	226	52.5	12.8	302	4	US-09-107-433-4866	Sequence 4866, Ap
154	53.5	13.0	175	3	US-08-448-716-85	Sequence 85, Appl	227	52.5	12.8	360	3	US-09-116-498-8	Sequence 8, Appli
155	53.5	13.0	175	3	US-09-304-186-85	Sequence 85, Appl	228	52.5	12.8	360	3	US-09-517-605-10	Sequence 10, Appl
156	53.5	13.0	175	4	US-09-754-532-85	Sequence 85, Appl	229	52.5	12.8	360	4	US-09-170-496D-28	Sequence 28, Appl
157	53.5	13.0	212	4	US-09-902-540-14863	Sequence 14863, A	230	52.5	12.8	360	4	US-09-170-496D-180	Sequence 180, App
158	53.5	13.0	456	3	US-09-134-001C-3448	Sequence 3448, Ap	231	52.5	12.8	360	4	US-09-852-156-8	Sequence 8, Appli
159	53.5	13.0	456	4	US-09-248-796A-17048	Sequence 17048, A	232	52.5	12.8	423	4	US-09-489-039A-9464	Sequence 9464, Ap
160	53	12.9	74	4	US-09-248-796A-22346	Sequence 22346, A	233	52.5	12.8	470	2	US-08-377-440A-1	Sequence 1, Appli
161	53	12.9	115	4	US-09-107-433-2869	Sequence 2869, Ap	234	52.5	12.8	470	3	US-09-440-530-1	Sequence 1, Appli
162	53	12.9	173	4	US-09-248-796A-15442	Sequence 15442, A	235	52.5	12.8	672	4	US-09-543-681A-5976	Sequence 5976, Ap
163	53	12.9	182	4	US-09-328-352-5885	Sequence 5885, Ap	236	52.5	12.8	2787	3	US-09-245-041-15	Sequence 15, Appl
164	53	12.9	207	4	US-08-811-519-22	Sequence 22, Appl	237	52.5	12.8	2787	4	US-09-358-055B-15	Sequence 15, Appl
165	53	12.9	248	4	US-09-248-796A-15839	Sequence 15839, A	238	52.5	12.8	2787	4	US-09-893-238-15	Sequence 15, Appl
166	53	12.9	287	4	US-09-328-352-7074	Sequence 7074, Ap	239	52.5	12.8	115	4	US-09-393-634-27	Sequence 27, Appl
167	53	12.9	308	4	US-09-248-796A-20449	Sequence 20449, A	240	52	12.7	141	4	US-09-621-976-3932	Sequence 3932, Ap
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169	53	12.9	327	3	US-08-513-974B-372	Sequence 372, App	242	52	12.7	212	2	US-09-006-491-2	Sequence 2, Appli
170	53	12.9	328	3	US-08-513-974B-39	Sequence 39, Appl	243	52	12.7	212	3	US-09-335-919-2	Sequence 2, Appli
171	53	12.9	328	3	US-08-513-974B-371	Sequence 371, App	244	52	12.7	234	4	US-09-270-767-44557	Sequence 44557, A
172	53	12.9	328	4	US-09-461-436B-39	Sequence 39, Appl	245	52	12.7	262	4	US-09-270-767-45003	Sequence 45003, A
173	53	12.9	350	1	US-08-202-056-1	Sequence 1, Appli	246	52	12.7				

247	52	12.7	310	3	US-08-605-284B-10	Sequence 10, Appl	320	51.5	12.6	174	6	5194592-26	Patent No. 5194592
248	52	12.7	361	2	US-08-902-237-2	Sequence 2, Appli	321	51.5	12.6	174	6	5194592-26	Patent No. 5194592
249	52	12.7	361	3	US-08-178-694-2	Sequence 2, Appli	322	51.5	12.6	175	1	US-08-010-099-2	Sequence 2, Appli
250	52	12.7	424	4	US-09-107-532A-5459	Sequence 10553, Ap	323	51.5	12.6	175	1	US-08-010-099-67	Sequence 67, Appl
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252	52	12.7	538	4	US-09-107-532A-5563	Sequence 5563, Ap	325	51.5	12.6	175	1	US-08-010-099-69	Sequence 69, Appl
253	52	12.7	583	4	US-09-489-039A-1318	Sequence 1318, A	326	51.5	12.6	175	1	US-08-010-099-70	Sequence 70, Appl
254	52	12.7	666	4	US-08-937-067-10	Sequence 10, Appl	327	51.5	12.6	175	1	US-08-010-099-71	Sequence 71, Appl
255	52	12.7	765	4	US-09-270-767-32645	Sequence 32645, A	328	51.5	12.6	175	1	US-08-010-099-72	Sequence 72, Appl
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257	52	12.7	1011	3	US-08-836-325-2	Sequence 2, Appli	330	51.5	12.6	175	1	US-08-010-099-74	Sequence 74, Appl
258	52	12.7	1011	4	US-09-457-571-2	Sequence 2, Appli	331	51.5	12.6	175	1	US-08-010-099-75	Sequence 75, Appl
259	52	12.7	1835	3	US-08-836-325-15	Sequence 15, Appl	332	51.5	12.6	175	1	US-08-010-099-76	Sequence 76, Appl
260	52	12.7	1835	4	US-09-457-571-15	Sequence 15, Appl	333	51.5	12.6	175	1	US-08-010-099-78	Sequence 78, Appl
261	52	12.7	1969	3	US-08-836-325-16	Sequence 16, Appl	334	51.5	12.6	175	1	US-08-010-099-79	Sequence 79, Appl
262	52	12.7	1969	4	US-09-457-571-16	Sequence 16, Appl	335	51.5	12.6	175	1	US-08-010-099-80	Sequence 80, Appl
263	52	12.7	1977	4	US-09-976-594-757	Sequence 757, App	336	51.5	12.6	175	1	US-08-010-099-81	Sequence 81, Appl
264	52	12.7	1977	4	US-09-919-039-367	Sequence 367, App	337	51.5	12.6	175	1	US-08-010-099-89	Sequence 89, Appl
265	52	12.7	1984	3	US-08-836-325-10	Sequence 10, Appl	338	51.5	12.6	175	1	US-08-010-099-90	Sequence 90, Appl
266	52	12.7	1984	4	US-09-457-571-10	Sequence 10, Appl	339	51.5	12.6	175	1	US-08-010-099-91	Sequence 91, Appl
267	52	12.7	1989	3	US-08-836-325-11	Sequence 11, Appl	340	51.5	12.6	175	1	US-08-010-099-92	Sequence 92, Appl
268	52	12.7	1989	3	US-08-836-325-12	Sequence 12, Appl	341	51.5	12.6	175	1	US-08-010-099-93	Sequence 93, Appl
269	52	12.7	1989	4	US-09-457-571-11	Sequence 11, Appl	342	51.5	12.6	175	1	US-08-010-099-94	Sequence 94, Appl
270	52	12.7	1989	4	US-09-457-571-12	Sequence 12, Appl	343	51.5	12.6	175	1	US-08-010-099-98	Sequence 98, Appl
271	51.5	12.6	172	4	US-08-663-600A-96	Sequence 96, Appl	344	51.5	12.6	175	1	US-08-010-099-99	Sequence 99, Appl
272	51.5	12.6	172	4	US-09-270-767-36922	Sequence 36922, A	345	51.5	12.6	175	1	US-08-010-099-100	Sequence 100, App
273	51.5	12.6	172	4	US-09-270-767-52139	Sequence 52139, A	346	51.5	12.6	175	1	US-08-010-099-101	Sequence 101, App
274	51.5	12.6	173	1	US-08-354-456A-7	Sequence 7, Appli	347	51.5	12.6	175	1	US-08-010-099-102	Sequence 102, App
275	51.5	12.6	174	1	US-08-010-099-82	Sequence 82, Appl	348	51.5	12.6	175	1	US-08-010-099-104	Sequence 104, App
276	51.5	12.6	174	1	US-08-225-224-5	Sequence 5, Appli	349	51.5	12.6	175	1	US-08-010-099-105	Sequence 105, App
277	51.5	12.6	174	1	US-08-448-716-82	Sequence 82, Appl	350	51.5	12.6	175	1	US-08-010-099-106	Sequence 106, App
278	51.5	12.6	174	2	US-08-431-459A-31	Sequence 31, Appl	351	51.5	12.6	175	1	US-08-010-099-107	Sequence 107, App
279	51.5	12.6	174	3	US-08-722-258-5	Sequence 5, Appli	352	51.5	12.6	175	1	US-08-010-099-108	Sequence 108, App
280	51.5	12.6	174	3	US-08-833-167-49	Sequence 49, Appl	353	51.5	12.6	175	1	US-08-010-099-109	Sequence 109, App
281	51.5	12.6	174	3	US-08-833-167-50	Sequence 50, Appl	354	51.5	12.6	175	1	US-08-010-099-110	Sequence 110, App
282	51.5	12.6	174	3	US-08-833-167-51	Sequence 51, Appl	355	51.5	12.6	175	1	US-08-167-721-1	Sequence 1, Appli
283	51.5	12.6	174	3	US-08-833-167-52	Sequence 52, Appl	356	51.5	12.6	175	1	US-08-428-732-6	Sequence 6, Appli
284	51.5	12.6	174	3	US-08-833-167-53	Sequence 53, Appl	357	51.5	12.6	175	1	US-08-448-716-2	Sequence 2, Appli
285	51.5	12.6	174	3	US-08-833-167-54	Sequence 54, Appl	358	51.5	12.6	175	1	US-08-448-716-67	Sequence 67, Appl
286	51.5	12.6	174	3	US-08-833-167-55	Sequence 55, Appl	359	51.5	12.6	175	1	US-08-448-716-68	Sequence 68, Appl
287	51.5	12.6	174	3	US-08-833-167-56	Sequence 56, Appl	360	51.5	12.6	175	1	US-08-448-716-69	Sequence 69, Appl
288	51.5	12.6	174	3	US-08-833-167-96	Sequence 96, Appl	361	51.5	12.6	175	1	US-08-448-716-70	Sequence 70, Appl
289	51.5	12.6	174	3	US-08-833-167-97	Sequence 97, Appl	362	51.5	12.6	175	1	US-08-448-716-71	Sequence 71, Appl
290	51.5	12.6	174	3	US-08-833-167-98	Sequence 98, Appl	363	51.5	12.6	175	1	US-08-448-716-72	Sequence 72, Appl
291	51.5	12.6	174	3	US-08-833-167-99	Sequence 99, Appl	364	51.5	12.6	175	1	US-08-448-716-73	Sequence 73, Appl
292	51.5	12.6	174	3	US-08-833-167-100	Sequence 100, App	365	51.5	12.6	175	1	US-08-448-716-74	Sequence 74, Appl
293	51.5	12.6	174	3	US-08-833-167-101	Sequence 101, App	366	51.5	12.6	175	1	US-08-448-716-75	Sequence 75, Appl
294	51.5	12.6	174	3	US-08-833-167-102	Sequence 102, App	367	51.5	12.6	175	1	US-08-448-716-76	Sequence 76, Appl
295	51.5	12.6	174	3	US-09-221-181-1	Sequence 1, Appli	368	51.5	12.6	175	1	US-08-448-716-77	Sequence 77, Appl
296	51.5	12.6	174	3	US-09-304-186-82	Sequence 82, Appl	369	51.5	12.6	175	1	US-08-448-716-79	Sequence 79, Appl
297	51.5	12.6	174	3	US-09-344-837A-49	Sequence 49, Appl	370	51.5	12.6	175	1	US-08-448-716-80	Sequence 80, Appl
298	51.5	12.6	174	3	US-09-344-837A-50	Sequence 50, Appl	371	51.5	12.6	175	1	US-08-448-716-81	Sequence 81, Appl
299	51.5	12.6	174	3	US-09-344-837A-51	Sequence 51, Appl	372	51.5	12.6	175	1	US-08-448-716-89	Sequence 89, Appl
300	51.5	12.6	174	3	US-09-344-837A-52	Sequence 52, Appl	373	51.5	12.6	175	1	US-08-448-716-90	Sequence 90, Appl
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302	51.5	12.6	174	3	US-09-344-837A-54	Sequence 54, Appl	375	51.5	12.6	175	1	US-08-448-716-92	Sequence 92, Appl
303	51.5	12.6	174	3	US-09-344-837A-55	Sequence 55, Appl	376	51.5	12.6	175	1	US-08-448-716-93	Sequence 93, Appl
304	51.5	12.6	174	3	US-09-344-837A-56	Sequence 56, Appl	377	51.5	12.6	175	1	US-08-448-716-94	Sequence 94, Appl
305	51.5	12.6	174	3	US-09-344-837A-96	Sequence 96, Appl	378	51.5	12.6	175	1	US-08-448-716-98	Sequence 98, Appl
306	51.5	12.6	174	3	US-09-344-837A-97	Sequence 97, Appl	379	51.5	12.6	175	1	US-08-448-716-99	Sequence 99, Appl
307	51.5	12.6	174	3	US-09-344-837A-98	Sequence 98, Appl	380	51.5	12.6	175	1	US-08-448-716-100	Sequence 100, App
308	51.5	12.6	174	3	US-09-344-837A-99	Sequence 99, Appl	381	51.5	12.6	175	1	US-08-448-716-101	Sequence 101, App
309	51.5	12.6	174	3	US-09-344-837A-100	Sequence 100, App	382	51.5	12.6	175	1	US-08-448-716-102	Sequence 102, App
310	51.5	12.6	174	3	US-09-344-837A-101	Sequence 101, App	383	51.5	12.6	175	1	US-08-448-716-104	Sequence 104, App
311	51.5	12.6	174	3	US-09-344-837A-102	Sequence 102, App	384	51.5	12.6	175	1	US-08-448-716-105	Sequence 105, App
312	51.5	12.6	174	4	US-09-904-196B-1	Sequence 1, Appli	385	51.5	12.6	175	1	US-08-448-716-106	Sequence 106, App
313	51.5	12.6	174	4	US-09-462-941-6	Sequence 6, Appli	386	51.5	12.6	175	1	US-08-448-716-107	Sequence 107, App
314	51.5	12.6	174	4	US-09-479-313B-2	Sequence 2, Appli	387	51.5	12.6	175	1	US-08-448-716-108	Sequence 108, App
315	51.5	12.6	174	4	US-09-754-532-82	Sequence 82, Appl	388	51.5	12.6	175	1	US-08-448-716-109	Sequence 109, App
316	51.5	12.6	174	4	US-09-760-008A-1	Sequence 1, Appli	389	51.5	12.6	175	1	US-08-448-716-110	Sequence 110, App
317	51.5	12.6	174	4	US-09-950-473-2	Sequence 2, Appli	390	51.5	12.6	175	2	US-08-321-510-2	Sequence 2, Appli
318	51.5	12.6	174	4	US-10-152-294-1	Sequence 1, Appli	391	51.5	12.6	175	2	US-08-570-943-1	Sequence 1, Appli
319	51.5	12.6	174	5	PCT-US95-04468-5	Sequence 5, Appli	392	51.5	12.6	175	2	US-08-879-760-2	Sequence 2, Appli

393	51.5	12.6	175	3	US-08-505-187-4	Sequence 4, Appli	466	51.5	12.6	175	4	US-09-754-532-108	Sequence 108, App
394	51.5	12.6	175	3	US-08-696-988-1	Sequence 1, Appli	467	51.5	12.6	175	4	US-09-754-532-109	Sequence 109, App
395	51.5	12.6	175	3	US-09-304-186-2	Sequence 2, Appli	468	51.5	12.6	175	4	US-09-754-532-110	Sequence 110, App
396	51.5	12.6	175	3	US-09-304-186-67	Sequence 67, Appl	469	51.5	12.6	175	5	PCT-US95-01729-2	Sequence 2, Appli
397	51.5	12.6	175	3	US-09-304-186-68	Sequence 68, Appl	470	51.5	12.6	175	5	PCT-US95-01752-2	Sequence 2, Appli
398	51.5	12.6	175	3	US-09-304-186-69	Sequence 69, Appl	471	51.5	12.6	176	3	US-08-469-318-161	Sequence 161, App
399	51.5	12.6	175	3	US-09-304-186-70	Sequence 70, Appl	472	51.5	12.6	176	3	US-08-469-318-162	Sequence 162, App
400	51.5	12.6	175	3	US-09-304-186-71	Sequence 71, Appl	473	51.5	12.6	176	3	US-08-468-609A-161	Sequence 161, App
401	51.5	12.6	175	3	US-09-304-186-72	Sequence 72, Appl	474	51.5	12.6	176	3	US-08-468-609A-162	Sequence 162, App
402	51.5	12.6	175	3	US-09-304-186-73	Sequence 73, Appl	475	51.5	12.6	176	3	US-08-149-101A-26	Sequence 26, Appl
403	51.5	12.6	175	3	US-09-304-186-74	Sequence 74, Appl	476	51.5	12.6	176	3	US-08-446-872A-161	Sequence 161, App
404	51.5	12.6	175	3	US-09-304-186-75	Sequence 75, Appl	477	51.5	12.6	176	3	US-08-446-872A-162	Sequence 162, App
405	51.5	12.6	175	3	US-09-304-186-76	Sequence 76, Appl	478	51.5	12.6	176	4	US-08-762-227A-161	Sequence 161, App
406	51.5	12.6	175	3	US-09-304-186-77	Sequence 77, Appl	479	51.5	12.6	176	4	US-08-762-227A-162	Sequence 162, App
407	51.5	12.6	175	3	US-09-304-186-79	Sequence 79, Appl	480	51.5	12.6	176	5	PCT-US94-12873-26	Sequence 26, Appl
408	51.5	12.6	175	3	US-09-304-186-80	Sequence 80, Appl	481	51.5	12.6	176	5	PCT-US95-01185-161	Sequence 161, App
409	51.5	12.6	175	3	US-09-304-186-81	Sequence 81, Appl	482	51.5	12.6	176	5	PCT-US95-01185-162	Sequence 162, App
410	51.5	12.6	175	3	US-09-304-186-89	Sequence 89, Appl	483	51.5	12.6	177	2	US-08-797-689-14	Sequence 14, Appl
411	51.5	12.6	175	3	US-09-304-186-90	Sequence 90, Appl	484	51.5	12.6	177	3	US-08-833-167-117	Sequence 117, App
412	51.5	12.6	175	3	US-09-304-186-91	Sequence 91, Appl	485	51.5	12.6	177	3	US-08-833-167-118	Sequence 118, App
413	51.5	12.6	175	3	US-09-304-186-92	Sequence 92, Appl	486	51.5	12.6	177	3	US-08-833-167-120	Sequence 120, App
414	51.5	12.6	175	3	US-09-304-186-93	Sequence 93, Appl	487	51.5	12.6	177	3	US-08-833-167-122	Sequence 122, App
415	51.5	12.6	175	3	US-09-304-186-94	Sequence 94, Appl	488	51.5	12.6	177	3	US-08-833-167-125	Sequence 125, App
416	51.5	12.6	175	3	US-09-304-186-98	Sequence 98, Appl	489	51.5	12.6	177	3	US-08-833-167-126	Sequence 126, App
417	51.5	12.6	175	3	US-09-304-186-99	Sequence 99, Appl	490	51.5	12.6	177	3	US-08-833-167-127	Sequence 127, App
418	51.5	12.6	175	3	US-09-304-186-100	Sequence 100, App	491	51.5	12.6	177	3	US-08-833-167-128	Sequence 128, App
419	51.5	12.6	175	3	US-09-304-186-101	Sequence 101, App	492	51.5	12.6	177	3	US-09-344-837A-117	Sequence 117, App
420	51.5	12.6	175	3	US-09-304-186-102	Sequence 102, App	493	51.5	12.6	177	3	US-09-344-837A-118	Sequence 118, App
421	51.5	12.6	175	3	US-09-304-186-104	Sequence 104, App	494	51.5	12.6	177	3	US-09-344-837A-120	Sequence 120, App
422	51.5	12.6	175	3	US-09-304-186-105	Sequence 105, App	495	51.5	12.6	177	3	US-09-344-837A-121	Sequence 121, App
423	51.5	12.6	175	3	US-09-304-186-106	Sequence 106, App	496	51.5	12.6	177	3	US-09-344-837A-125	Sequence 125, App
424	51.5	12.6	175	3	US-09-304-186-107	Sequence 107, App	497	51.5	12.6	177	3	US-09-344-837A-126	Sequence 126, App
425	51.5	12.6	175	3	US-09-304-186-108	Sequence 108, App	498	51.5	12.6	177	3	US-09-344-837A-127	Sequence 127, App
426	51.5	12.6	175	3	US-09-304-186-109	Sequence 109, App	499	51.5	12.6	177	3	US-09-344-837A-128	Sequence 128, App
427	51.5	12.6	175	3	US-09-304-186-110	Sequence 110, App	500	51.5	12.6	177	4	US-09-384-186-14	Sequence 14, Appl
428	51.5	12.6	175	4	US-09-230-733-1	Sequence 1, Appli	501	51.5	12.6	177	4	US-09-510-238A-301	Sequence 301, App
429	51.5	12.6	175	4	US-09-479-313B-7	Sequence 7, Appli	502	51.5	12.6	177	4	US-09-510-238A-302	Sequence 302, App
430	51.5	12.6	175	4	US-09-479-313B-10	Sequence 10, Appl	503	51.5	12.6	177	4	US-09-510-238A-304	Sequence 304, App
431	51.5	12.6	175	4	US-09-479-313B-11	Sequence 11, Appl	504	51.5	12.6	177	4	US-09-510-238A-306	Sequence 306, App
432	51.5	12.6	175	4	US-09-479-313B-12	Sequence 12, Appl	505	51.5	12.6	177	4	US-09-510-238A-309	Sequence 309, App
433	51.5	12.6	175	4	US-09-479-313B-13	Sequence 13, Appl	506	51.5	12.6	177	4	US-09-510-238A-310	Sequence 310, App
434	51.5	12.6	175	4	US-09-479-313B-14	Sequence 14, Appl	507	51.5	12.6	177	4	US-09-510-238A-311	Sequence 311, App
435	51.5	12.6	175	4	US-09-479-313B-15	Sequence 15, Appl	508	51.5	12.6	177	4	US-09-510-238A-312	Sequence 312, App
436	51.5	12.6	175	4	US-09-754-532-2	Sequence 2, Appli	509	51.5	12.6	178	4	US-09-134-000C-4464	Sequence 4464, Ap
437	51.5	12.6	175	4	US-09-754-532-67	Sequence 67, Appl	510	51.5	12.6	204	1	US-08-792-019B-10	Sequence 10, Appl
438	51.5	12.6	175	4	US-09-754-532-68	Sequence 68, Appl	511	51.5	12.6	204	3	US-08-588-819-10	Sequence 10, Appl
439	51.5	12.6	175	4	US-09-754-532-69	Sequence 69, Appl	512	51.5	12.6	204	3	US-09-016-534-10	Sequence 10, Appl
440	51.5	12.6	175	4	US-09-754-532-70	Sequence 70, Appl	513	51.5	12.6	204	3	US-08-097-869-5	Sequence 5, Appli
441	51.5	12.6	175	4	US-09-754-532-71	Sequence 71, Appl	514	51.5	12.6	219	4	US-09-543-681A-5930	Sequence 5930, Ap
442	51.5	12.6	175	4	US-09-754-532-72	Sequence 72, Appl	515	51.5	12.6	222	4	US-09-593-887-20	Sequence 20, Appl
443	51.5	12.6	175	4	US-09-754-532-73	Sequence 73, Appl	516	51.5	12.6	224	4	US-09-270-767-32067	Sequence 32067, A
444	51.5	12.6	175	4	US-09-754-532-74	Sequence 74, Appl	517	51.5	12.6	224	4	US-09-270-767-47284	Sequence 47284, A
445	51.5	12.6	175	4	US-09-754-532-75	Sequence 75, Appl	518	51.5	12.6	236	4	US-09-583-110-4569	Sequence 4569, Ap
446	51.5	12.6	175	4	US-09-754-532-76	Sequence 76, Appl	519	51.5	12.6	237	4	US-09-270-767-35063	Sequence 35063, A
447	51.5	12.6	175	4	US-09-754-532-77	Sequence 77, Appl	520	51.5	12.6	237	4	US-09-270-767-50280	Sequence 50280, A
448	51.5	12.6	175	4	US-09-754-532-78	Sequence 78, Appl	521	51.5	12.6	249	4	US-08-818-581B-10	Sequence 10, Appl
449	51.5	12.6	175	4	US-09-754-532-80	Sequence 80, Appl	522	51.5	12.6	254	2	US-08-948-616-9	Sequence 9, Appli
450	51.5	12.6	175	4	US-09-754-532-81	Sequence 81, Appl	523	51.5	12.6	254	2	US-09-193-510-9	Sequence 9, Appli
451	51.5	12.6	175	4	US-09-754-532-89	Sequence 89, Appl	524	51.5	12.6	254	3	US-09-368-402-9	Sequence 9, Appli
452	51.5	12.6	175	4	US-09-754-532-90	Sequence 90, Appl	525	51.5	12.6	264	4	US-09-248-796A-20427	Sequence 20427, A
453	51.5	12.6	175	4	US-09-754-532-91	Sequence 91, Appl	526	51.5	12.6	267	4	US-09-663-600A-190	Sequence 190, App
454	51.5	12.6	175	4	US-09-754-532-92	Sequence 92, Appl	527	51.5	12.6	279	2	US-08-326-286-5	Sequence 5, Appli
455	51.5	12.6	175	4	US-09-754-532-93	Sequence 93, Appl	528	51.5	12.6	281	4	US-08-818-581B-8	Sequence 8, Appli
456	51.5	12.6	175	4	US-09-754-532-94	Sequence 94, Appl	529	51.5	12.6	281	4	US-09-107-532A-4147	Sequence 4147, Ap
457	51.5	12.6	175	4	US-09-754-532-98	Sequence 98, Appl	530	51.5	12.6	305	4	US-09-510-238A-178	Sequence 178, App
458	51.5	12.6	175	4	US-09-754-532-99	Sequence 99, Appl	531	51.5	12.6	305	4	US-09-510-238A-180	Sequence 180, App
459	51.5	12.6	175	4	US-09-754-532-100	Sequence 100, App	532	51.5	12.6	305	4	US-09-510-238A-182	Sequence 182, App
460	51.5	12.6	175	4	US-09-754-532-101	Sequence 101, App	533	51.5	12.6	305	4	US-09-510-238A-184	Sequence 184, App
461	51.5	12.6	175	4	US-09-754-532-102	Sequence 102, App	534	51.5	12.6	307	3	US-08-469-318-121	Sequence 121, App
462	51.5	12.6	175	4	US-09-754-532-104	Sequence 104, App	535	51.5	12.6	307	3	US-08-469-318-122	Sequence 122, App
463	51.5	12.6	175	4	US-09-754-532-105	Sequence 105, App	536	51.5	12.6	307	3	US-08-469-318-123	Sequence 123, App
464	51.5	12.6	175	4	US-09-754-532-106	Sequence 106, App	537	51.5	12.6	307	3	US-08-469-318-124	Sequence 124, App
465	51.5	12.6	175	4	US-09-754-532-107	Sequence 107, App	538	51.5	12.6	307	3	US-08-469-318-134	Sequence 134, App

539	51.5	12.6	307	3	US-08-469-318-135	Sequence 135, App	612	51.5	12.6	322	3	US-08-446-872A-128	Sequence 128, App
540	51.5	12.6	307	3	US-08-469-318-146	Sequence 146, App	613	51.5	12.6	322	3	US-08-446-872A-129	Sequence 129, App
541	51.5	12.6	307	3	US-08-469-318-147	Sequence 147, App	614	51.5	12.6	322	3	US-08-446-872A-130	Sequence 130, App
542	51.5	12.6	307	3	US-08-469-318-152	Sequence 152, App	615	51.5	12.6	322	3	US-08-446-872A-138	Sequence 138, App
543	51.5	12.6	307	3	US-08-469-318-158	Sequence 158, App	616	51.5	12.6	322	3	US-08-446-872A-149	Sequence 149, App
544	51.5	12.6	307	3	US-08-469-318-159	Sequence 159, App	617	51.5	12.6	322	3	US-08-446-872A-150	Sequence 150, App
545	51.5	12.6	307	3	US-08-468-609A-121	Sequence 121, App	618	51.5	12.6	322	3	US-08-446-872A-154	Sequence 154, App
546	51.5	12.6	307	3	US-08-468-609A-122	Sequence 122, App	619	51.5	12.6	322	3	US-08-446-872A-156	Sequence 156, App
547	51.5	12.6	307	3	US-08-468-609A-123	Sequence 123, App	620	51.5	12.6	322	3	US-08-446-872A-157	Sequence 157, App
548	51.5	12.6	307	3	US-08-468-609A-124	Sequence 124, App	621	51.5	12.6	322	3	US-08-762-227A-128	Sequence 128, App
549	51.5	12.6	307	3	US-08-468-609A-134	Sequence 134, App	622	51.5	12.6	322	4	US-08-762-227A-129	Sequence 129, App
550	51.5	12.6	307	3	US-08-468-609A-135	Sequence 135, App	623	51.5	12.6	322	4	US-08-762-227A-130	Sequence 130, App
551	51.5	12.6	307	3	US-08-468-609A-146	Sequence 146, App	624	51.5	12.6	322	4	US-08-762-227A-138	Sequence 138, App
552	51.5	12.6	307	3	US-08-468-609A-147	Sequence 147, App	625	51.5	12.6	322	4	US-08-762-227A-149	Sequence 149, App
553	51.5	12.6	307	3	US-08-468-609A-152	Sequence 152, App	626	51.5	12.6	322	4	US-08-762-227A-150	Sequence 150, App
554	51.5	12.6	307	3	US-08-468-609A-158	Sequence 158, App	627	51.5	12.6	322	4	US-08-762-227A-154	Sequence 154, App
555	51.5	12.6	307	3	US-08-468-609A-159	Sequence 159, App	628	51.5	12.6	322	4	US-08-762-227A-156	Sequence 156, App
556	51.5	12.6	307	3	US-08-446-872A-121	Sequence 121, App	629	51.5	12.6	322	4	US-08-762-227A-157	Sequence 157, App
557	51.5	12.6	307	3	US-08-446-872A-122	Sequence 122, App	630	51.5	12.6	322	4	US-09-510-238A-200	Sequence 200, App
558	51.5	12.6	307	3	US-08-446-872A-123	Sequence 123, App	631	51.5	12.6	322	4	US-09-510-238A-202	Sequence 202, App
559	51.5	12.6	307	3	US-08-446-872A-124	Sequence 124, App	632	51.5	12.6	322	4	US-09-902-540-15348	Sequence 15348, A
560	51.5	12.6	307	3	US-08-446-872A-134	Sequence 134, App	633	51.5	12.6	322	5	PCT-US95-01185-128	Sequence 128, App
561	51.5	12.6	307	3	US-08-446-872A-135	Sequence 135, App	634	51.5	12.6	322	5	PCT-US95-01185-129	Sequence 129, App
562	51.5	12.6	307	3	US-08-446-872A-146	Sequence 146, App	635	51.5	12.6	322	5	PCT-US95-01185-130	Sequence 130, App
563	51.5	12.6	307	3	US-08-446-872A-147	Sequence 147, App	636	51.5	12.6	322	5	PCT-US95-01185-138	Sequence 138, App
564	51.5	12.6	307	3	US-08-446-872A-152	Sequence 152, App	637	51.5	12.6	322	5	PCT-US95-01185-149	Sequence 149, App
565	51.5	12.6	307	3	US-08-446-872A-158	Sequence 158, App	638	51.5	12.6	322	5	PCT-US95-01185-150	Sequence 150, App
566	51.5	12.6	307	3	US-08-446-872A-159	Sequence 159, App	639	51.5	12.6	322	5	PCT-US95-01185-154	Sequence 154, App
567	51.5	12.6	307	4	US-08-762-227A-121	Sequence 121, App	640	51.5	12.6	322	5	PCT-US95-01185-156	Sequence 156, App
568	51.5	12.6	307	4	US-08-762-227A-122	Sequence 122, App	641	51.5	12.6	322	5	PCT-US95-01185-157	Sequence 157, App
569	51.5	12.6	307	4	US-08-762-227A-123	Sequence 123, App	642	51.5	12.6	325	4	US-09-510-238A-271	Sequence 271, App
570	51.5	12.6	307	4	US-08-762-227A-124	Sequence 124, App	643	51.5	12.6	325	4	US-09-510-238A-272	Sequence 272, App
571	51.5	12.6	307	4	US-08-762-227A-134	Sequence 134, App	644	51.5	12.6	325	4	US-09-510-238A-277	Sequence 277, App
572	51.5	12.6	307	4	US-08-762-227A-135	Sequence 135, App	645	51.5	12.6	325	4	US-09-510-238A-278	Sequence 278, App
573	51.5	12.6	307	4	US-08-762-227A-146	Sequence 146, App	646	51.5	12.6	325	4	US-09-510-238A-279	Sequence 279, App
574	51.5	12.6	307	4	US-08-762-227A-147	Sequence 147, App	647	51.5	12.6	325	4	US-09-510-238A-280	Sequence 280, App
575	51.5	12.6	307	4	US-08-762-227A-152	Sequence 152, App	648	51.5	12.6	325	4	US-09-510-238A-281	Sequence 281, App
576	51.5	12.6	307	4	US-08-762-227A-158	Sequence 158, App	649	51.5	12.6	325	4	US-09-510-238A-282	Sequence 282, App
577	51.5	12.6	307	4	US-08-762-227A-159	Sequence 159, App	650	51.5	12.6	329	4	US-09-510-238A-195	Sequence 195, App
578	51.5	12.6	307	5	PCT-US95-01185-121	Sequence 121, App	651	51.5	12.6	329	4	US-09-510-238A-196	Sequence 196, App
579	51.5	12.6	307	5	PCT-US95-01185-122	Sequence 122, App	652	51.5	12.6	329	4	US-09-510-238A-197	Sequence 197, App
580	51.5	12.6	307	5	PCT-US95-01185-123	Sequence 123, App	653	51.5	12.6	329	4	US-09-510-238A-198	Sequence 198, App
581	51.5	12.6	307	5	PCT-US95-01185-124	Sequence 124, App	654	51.5	12.6	335	3	US-08-469-318-143	Sequence 143, App
582	51.5	12.6	307	5	PCT-US95-01185-134	Sequence 134, App	655	51.5	12.6	335	3	US-08-468-609A-143	Sequence 143, App
583	51.5	12.6	307	5	PCT-US95-01185-135	Sequence 135, App	656	51.5	12.6	335	3	US-08-446-872A-143	Sequence 143, App
584	51.5	12.6	307	5	PCT-US95-01185-146	Sequence 146, App	657	51.5	12.6	335	4	US-08-762-227A-143	Sequence 143, App
585	51.5	12.6	307	5	PCT-US95-01185-147	Sequence 147, App	658	51.5	12.6	335	5	PCT-US95-01185-143	Sequence 143, App
586	51.5	12.6	307	5	PCT-US95-01185-152	Sequence 152, App	659	51.5	12.6	337	3	US-08-469-318-148	Sequence 148, App
587	51.5	12.6	307	5	PCT-US95-01185-158	Sequence 158, App	660	51.5	12.6	337	3	US-08-468-609A-148	Sequence 148, App
588	51.5	12.6	319	4	US-09-489-039A-12160	Sequence 12160, A	661	51.5	12.6	337	4	US-08-446-872A-148	Sequence 148, App
589	51.5	12.6	319	4	US-09-510-238A-179	Sequence 179, App	662	51.5	12.6	337	4	US-08-762-227A-148	Sequence 148, App
590	51.5	12.6	320	4	US-09-510-238A-181	Sequence 181, App	663	51.5	12.6	337	5	PCT-US95-01185-148	Sequence 148, App
591	51.5	12.6	320	4	US-09-510-238A-183	Sequence 183, App	664	51.5	12.6	347	3	US-09-188-930-326	Sequence 326, App
592	51.5	12.6	320	4	US-09-510-238A-185	Sequence 185, App	665	51.5	12.6	347	3	US-09-312-283C-326	Sequence 326, App
593	51.5	12.6	320	4	US-08-469-318-128	Sequence 128, App	666	51.5	12.6	349	3	US-08-469-318-139	Sequence 139, App
594	51.5	12.6	322	3	US-08-469-318-129	Sequence 129, App	667	51.5	12.6	349	3	US-08-469-318-151	Sequence 151, App
595	51.5	12.6	322	3	US-08-469-318-130	Sequence 130, App	668	51.5	12.6	349	3	US-08-468-609A-139	Sequence 139, App
596	51.5	12.6	322	3	US-08-469-318-138	Sequence 138, App	669	51.5	12.6	349	3	US-08-468-609A-151	Sequence 151, App
597	51.5	12.6	322	3	US-08-469-318-149	Sequence 149, App	670	51.5	12.6	349	3	US-08-446-872A-139	Sequence 139, App
598	51.5	12.6	322	3	US-08-469-318-150	Sequence 150, App	671	51.5	12.6	349	3	US-08-446-872A-151	Sequence 151, App
599	51.5	12.6	322	3	US-08-469-318-154	Sequence 154, App	672	51.5	12.6	349	4	US-08-762-227A-139	Sequence 139, App
600	51.5	12.6	322	3	US-08-469-318-156	Sequence 156, App	673	51.5	12.6	349	4	US-08-762-227A-151	Sequence 151, App
601	51.5	12.6	322	3	US-08-469-318-157	Sequence 157, App	674	51.5	12.6	349	5	PCT-US95-01185-139	Sequence 139, App
602	51.5	12.6	322	3	US-08-468-609A-128	Sequence 128, App	675	51.5	12.6	349	5	PCT-US95-01185-151	Sequence 151, App
603	51.5	12.6	322	3	US-08-468-609A-129	Sequence 129, App	676	51.5	12.6	357	4	US-09-949-016-6443	Sequence 6443, App
604	51.5	12.6	322	3	US-08-468-609A-130	Sequence 130, App	677	51.5	12.6	368	4	US-08-879-337-1	Sequence 1, App11
605	51.5	12.6	322	3	US-08-468-609A-138	Sequence 138, App	678	51.5	12.6	380	4	US-09-328-352-5640	Sequence 5640, App
606	51.5	12.6	322	3	US-08-468-609A-149	Sequence 149, App	679	51.5	12.6	390	4	US-09-949-016-9484	Sequence 9484, App
607	51.5	12.6	322	3	US-08-468-609A-150	Sequence 150, App	680	51.5	12.6	396	4	US-09-830-428A-1	Sequence 1, App11
608	51.5	12.6	322	3	US-08-468-609A-154	Sequence 154, App	681	51.5	12.6	404	4	US-09-270-767-45393	Sequence 45393, A
609	51.5	12.6	322	3	US-08-468-609A-156	Sequence 156, App	682	51.5	12.6	447	4	US-09-968-362A-22	Sequence 22, App1
610	51.5	12.6	322	3	US-08-468-609A-157	Sequence 157, App	683	51.5	12.6	448	4	US-09-968-362A-18	Sequence 18, App1
611	51.5	12.6	322	3	US-08-468-609A-157	Sequence 157, App	684	51.5	12.6	449	4	US-09-968-362A-20	Sequence 20, App1

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686	51.5	12.6	476	4	US-09-328-352-6735	Sequence 6735, Ap	759	50.5	12.3	86	4	US-09-621-976-5439	Sequence 5439, Ap
687	51.5	12.6	514	4	US-09-252-991A-25845	Sequence 25845, A	760	50.5	12.3	114	4	US-09-270-767-41159	Sequence 41199, A
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690	51.5	12.6	548	4	US-09-398-395A-8	Sequence 6, Appl	763	50.5	12.3	116	4	US-09-270-767-47156	Sequence 47156, A
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693	51.5	12.6	548	4	US-09-398-395A-12	Sequence 12, Appl	766	50.5	12.3	175	1	US-08-010-099-96	Sequence 96, Appl
694	51.5	12.6	548	4	US-09-887-586A-2	Sequence 2, Appl	767	50.5	12.3	175	1	US-08-448-716-95	Sequence 95, Appl
695	51.5	12.6	548	4	US-09-887-586A-4	Sequence 4, Appl	768	50.5	12.3	175	1	US-08-448-716-96	Sequence 96, Appl
696	51.5	12.6	548	4	US-09-887-586A-6	Sequence 6, Appl	769	50.5	12.3	175	3	US-09-304-186-95	Sequence 95, Appl
697	51.5	12.6	548	4	US-09-887-586A-8	Sequence 8, Appl	770	50.5	12.3	175	3	US-09-304-186-96	Sequence 96, Appl
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699	51.5	12.6	548	4	US-09-887-586A-12	Sequence 12, Appl	772	50.5	12.3	175	4	US-09-754-532-95	Sequence 95, Appl
700	51.5	12.6	548	4	US-09-895-752-2	Sequence 2, Appl	773	50.5	12.3	175	4	US-09-754-532-96	Sequence 96, Appl
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705	51.5	12.6	548	4	US-09-895-752-12	Sequence 12, Appl	778	50.5	12.3	207	4	US-08-811-519-29	Sequence 29, Appl
706	51.5	12.6	548	4	US-09-903-012B-2	Sequence 2, Appl	779	50.5	12.3	229	4	US-09-489-039A-9242	Sequence 9242, Ap
707	51.5	12.6	548	4	US-09-903-012B-4	Sequence 4, Appl	780	50.5	12.3	238	3	US-09-111-470-8	Sequence 8, Appl
708	51.5	12.6	548	4	US-09-903-012B-6	Sequence 6, Appl	781	50.5	12.3	238	4	US-09-862-802A-8	Sequence 8, Appl
709	51.5	12.6	548	4	US-09-903-012B-8	Sequence 8, Appl	782	50.5	12.3	261	4	US-09-903-456-60	Sequence 58, Appl
710	51.5	12.6	548	4	US-09-903-012B-10	Sequence 10, Appl	783	50.5	12.3	278	4	US-09-903-456-58	Sequence 38484, A
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712	51.5	12.6	548	4	US-09-900-797-2	Sequence 2, Appl	785	50.5	12.3	324	4	US-09-716-129-62	Sequence 62, Appl
713	51.5	12.6	548	4	US-09-900-797-4	Sequence 4, Appl	786	50.5	12.3	336	4	US-09-902-540-14418	Sequence 14418, A
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715	51.5	12.6	548	4	US-09-900-797-8	Sequence 8, Appl	788	50.5	12.3	434	4	US-09-328-352-7304	Sequence 7304, Ap
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718	51.5	12.6	550	2	US-08-443-639-8	Sequence 8, Appl	791	50.5	12.3	462	2	US-09-790-838-5	Sequence 5, Appl
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724	51.5	12.6	787	2	US-08-797-689-16	Sequence 16, Appl	797	50.5	12.3	600	6	5268463-2	Patent No. 5268463
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726	51	12.4	216	4	US-09-270-767-60948	Sequence 60948, A	799	50.5	12.3	602	2	US-09-151-957-5	Sequence 5, Appl
727	51	12.4	232	4	US-09-107-532A-6747	Sequence 6747, Ap	800	50.5	12.3	602	4	US-09-252-991A-22527	Sequence 22527, A
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730	51	12.4	359	2	US-08-103-170-4	Sequence 4, Appl	803	50.5	12.3	602	6	5432081-2	Patent No. 5432081
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732	51	12.4	359	2	US-08-103-170-7	Sequence 7, Appl	805	50.5	12.3	693	4	US-09-838-586-11	Sequence 11, Appl
733	51	12.4	359	3	US-09-328-314-19	Sequence 19, Appl	806	50.5	12.3	757	4	US-09-725-735A-20	Sequence 20, Appl
734	51	12.4	360	4	US-09-543-681A-7051	Sequence 7051, Ap	807	50.5	12.3	835	3	US-09-284-819-6	Sequence 6, Appl
735	51	12.4	360	4	US-09-826-509-471	Sequence 471, App	808	50.5	12.3	835	3	US-09-262-537-12	Sequence 12, Appl
736	51	12.4	403	4	US-09-270-767-38792	Sequence 38792, A	809	50.5	12.3	835	4	US-09-631-603-9	Sequence 9, Appl
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739	51	12.4	466	3	US-09-134-001C-3066	Sequence 13478, A	812	50	12.2	51	3	US-09-052-089A-6	Sequence 6, Appl
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833	50	12.2	376	4	US-09-949-016-7545	Sequence 7545, Ap	906	49.5	12.1	937	3	US-09-005-180A-4	Sequence 4, Appli
834	50	12.2	457	4	US-09-489-039A-8293	Sequence 8293, Ap	907	49.5	12.1	940	4	US-09-328-052-8165	Sequence 8165, Ap
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841	50	12.2	1243	4	US-09-354-147C-8	Sequence 8, Appli	914	49	12.0	150	4	US-09-107-433-3841	Sequence 3841, Ap
842	50	12.2	1284	4	US-09-343-494-9	Sequence 9, Appli	915	49	12.0	192	4	US-09-540-236-3328	Sequence 3328, Ap
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844	50	12.2	1791	4	US-10-160-224-9	Sequence 9, Appli	917	49	12.0	229	4	US-09-328-352-6458	Sequence 6458, Ap
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849	49.5	12.1	50	4	US-09-621-976-6194	Sequence 6194, Ap	922	49	12.0	342	4	US-09-248-796A-27396	Sequence 27396, A
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851	49.5	12.1	110	4	US-09-384-302A-27	Sequence 27, Appli	924	49	12.0	380	4	US-09-902-540-14637	Sequence 14637, A
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857	49.5	12.1	175	4	US-09-479-313B-9	Sequence 9, Appli	930	49	12.0	535	4	US-09-489-039A-12980	Sequence 12980, A
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860	49.5	12.1	206	3	US-08-776-971-22	Sequence 22, Appli	933	49	12.0	727	4	US-08-987-289-2	Sequence 2, Appli
861	49.5	12.1	206	4	US-09-461-436B-27	Sequence 27, Appli	934	49	12.0	1019	4	US-09-543-681A-7968	Sequence 7968, Ap
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863	49.5	12.1	223	3	US-08-513-974B-315	Sequence 315, App	936	49	12.0	1065	4	US-09-397-550-11	Sequence 11, Appli
864	49.5	12.1	223	3	US-08-513-974B-364	Sequence 364, App	937	49	12.0	1085	4	US-09-397-550-12	Sequence 12, Appli
865	49.5	12.1	223	3	US-08-513-974B-368	Sequence 368, App	938	49	12.0	1091	4	US-09-397-550-22	Sequence 22, Appli
866	49.5	12.1	223	3	US-08-776-971-100	Sequence 100, App	939	49	12.0	1765	4	US-10-162-012-15	Sequence 15, Appli
867	49.5	12.1	223	3	US-08-776-971-102	Sequence 102, App	940	49	12.0	1897	4	US-09-354-147C-5	Sequence 5, Appli
868	49.5	12.1	223	3	US-08-776-971-108	Sequence 108, App	941	49	12.0	56	4	US-09-752-024-98	Sequence 98, Appli
869	49.5	12.1	223	4	US-09-576-290-100	Sequence 100, App	942	48.5	11.8	56	4	US-09-621-976-6408	Sequence 6408, Ap
870	49.5	12.1	223	4	US-09-576-290-102	Sequence 102, App	943	48.5	11.8	61	4	US-09-540-236-3297	Sequence 3297, Ap
871	49.5	12.1	223	4	US-09-576-290-108	Sequence 108, App	944	48.5	11.8	100	4	US-09-270-767-33399	Sequence 33399, A
872	49.5	12.1	240	4	US-09-270-767-38489	Sequence 38489, A	945	48.5	11.8	100	4	US-09-270-767-48616	Sequence 48616, A
873	49.5	12.1	240	4	US-09-270-767-53706	Sequence 53706, A	946	48.5	11.8	109	4	US-09-328-352-6204	Sequence 6204, Ap
874	49.5	12.1	263	4	US-10-000-489-40	Sequence 40, Appli	947	48.5	11.8	109	4	US-09-328-352-7123	Sequence 7123, Ap
875	49.5	12.1	289	4	US-09-134-000C-5932	Sequence 5932, Ap	948	48.5	11.8	125	4	US-09-489-039A-11686	Sequence 11686, A
876	49.5	12.1	303	4	US-09-949-016-9114	Sequence 9114, Ap	949	48.5	11.8	133	4	US-09-252-991A-18682	Sequence 18682, A
877	49.5	12.1	308	4	US-09-328-352-7093	Sequence 7093, Ap	950	48.5	11.8	153	4	US-09-270-767-35496	Sequence 35496, A
878	49.5	12.1	311	4	US-09-252-991A-17395	Sequence 17395, A	951	48.5	11.8	153	4	US-09-270-767-50713	Sequence 50713, A
879	49.5	12.1	317	4	US-09-489-039A-9602	Sequence 9602, Ap	952	48.5	11.8	154	4	US-09-489-847-233	Sequence 233, App
880	49.5	12.1	338	4	US-09-270-767-46192	Sequence 46192, A	953	48.5	11.8	166	4	US-08-311-731A-299	Sequence 299, App
881	49.5	12.1	344	3	US-08-681-192-2	Sequence 2, Appli	954	48.5	11.8	171	4	US-09-489-847-152	Sequence 152, App
882	49.5	12.1	348	4	US-09-360-376-13	Sequence 13, Appli	955	48.5	11.8	175	4	US-09-479-313B-4	Sequence 4, Appli
883	49.5	12.1	356	4	US-10-039-659A-12	Sequence 12, Appli	956	48.5	11.8	175	4	US-09-479-313B-6	Sequence 6, Appli
884	49.5	12.1	382	4	US-09-134-000C-5889	Sequence 5889, Ap	957	48.5	11.8	207	4	US-09-489-847-312	Sequence 312, App
885	49.5	12.1	422	4	US-09-489-039A-10842	Sequence 10842, A	958	48.5	11.8	254	4	US-09-107-532A-4025	Sequence 4025, Ap
886	49.5	12.1	428	4	US-09-252-991A-30846	Sequence 30846, A	959	48.5	11.8	292	4	US-09-543-681A-7272	Sequence 7272, Ap
887	49.5	12.1	445	4	US-09-543-681A-6887	Sequence 6887, Ap	960	48.5	11.8	295	4	US-09-710-279-654	Sequence 654, App
888	49.5	12.1	473	1	US-08-597-236-13	Sequence 13, Appli	961	48.5	11.8	307	2	US-08-948-616-3	Sequence 3, Appli
889	49.5	12.1	473	1	US-08-746-682A-13	Sequence 13, Appli	962	48.5	11.8	307	2	US-09-193-510-3	Sequence 3, Appli
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891	49.5	12.1	516	4	US-09-107-532A-5467	Sequence 5467, Ap	964	48.5	11.8	308	4	US-09-248-796A-15413	Sequence 15413, A
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893	49.5	12.1	560	3	US-08-851-843A-6	Sequence 6, Appli	966	48.5	11.8	330	4	US-09-543-681A-4735	Sequence 4735, Ap
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898	49.5	12.1	603	4	US-09-270-957-17	Sequence 17, Appli	971	48.5	11.8	361	1	US-08-746-682A-11	Sequence 11, Appli
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900	49.5	12.1	604	4	US-09-893-525-40	Sequence 40, Appli	973	48.5	11.8	434	2	US-08-529-600D-2	Sequence 2, Appli
901	49.5	12.1	659	4	US-09-893-525-40	Sequence 40, Appli	974	48.5	11.8	434	2	US-08-973-275-4	Sequence 4, Appli
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903	49.5	12.1	832	3	US-08-630-820-7	Sequence 7, Appli	976	48.5	11.8	469	3	US-09-052-089A-1	Sequence 1, Appli

977	48.5	11.8	469	4	US-09-949-016-6664	Sequence 6664, Ap	1050	48	11.7	550	3	US-09-166-460-19	Sequence 19, Appl
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980	48.5	11.8	529	4	US-09-732-234-6	Sequence 6, Appl	1053	48	11.7	550	3	US-09-166-460-22	Sequence 22, Appl
981	48.5	11.8	529	4	US-09-784-859-6	Sequence 6, Appl	1054	48	11.7	550	3	US-09-166-460-23	Sequence 23, Appl
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985	48.5	11.8	544	4	US-09-540-236-2905	Sequence 2905, Ap	1058	48	11.7	550	3	US-09-166-460-27	Sequence 27, Appl
986	48.5	11.8	557	4	US-09-252-991A-21787	Sequence 21787, A	1059	48	11.7	550	3	US-09-166-460-28	Sequence 28, Appl
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992	48.5	11.8	886	4	US-09-631-603-14	Sequence 14, Appl	1065	48	11.7	550	3	US-09-361-718-13	Sequence 15, Appl
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996	48	11.7	73	4	US-09-149-476-579	Sequence 579, App	1069	48	11.7	550	3	US-09-361-718-20	Sequence 21, Appl
997	48	11.7	101	4	US-09-270-767-40263	Sequence 40263, A	1070	48	11.7	550	3	US-09-361-718-21	Sequence 22, Appl
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1005	48	11.7	135	4	US-09-270-767-50698	Sequence 50698, A	1078	48	11.7	550	4	US-09-887-586A-28	Sequence 28, Appl
1006	48	11.7	136	4	US-09-270-767-36748	Sequence 36748, A	1079	48	11.7	550	4	US-09-895-752-28	Sequence 28, Appl
1007	48	11.7	136	4	US-09-270-767-51965	Sequence 51965, A	1080	48	11.7	550	4	US-09-903-012B-28	Sequence 28, Appl
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1023	48	11.7	312	5	US-09-465-901-48	Sequence 48, Appl	1096	48	11.7	1765	4	US-09-354-147C-3	Sequence 3, Appl
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1025	48	11.7	352	4	US-09-170-496D-108	Sequence 108, App	1099	48	11.7	2005	4	US-09-457-571-7	Sequence 7, Appl
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1027	48	11.7	387	4	US-09-270-767-59513	Sequence 59513, A	1101	47.5	11.6	115	4	US-08-461-436B-38	Sequence 38, Appl
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1030	48	11.7	408	4	US-09-134-001C-2981	Sequence 2981, Ap	1104	47.5	11.6	132	3	US-08-513-974B-326	Sequence 326, App
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1046	48	11.7	550	3	US-09-166-460-15	Sequence 15, Appl	1120	47.5	11.6	333	4	US-09-170-496D-8	Sequence 8, Appl
1047	48	11.7	550	3	US-09-166-460-17	Sequence 17, Appl	1121	47.5	11.6	341	4	US-09-248-796A-16208	Sequence 16208, A
1048	48	11.7	550	3	US-09-166-460-19	Sequence 19, Appl	1122	47.5	11.6	372	4	US-09-270-957-3	Sequence 3, Appl
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1125	47.5	11.6	405	4	US-09-248-796A-15148	Sequence 15148, A	1198	47	11.5	237	1	US-08-818-514-3	Sequence 3, Appl
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1127	47.5	11.6	415	4	US-09-328-352-4420	Sequence 4420, Ap	1200	47	11.5	237	2	US-08-465-273-16	Sequence 16, Appl
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1133	47.5	11.6	491	4	US-09-543-681A-8251	Sequence 8251, Ap	1206	47	11.5	237	3	US-09-196-131-2	Sequence 2, Appl
1134	47.5	11.6	556	4	US-09-398-395A-32	Sequence 32, Appl	1207	47	11.5	237	3	US-09-196-131-16	Sequence 16, Appl
1135	47.5	11.6	556	4	US-08-887-586A-32	Sequence 32, Appl	1208	47	11.5	237	3	US-08-643-732-2	Sequence 2, Appl
1136	47.5	11.6	556	4	US-09-895-752-32	Sequence 32, Appl	1209	47	11.5	237	4	US-09-611-175-3	Sequence 3, Appl
1137	47.5	11.6	556	4	US-09-903-012B-32	Sequence 32, Appl	1210	47	11.5	237	4	US-09-836-169-2	Sequence 2, Appl
1138	47.5	11.6	556	4	US-09-900-797-32	Sequence 32, Appl	1211	47	11.5	237	4	US-09-836-169-16	Sequence 16, Appl
1139	47.5	11.6	615	4	US-09-248-796A-20833	Sequence 20833, A	1212	47	11.5	237	4	US-09-244-130-2	Sequence 2, Appl
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1146	47	11.5	38	4	US-09-270-767-34516	Sequence 34516, A	1219	47	11.5	249	4	US-09-949-016-7192	Sequence 7192, Ap
1147	47	11.5	38	4	US-09-270-767-49733	Sequence 49733, A	1220	47	11.5	251	3	US-09-627-376-13	Sequence 13, Appl
1148	47	11.5	51	4	US-09-513-999C-4406	Sequence 4406, Ap	1221	47	11.5	251	4	US-09-328-352-4178	Sequence 4178, Ap
1149	47	11.5	64	4	US-09-134-000C-4532	Sequence 4532, Ap	1222	47	11.5	251	4	US-10-047-676B-13	Sequence 13, Appl
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1155	47	11.5	102	3	US-09-483-665-2	Sequence 2, Appl	1228	47	11.5	318	4	US-09-252-991A-27319	Sequence 27319, A
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1161	47	11.5	134	4	US-09-270-767-38963	Sequence 38963, A	1234	47	11.5	346	4	US-09-614-124B-329	Sequence 329, App
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1164	47	11.5	139	4	US-09-270-767-44805	Sequence 44805, A	1237	47	11.5	346	4	US-09-658-824-329	Sequence 329, App
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1167	47	11.5	162	4	US-09-583-110-3336	Sequence 3336, Ap	1240	47	11.5	360	3	US-09-116-498-10	Sequence 10, Appl
1168	47	11.5	167	4	US-09-492-709A-297	Sequence 297, App	1241	47	11.5	360	4	US-09-852-156-10	Sequence 10, Appl
1169	47	11.5	168	4	US-09-673-395A-159	Sequence 159, App	1242	47	11.5	371	2	US-08-591-629-2	Sequence 2, Appl
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1174	47	11.5	192	4	US-09-252-991A-20344	Sequence 20344, A	1247	47	11.5	414	4	US-09-438-185A-396	Sequence 396, App
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1185	47	11.5	235	2	US-09-119-024-4	Sequence 4, Appl	1258	47	11.5	618	3	US-09-345-473E-49	Sequence 49, Appl
1186	47	11.5	235	2	US-08-417-226-4	Sequence 4, Appl	1259	47	11.5	662	3	US-09-134-001C-4039	Sequence 4039, Ap
1187	47	11.5	235	2	US-09-196-131-4	Sequence 4, Appl	1260	47	11.5	662	3	US-09-232-201-11	Sequence 11, Appl
1188	47	11.5	235	3	US-08-643-732-4	Sequence 4, Appl	1261	47	11.5	662	3	US-09-232-200-96	Sequence 96, Appl
1189	47	11.5	235	3	US-09-836-169-4	Sequence 4, Appl	1262	47	11.5	662	3	US-09-232-197-11	Sequence 11, Appl
1190	47	11.5	235	4	US-09-244-130-4	Sequence 4, Appl	1263	47	11.5	662	3	US-09-232-197-96	Sequence 96, Appl
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1194	47	11.5	237	1	US-07-971-160-16	Sequence 16, Appl	1267	47	11.5	662	4	US-09-232-195-96	Sequence 96, Appl
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1270	47	11.5	689	3	US-09-232-197-73	Sequence 73, Appl	1343	46.5	11.3	433	4	US-09-390-287A-6	Sequence 6, Appl
1271	47	11.5	689	3	US-09-232-201-73	Sequence 73, Appl	1344	46.5	11.3	435	6	5268463-9	Patent No. 5268463
1272	47	11.5	689	4	US-09-232-195-73	Sequence 73, Appl	1345	46.5	11.3	435	6	5268463-9	Patent No. 5268463
1273	47	11.5	690	4	US-09-302-6268-171	Sequence 171, App	1346	46.5	11.3	436	6	5432081-10	Patent No. 5432081
1274	47	11.5	710	4	US-09-302-6268-28	Sequence 28, Appl	1347	46.5	11.3	436	6	5432081-10	Patent No. 5432081
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1277	47	11.5	750	4	US-09-248-796A-20376	Sequence 20376, A	1350	46.5	11.3	445	2	US-08-630-118A-4	Sequence 4, Appl
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1280	47	11.5	885	3	US-08-841-089-2	Sequence 2, Appl	1353	46.5	11.3	445	2	US-09-003-199-23	Sequence 23, Appl
1281	47	11.5	885	3	US-09-301-085-2	Sequence 2, Appl	1354	46.5	11.3	445	3	US-09-235-839-2	Sequence 2, Appl
1282	47	11.5	885	5	PCT-US95-04570-2	Sequence 2, Appl	1355	46.5	11.3	445	3	US-09-235-839-4	Sequence 4, Appl
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1284	47	11.5	909	2	US-08-310-912A-142	Sequence 142, App	1357	46.5	11.3	445	3	US-09-327-035-4	Sequence 4, Appl
1285	47	11.5	909	3	US-09-301-085-142	Sequence 142, App	1358	46.5	11.3	445	4	US-09-065-027-6	Sequence 6, Appl
1286	47	11.5	909	5	PCT-US95-04589-142	Sequence 142, App	1359	46.5	11.3	451	4	US-09-270-767-45139	Sequence 45139, A
1287	47	11.5	924	2	US-08-588-983-18	Sequence 18, Appl	1360	46.5	11.3	454	4	US-09-489-039A-8351	Sequence 8351, Ap
1288	47	11.5	924	2	US-08-588-976-18	Sequence 18, Appl	1361	46.5	11.3	456	1	US-08-349-025-2	Sequence 2, Appl
1289	47	11.5	1720	2	US-08-477-451-12	Sequence 12, Appl	1362	46.5	11.3	456	2	US-08-566-096A-2	Sequence 2, Appl
1290	47	11.5	1836	4	US-10-162-012-24	Sequence 24, Appl	1363	46.5	11.3	456	2	US-08-668-650B-2	Sequence 2, Appl
1291	46.5	11.3	60	4	US-09-513-999C-6864	Sequence 6864, Ap	1364	46.5	11.3	456	3	US-09-200-673-2	Sequence 2, Appl
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1293	46.5	11.3	81	4	US-09-107-532A-4571	Sequence 4571, Ap	1366	46.5	11.3	456	4	US-09-447-907-2	Sequence 2, Appl
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1298	46.5	11.3	132	4	US-09-328-352-5435	Sequence 5435, App	1371	46.5	11.3	484	3	US-09-457-040B-12	Sequence 12, Appl
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1304	46.5	11.3	149	4	US-09-198-452A-878	Sequence 878, App	1377	46.5	11.3	526	4	US-09-722-377-19	Sequence 19, Appl
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1306	46.5	11.3	156	4	US-09-270-767-52598	Sequence 52598, A	1379	46.5	11.3	548	3	US-09-601-091-2	Sequence 2, Appl
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1312	46.5	11.3	210	3	US-09-103-434-1	Sequence 1, Appl	1385	46.5	11.3	548	4	US-09-900-797-52	Sequence 52, Appl
1313	46.5	11.3	210	3	US-09-687-594-1	Sequence 1, Appl	1386	46.5	11.3	584	4	US-09-107-532A-6329	Sequence 6329, Ap
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1315	46.5	11.3	211	4	US-09-270-767-50674	Sequence 50674, A	1388	46.5	11.3	619	4	US-09-489-039A-12704	Sequence 12704, A
1316	46.5	11.3	219	4	US-09-270-767-33673	Sequence 33673, A	1389	46.5	11.3	628	2	US-08-817-436A-2	Sequence 2, Appl
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1318	46.5	11.3	235	3	US-09-370-098-6	Sequence 6, Appl	1391	46.5	11.3	726	3	US-09-476-482-2	Sequence 2, Appl
1319	46.5	11.3	236	4	US-09-489-039A-7800	Sequence 7800, Ap	1392	46.5	11.3	726	3	US-09-517-605-6	Sequence 6, Appl
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1324	46.5	11.3	275	3	US-09-134-001C-3290	Sequence 3290, Ap	1397	46.5	11.3	979	4	US-09-538-092-990	Sequence 990, App
1325	46.5	11.3	311	3	US-09-198-092-2	Sequence 2, Appl	1398	46.5	11.3	980	2	US-08-473-553A-6	Sequence 6, Appl
1326	46.5	11.3	319	4	US-09-170-496D-60	Sequence 60, Appl	1399	46.5	11.3	985	2	US-08-473-553A-2	Sequence 2, Appl
1327	46.5	11.3	319	4	US-09-170-496D-196	Sequence 196, App	1400	46.5	11.3	993	4	US-09-949-016-10335	Sequence 10335, A
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1331	46.5	11.3	376	4	US-09-902-540-15516	Sequence 15516, A	1404	46.5	11.3	1079	2	US-08-943-986-8	Sequence 8, Appl
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1333	46.5	11.3	405	1	US-07-914-281-8	Sequence 8, Appl	1406	46.5	11.3	1079	3	US-08-484-719B-8	Sequence 8, Appl
1334	46.5	11.3	405	1	US-08-393-246-8	Sequence 8, Appl	1407	46.5	11.3	1079	3	US-08-484-159-8	Sequence 8, Appl
1335	46.5	11.3	405	1	US-08-525-058A-8	Sequence 8, Appl	1408	46.5	11.3	1411	4	US-09-538-092-413	Sequence 413, App
1336	46.5	11.3	405	2	US-08-483-151-4	Sequence 4, Appl	1409	46	11.2	51	4	US-09-471-276-1452	Sequence 1452, Ap
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1338	46.5	11.3	405	3	US-09-042-531-8	Sequence 8, Appl	1411	46	11.2	64	4	US-09-107-433-3164	Sequence 3164, Ap
1339	46.5	11.3	428	4	US-08-311-731A-380	Sequence 380, App	1412	46	11.2	64	4	US-09-107-433-3165	Sequence 3165, Ap
1340	46.5	11.3	429	4	US-09-810-671-5	Sequence 5, Appl	1413	46	11.2	64	4	US-09-107-433-3166	Sequence 3166, Ap
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1419	46	11.2	94	5	PCT-US92-02750-6	Sequence 6, Appl	1492	46	11.2	542	4	US-09-489-039A-7419	Sequence 7419, Ap
1420	46	11.2	109	4	US-09-252-991A-20785	Sequence 20785, A	1493	46	11.2	552	4	US-09-252-991A-32570	Sequence 32570, A
1421	46	11.2	115	3	US-08-513-974B-356	Sequence 356, App	1494	46	11.2	565	4	US-09-543-681A-5889	Sequence 5889, Ap
1422	46	11.2	115	3	US-09-097-889-20	Sequence 20, Appl	1495	46	11.2	570	4	US-09-649-747A-21	Sequence 21, Appl
1423	46	11.2	115	4	US-09-098-079-20	Sequence 20, Appl	1496	46	11.2	581	4	US-09-710-279-1060	Sequence 1060, Ap
1424	46	11.2	149	4	US-09-328-352-7196	Sequence 7196, Ap	1497	46	11.2	648	3	US-09-134-001C-3430	Sequence 3430, Ap
1425	46	11.2	155	4	US-09-107-532A-5926	Sequence 5926, Ap	1498	46	11.2	719	4	US-09-328-352-6274	Sequence 6274, Ap
1426	46	11.2	162	4	US-09-663-600A-126	Sequence 126, App	1499	46	11.2	852	1	US-08-190-802A-59	Sequence 59, Appl
1427	46	11.2	162	4	US-09-663-600A-220	Sequence 220, App	1500	46	11.2	852	1	US-08-190-802A-67	Sequence 67, Appl
1428	46	11.2	163	4	US-09-149-476-422	Sequence 462, App							
1429	46	11.2	176	4	US-09-252-991A-31051	Sequence 31051, A							
1430	46	11.2	211	4	US-09-489-039A-9608	Sequence 9608, Ap							
1431	46	11.2	212	4	US-09-248-796A-21132	Sequence 21132, A							
1432	46	11.2	223	4	US-09-465-901-40	Sequence 40, Appl							
1433	46	11.2	228	4	US-09-252-991A-26379	Sequence 26379, A							
1434	46	11.2	244	1	US-07-869-933-32	Sequence 32, Appl							
1435	46	11.2	244	1	US-08-201-879A-3	Sequence 3, Appl							
1436	46	11.2	244	3	US-09-103-663-32	Sequence 32, Appl							
1437	46	11.2	244	4	US-09-949-016-5892	Sequence 5892, Ap							
1438	46	11.2	246	4	US-09-198-452A-22	Sequence 22, Appl							
1439	46	11.2	246	4	US-09-438-185A-13	Sequence 13, Appl							
1440	46	11.2	249	4	US-09-649-747A-14	Sequence 14, Appl							
1441	46	11.2	256	4	US-09-949-016-8329	Sequence 8329, Ap							
1442	46	11.2	261	4	US-09-538-092-318	Sequence 318, Ap							
1443	46	11.2	268	4	US-09-543-681A-7689	Sequence 7689, Ap							
1444	46	11.2	269	4	US-09-270-767-31896	Sequence 31896, A							
1445	46	11.2	269	4	US-09-270-767-47113	Sequence 47113, A							
1446	46	11.2	299	4	US-09-520-781-28	Sequence 28, Appl							
1447	46	11.2	300	4	US-09-170-496D-250	Sequence 250, App							
1448	46	11.2	300	4	US-09-170-496D-272	Sequence 272, App							
1449	46	11.2	309	4	US-09-543-681A-4820	Sequence 4820, Ap							
1450	46	11.2	312	2	US-09-014-969-17	Sequence 17, Appl							
1451	46	11.2	320	4	US-09-252-991A-19560	Sequence 19560, A							
1452	46	11.2	320	4	US-09-328-352-7611	Sequence 7611, Ap							
1453	46	11.2	328	4	US-09-543-681A-6070	Sequence 6070, Ap							
1454	46	11.2	337	4	US-09-828-303-18	Sequence 18, Appl							
1455	46	11.2	340	2	US-08-790-572-1	Sequence 1, Appl							
1456	46	11.2	340	2	US-09-213-398-1	Sequence 1, Appl							
1457	46	11.2	342	4	US-09-149-476-695	Sequence 695, App							
1458	46	11.2	345	4	US-09-949-016-10427	Sequence 10427, A							
1459	46	11.2	347	4	US-09-949-016-9849	Sequence 9849, Ap							
1460	46	11.2	354	4	US-09-134-000C-4922	Sequence 4922, Ap							
1461	46	11.2	357	4	US-09-252-991A-17970	Sequence 17970, A							
1462	46	11.2	358	4	US-09-151-771B-8	Sequence 8, Appl							
1463	46	11.2	358	4	US-09-151-771B-9	Sequence 9, Appl							
1464	46	11.2	359	4	US-09-154-750A-30	Sequence 30, Appl							
1465	46	11.2	359	4	US-09-949-016-6561	Sequence 6561, Ap							
1466	46	11.2	361	4	US-09-710-279-160	Sequence 160, App							
1467	46	11.2	362	4	US-09-270-767-39855	Sequence 39855, A							
1468	46	11.2	362	4	US-09-270-767-55072	Sequence 55072, A							
1469	46	11.2	379	4	US-09-710-279-1512	Sequence 1512, Ap							
1470	46	11.2	391	4	US-09-198-452A-364	Sequence 364, App							
1471	46	11.2	392	4	US-09-826-509-547	Sequence 547, App							
1472	46	11.2	400	4	US-09-668-097A-16	Sequence 16, Appl							
1473	46	11.2	400	4	US-09-826-509-545	Sequence 545, App							
1474	46	11.2	405	3	US-09-134-001C-3496	Sequence 3496, Ap							
1475	46	11.2	405	4	US-09-252-991A-31137	Sequence 31137, App							
1476	46	11.2	413	4	US-09-976-594-562	Sequence 562, App							
1477	46	11.2	415	4	US-09-540-236-2600	Sequence 2600, Ap							
1478	46	11.2	419	4	US-09-948-774-2	Sequence 2, Appl							
1479	46	11.2	430	4	US-09-270-767-41868	Sequence 41868, A							
1480	46	11.2	432	4	US-09-902-540-10469	Sequence 10469, A							
1481	46	11.2	433	3	US-09-134-001C-3085	Sequence 3085, Ap							
1482	46	11.2	451	4	US-09-270-767-42866	Sequence 42866, A							
1483	46	11.2	467	4	US-09-438-185A-349	Sequence 349, App							
1484	46	11.2	486	4	US-09-328-352-6007	Sequence 6007, Ap							
1485	46	11.2	494	4	US-09-328-352-7016	Sequence 7016, Ap							
1486	46	11.2	495	4	US-09-328-352-4637	Sequence 4637, Ap							
1487	46	11.2	495	4	US-09-275-252A-5	Sequence 5, Appl							

ALIGNMENTS

RESULT 1

US-09-270-767-32997  
 ; Sequence 32997, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 32997  
 ; LENGTH: 168  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-270-767-32997

Query Match 57.3%; Score 235; DB 4; Length 168;  
 Best Local Similarity 62.2%; Pred. No. Se-22;  
 Matches 46; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MGPVKQLKRMPEPTRLIATIMVLLCFALTLCSAFWHNKGLALIFCILOSLALTWYSLSF 60  
 DB 92 MGPFKQIKKMFATRLIATIIIVMMVLTFTAIIVKKAGLTIIIFIIQSLANTWYSLSY 151  
 QY 61 IPFARDVAKKCFV 74  
 DB 152 IPYARDVAKTMSAI 165

RESULT 2

US-09-270-767-48214  
 ; Sequence 48214, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 48214  
 ; LENGTH: 168  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-270-767-48214

Query Match 57.3%; Score 235; DB 4; Length 168;  
 Best Local Similarity 62.2%; Pred. No. Se-22;  
 Matches 46; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MGPVKQLKRMPEPTRLIATIMVLLCFALTLCSAFWHNKGLALIFCILOSLALTWYSLSF 60  
 DB 92 MGPFKQIKKMFATRLIATIIIVMMVLTFTAIIVKKAGLTIIIFIIQSLANTWYSLSY 151

Db 92 MGPFQIKQKPAETRLIATIVLVMMVLTFIAAIVWKKAGLTLFIILIIQSLAMTWYSLSY 151  
Qy 61 IPFARDVKKCFAY 74  
Db 152 IPYARDVAKTWSAI 165

RESULT 3  
US-09-248-796A-20672  
; Sequence 20672, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 20672  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-20672

Query Match 22.9%; Score 94; DB 4; Length 255;  
Best Local Similarity 33.9%; Pred. No. 0.00053;  
Matches 20; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Qy 10 MFETRLIATIMVLCFALTCGSAFWHKNKGLAIFCIQLSALATWTWYSLSPFARDAY 68  
Db 180 LFLSTRIIFTIVFGASIIITLISSVSLKSTLLSIIFAVIQLAALWTWTSYFPFGKQTL 238

RESULT 4  
US-09-538-092-22  
; Sequence 22, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuratPatSeqFormatter Version 0.9  
; SEQ ID NO 22  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number YBL102W  
US-09-538-092-22

Query Match 18.3%; Score 75; DB 4; Length 215;  
Best Local Similarity 27.1%; Pred. No. 0.11;  
Matches 19; Conservative 17; Mismatches 33; Indels 2; Gaps 2;

Qy 1 MGVPKQKRMFETRL-IATIMVLCFALTCGSAFWHKNKGLAIFCIQLSALATWTWYSLS 59  
Db 131 MGPLAYLKHLTARLRLPSPMFFATCF-MTIFYAFASKNVTLTITCALLELVAVIYVIAIS 189

Qy 60 FIPFARDVAVK 69  
Db 190 YFPFGATGLR 199

RESULT 5  
US-09-489-039A-11699  
; Sequence 11699, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 11699  
; LENGTH: 404  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11699

Query Match 16.2%; Score 66.5; DB 4; Length 404;  
Best Local Similarity 26.9%; Pred. No. 2.7;  
Matches 21; Conservative 11; Mismatches 33; Indels 13; Gaps 2;

Qy 1 MGVPKQKRMFETRLIATIMVLCFALTCGSAFWHKNK-----GLALIFC-----I 47  
Db 80 LGSLLIAPRVSDPSRLAALRVLALLTLFALAFWAGSHVAVLLAIIIGFNLFPSPLVPL 139

Qy 48 LQSLALTWYSLSFIPFAR 65  
Db 140 TDALANTWQKQITMDYGR 157

RESULT 6  
US-09-489-039A-12390  
; Sequence 12390, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12390  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12390

Query Match 16.1%; Score 66; DB 4; Length 289;  
Best Local Similarity 37.5%; Pred. No. 2.1;  
Matches 15; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy 20 IMVLLICFALTCGSAFWHKNKGLAIFCIQLSALATWTWYSLS 59  
Db 102 VALLLVUSPASAAFWRHRSKVLRLIFGLITIVPFFWGMIA 141

RESULT 7  
US-09-252-991A-24117  
; Sequence 24117, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24117
; LENGTH: 416
; TYPE: PRP
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-24117

Query Match          15.6%   Score 64; DB 4; Length 416;
Best Local Similarity 38.2%; Pred. No. 5-7;
Matches 13; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy      34 FWHNKGLALIFCIIQSALTWTYSLSLTFPPARDA 67
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RESULT 8
US-08-937-067-14
; Sequence 14, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-937-067-14

Query Match          15.6%   Score 64; DB 4; Length 685;
Best Local Similarity 22.1%; Pred. No. 10;
Matches 15; Conservative 15; Mismatches 26; Indels 12; Gaps 1;

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; APPLICANT: Wensvoort, Gert
; APPLICANT: Terpstra, Catharinus
; APPLICANT: Pol, Johannes M
; APPLICANT: Moorman, Robertus J
; APPLICANT: Meulenbergh, Johanna J
; TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Traak, Britt & Rossa
; STREET: 525 South 300 East
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,863
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/157,005
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91201398.4
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92200781.0
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL92/00096
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33041
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 532-1922
; TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-747-863-2

Query Match          15.0%; Score 61.5; DB 3; Length 2396;
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Matches 22; Conservative 14; Mismatches 26; Indels 11; Gaps 5;

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Qy      64 ARDAVKCFACVL 76
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Db      1273 SQRCHCKWGKCI 1285

RESULT 13
US-09-565-864-2
; Sequence 2, Application US/09565864
; Patent No. 6455245
; GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
;             Terpstra, Catharinus
;             Pol, Johannes M
;             Moorman, Robertus J

```

Meulenbergh, Johanna J  
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,  
VACCINE COMPOSITIONS AND DIAGNOSTIC KITS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC-compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION NUMBER: US/09/565,864  
FILING DATE: 05-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION NUMBER: 08/157,005  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 91201398.4  
FILING DATE: 06-JUN-1991  
APPLICATION NUMBER: EP 92200781.0  
FILING DATE: 18-MAR-1992  
APPLICATION NUMBER: PCT/NL92/00096  
FILING DATE: 05-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Moran, Thomas F  
REGISTRATION NUMBER: 16,579  
REFERENCE/DOCKET NUMBER: 44819  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 315-1931  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2396 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-565-864-2  
Query Match 15.0%; Score 61.5; DB 4; Length 2396;  
Best Local Similarity 30.1%; Pred. No. 85;  
Matches 22; Conservative 14; Mismatches 26; Indels 11; Gaps 5;  
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Db 1273 SQGRCHKWGKCI 1285  
RESULT 14  
US-10-226-065-2  
Sequence 2, Application US/10226065  
Patent No. 6806086  
GENERAL INFORMATION:  
APPLICANT: Wensvoort, Gert  
Terpetra, Catharinus  
Poi, Johannes M  
Moorman, Robertus J  
Meulenbergh, Johanna J  
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,  
VACCINE COMPOSITIONS AND DIAGNOSTIC KITS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC-compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION NUMBER: US/10/226,065  
FILING DATE: 21-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION NUMBER: US/09/565,864  
FILING DATE: 05-May-2000  
APPLICATION NUMBER: 08/157,005  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 91201398.4  
FILING DATE: 06-JUN-1991  
APPLICATION NUMBER: EP 92200781.0  
FILING DATE: 18-MAR-1992  
APPLICATION NUMBER: PCT/NL92/00096  
FILING DATE: 05-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Moran, Thomas F  
REGISTRATION NUMBER: 16,579  
REFERENCE/DOCKET NUMBER: 44819  
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INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2396 amino acids  
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TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
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RESULT 15  
US-09-248-796A-17451  
Sequence 17451, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
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US-09-248-796A-17451

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885	58	14.1	565	14	US-10-225-567A-382	Sequence 382, App	958	56.5	13.8	588	16	US-10-437-963-171859	Sequence 171859, A
886	58	14.1	565	14	US-10-285-976-41	Sequence 41, Appl	959	56.5	13.8	614	15	US-10-332-447-26	Sequence 26, Appl
887	58	14.1	565	15	US-10-301-764-8	Sequence 8, Appli	960	56.5	13.8	634	14	US-10-157-031-24	Sequence 24, Appl
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972	56	13.7	242	16	US-10-179-373-13	Sequence 13, Appl	1045	55	13.4	137	15	US-10-179-373-12	Sequence 12, Appl
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976	56	13.7	289	15	US-10-179-373-13	Sequence 13, Appl	1049	55	13.4	137	16	US-10-179-373-12	Sequence 12, Appl
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979	56	13.7	355	14	US-10-237-563-34	Sequence 34, Appl	1052	55	13.4	265	15	US-10-237-563-34	Sequence 34, Appl
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984	56	13.7	429	15	US-10-282-122A-58861	Sequence 58861, A	1057	55	13.4	355	14	US-10-237-563-27	Sequence 27, Appl
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986	56	13.7	626	16	US-10-437-963-188691	Sequence 188691, A	1059	55	13.4	355	14	US-10-237-563-29	Sequence 29, Appl
987	56	13.7	645	15	US-10-369-493-5619	Sequence 5619, Ap	1060	55	13.4	355	14	US-10-237-563-30	Sequence 30, Appl
988	56	13.7	1346	16	US-10-437-963-189131	Sequence 189131, A	1061	55	13.4	355	14	US-10-237-563-31	Sequence 31, Appl
989	56	13.7	1603	15	US-10-220-120-315	Sequence 315, App	1062	55	13.4	355	14	US-10-237-563-33	Sequence 33, Appl
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994	56	13.7	2016	9	US-09-840-125-4	Sequence 4, Appl	1067	55	13.4	360	14	US-10-101-148-4	Sequence 4, Appl
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998	56	13.7	2016	16	US-10-632-342-4	Sequence 4, Appl	1071	55	13.4	402	17	US-10-869-630-58	Sequence 58, Appl
999	56	13.7	2016	16	US-10-914-133-4	Sequence 4, Appl	1072	55	13.4	420	15	US-10-425-114-68141	Sequence 68141, A
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1305	54.5	13.3	403	9	US-09-895-686-5	Sequence 5, Appli	1378	53.5	13.0	174	10	US-09-950-123-8	Sequence 8, Appli
1306	54.5	13.3	403	14	US-10-097-340-121	Sequence 121, App	1379	53.5	13.0	175	9	US-09-754-532-85	Sequence 85, Appl
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1308	54.5	13.3	403	14	US-10-016-656-2	Sequence 2, Appli	1381	53.5	13.0	214	15	US-10-389-566-375	Sequence 375, App
1309	54.5	13.3	403	16	US-10-600-816-6	Sequence 6, Appli	1382	53.5	13.0	232	16	US-10-437-963-11250	Sequence 11250, A
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1326	54	13.2	188	15	US-10-094-749-3153	Sequence 3153, Ap	1399	53.5	13.0	706	15	US-10-282-122A-65643	Sequence 65643, A
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1328	54	13.2	242	14	US-10-166-225A-181	Sequence 181, App	1401	53.5	13.0	1030	16	US-10-408-765A-497	Sequence 497, App
1329	54	13.2	242	15	US-10-695-980-32	Sequence 32, Appl	1402	53.5	13.0	1083	14	US-10-080-170-330	Sequence 330, App
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1331	54	13.2	288	15	US-10-424-599-209811	Sequence 209811, A	1404	53.5	13.0	1083	16	US-10-468-356-330	Sequence 330, App
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OM protein - protein search, using sw model

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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hypothetical prote  
hypothetical prote  
probable transport  
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probable membrane  
hypothetical prote  
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NADH2 dehydrogenas  
P2Y6 receptor - hu  
interleukin-8 rece  
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Frizzled-2 protein  
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Frizzled-1 protein  
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hypothetical prote  
hypothetical prote  
ABC transporter tr  
prolipoprotein dia  
hypothetical prote  
ubiquinol-cytochro  
hypothetical prote  
methyl-accepting c  
methyl-accepting c  
hypothetical prote  
hypothetical prote  
yfeA protein - Esc  
hypothetical prote  
sodium-chloride tr  
AcrB/AcrD/AcrF fam  
hypothetical prote  
E5 protein - rhesu  
probable membrane  
heme O oxygenase h  
heme O oxygenase h  
cell division prot

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104	57	13.9	712	2	AG0175	probable membrane	177	55	13.4	459	2	C91257	DNA-damage-inducib
105	57	13.9	745	1	OPH0M	myeloperoxidase (E	178	55	13.4	481	2	E86285	hypothetical prote
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111	57	13.9	3473	2	S27927	polyprotein - rice	184	55	13.4	1017	2	A37227	Na+/K+-exchanging
112	56.5	13.8	89	2	S51911	cryptogene protein	185	55	13.4	1139	2	AI0379	probable potassium
113	56.5	13.8	229	2	E70838	hypothetical prote	186	54.5	13.3	169	2	C36807	hypothetical prote
114	56.5	13.8	250	2	AB1555	ABC transporter tr	187	54.5	13.3	174	2	B54853	amatigote surface
115	56.5	13.8	338	2	S22623	undecaprenyl-phosp	188	54.5	13.3	234	2	E86975	probable membrane
116	56.5	13.8	402	2	B69843	conserved hypother	189	54.5	13.3	245	2	A59258	tetraspan TSPAN-6
117	56.5	13.8	437	2	A69172	conserved hypother	190	54.5	13.3	284	2	A82729	phosphatidate cyti
118	56.5	13.8	455	1	T03024	calcium-dependent	191	54.5	13.3	287	2	AE1431	B. subtilis SpoIII
119	56.5	13.8	475	2	A12439	hypothetical prote	192	54.5	13.3	287	2	AG1805	B. subtilis SpoIII
120	56.5	13.8	514	2	T35371	probable Na+/H+ an	193	54.5	13.3	300	2	G89103	protein ClH810.2 l
121	56.5	13.8	533	2	T38644	conserved hypother	194	54.5	13.3	300	2	AE0010	probable integral
122	56.5	13.8	607	2	T11032	NADH2 dehydrogenas	195	54.5	13.3	306	2	I49068	protein kinase STY
123	56.5	13.8	653	2	A39922	potassium channel	196	54.5	13.3	315	1	QXMS1M	NADH2 dehydrogenas
124	56.5	13.8	658	2	T16040	hypothetical prote	197	54.5	13.3	348	2	T12591	NADH2 dehydrogenas
125	56.5	13.8	1202	2	T37867	hypothetical prote	198	54.5	13.3	362	2	C71311	probable phosphata
126	56	13.7	193	2	A53697	insulin-like growt	199	54.5	13.3	363	2	G83954	flagella-associate
127	56	13.7	269	2	H64146	hypothetical prote	200	54.5	13.3	378	2	T34372	hypothetical prote
128	56	13.7	321	2	T24572	hypothetical prote	201	54.5	13.3	413	2	E64536	serine transport p
129	56	13.7	324	2	T17978	probable ribonucle	202	54.5	13.3	421	2	AB2189	hypothetical prote
130	56	13.7	351	2	T15112	hypothetical prote	203	54.5	13.3	438	1	WQSCFP	L-fucose permease
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133	56	13.7	429	2	G64649	hypothetical prote	206	54.5	13.3	442	2	S14145	depressed growth-r
134	56	13.7	527	1	S75063	Na+/H+-exchanging	207	54.5	13.3	461	2	G64206	hexosephosphate tr
135	56	13.7	558	2	E83905	hypothetical prote	208	54.5	13.3	483	2	A39676	protein kinase STY
136	56	13.7	645	2	T27186	hypothetical prote	209	54.5	13.3	488	2	T33197	hypothetical prote
137	56	13.7	684	2	T37875	hypothetical prote	210	54.5	13.3	492	2	E58931	NADH2 dehydrogenas
138	56	13.7	694	2	S71786	wingless receptor	211	54.5	13.3	499	2	A48672	delayed rectifier
139	56	13.7	1682	2	A45380	sodium channel pro	212	54.5	13.3	499	2	I84204	potassium channel
140	56	13.7	2016	2	A38195	sodium channel pro	213	54.5	13.3	499	2	A33814	potassium channel
141	56	13.7	2019	2	A33996	sodium channel pro	214	54.5	13.3	510	2	P82566	GumJ protein XF236
142	55.5	13.5	100	2	C97798	hypothetical prote	215	54.5	13.3	560	2	S51600	phosphorylase kina
143	55.5	13.5	198	2	PC1134	hypothetical prote	216	54.5	13.3	563	2	T34479	hypothetical prote
144	55.5	13.5	210	1	A49872	cytochrome-c oxida	217	54.5	13.3	602	2	S47880	NADH2 dehydrogenas
145	55.5	13.5	268	2	G64234	proline iminopepti	218	54.5	13.3	616	2	S64156	probable membrane
146	55.5	13.5	298	2	S15433	hypothetical prote	219	54.5	13.3	660	2	S24125	potassium channel
147	55.5	13.5	321	2	S39586	peptide transport	220	54.5	13.3	720	1	A55160	Trg protein - frui
148	55.5	13.5	322	2	B83579	hypothetical prote	221	54.5	13.3	2818	2	B55282	neurofibromatosis-
149	55.5	13.5	355	2	AD2926	exopolysaccharide	222	54.5	13.3	2820	2	JC5196	neurofibromin I -
150	55.5	13.5	355	2	D98356	hypothetical prote	223	54.5	13.3	2825	2	I54352	neurofibromin - mo
151	55.5	13.5	359	2	S55653	hypothetical prote	224	54	13.2	167	2	S52831	probable membrane
152	55.5	13.5	476	2	S15314	undecaprenyl-phosp	225	54	13.2	193	2	T11234	hypothetical prote
153	55.5	13.5	539	2	T22041	hypothetical prote	226	54	13.2	259	2	S58988	cytochrome-c oxida
154	55.5	13.5	552	2	T23755	hypothetical prote	227	54	13.2	264	2	AE2100	phosphonate ABC tr
155	55.5	13.5	720	2	E82561	toxin secreted AB	228	54	13.2	265	2	H81155	conserved hypother
156	55.5	13.5	734	2	T24908	hypothetical prote	229	54	13.2	315	2	E64426	phosphate transpor
157	55.5	13.5	1063	2	A33683	hypothetical prote	230	54	13.2	325	2	T33297	hypothetical prote
158	55.5	13.5	1063	2	JC4700	cation efflux syst	231	54	13.2	337	2	B97271	uncharacterized co
159	55.5	13.5	1275	2	AD0332	cadmium, zinc, cob	232	54	13.2	338	2	T04734	cytochrome P450 ho
160	55.5	13.5	1321	2	A60165	probable membrane	233	54	13.2	347	2	G83171	hypothetical prote
161	55	13.4	98	2	T11083	sodium channel pro	234	54	13.2	348	2	T21627	hypothetical prote
162	55	13.4	118	2	F34792	Ig heavy chain pre	235	54	13.2	358	2	AE3752	interleukin-8 rece
163	55	13.4	128	2	E88449	protein F54D8.2 [i	236	54	13.2	387	2	AF2115	hypothetical prote
164	55	13.4	176	2	B90343	hypothetical prote	237	54	13.2	432	2	B65190	potassium uptake p
165	55	13.4	321	2	AD3367	sodium/bile acid c	238	54	13.2	498	2	B99946	hypothetical prote
166	55	13.4	340	2	AB2183	hypothetical prote	239	54	13.2	499	2	G97761	apolipoprotein N-a
167	55	13.4	347	2	S70364	cannabinoid recept	240	54	13.2	558	2	AE3580	iron(III)-transpor
168	55	13.4	354	2	A23669	interleukin-8 rece	241	54	13.2	566	1	HMIVT1	hemagglutinin prec
169	55	13.4	355	2	J01231	interleukin-8 rece	242	54	13.2	574	2	JE0339	Frizzled-7 protein
170	55	13.4	360	2	A53611	na+/h+ antiporter	243	54	13.2	599	2	A48863	limonene cyclase -
171	55	13.4	375	2	C75201	branched-chain ami	244	54	13.2	662	2	G82721	regulator of patho
172	55	13.4	439	2	A64769	branched-chain ami	245	54	13.2	690	2	T014639	probable potassium
173	55	13.4	439	2	C90685	branched-chain ami	246	54	13.2	764	2	T01493	probable membrane
174	55	13.4	439	2	G85535	branched-chain ami	247	54	13.2	894	2	S45135	probable membrane
175	55	13.4	449	2	H69862	Na+-transporting A	248	54	13.2	1272	2	C96637	hypothetical prote

249	53.5	13.0	139	2	PC4217	hypothetical 139 p	322	53	12.9	849	2	D83368	protein FlrH8.4 [i
250	53.5	13.0	184	2	S76935	hypothetical prote	323	53	12.9	1091	2	T30256	calcium channel al
251	53.5	13.0	226	1	JQ1574	major surface anti	324	52.5	12.8	83	2	F84510	hypothetical prote
252	53.5	13.0	226	1	JQ1576	major surface anti	325	52.5	12.8	90	2	S34798	nodulin (clone GmN
253	53.5	13.0	226	1	JQ2101	surface antigen -	326	52.5	12.8	111	2	AI2312	hypothetical prote
254	53.5	13.0	226	2	JQ2106	surface antigen -	327	52.5	12.8	133	2	E97400	hypothetical prote
255	53.5	13.0	263	2	A80585	probable membrane	328	52.5	12.8	133	2	AC2618	conserved hypothet
256	53.5	13.0	265	2	T46952	probable membrane	329	52.5	12.8	137	2	H90546	hypothetical prote
257	53.5	13.0	298	2	A83892	hypothetical prote	330	52.5	12.8	148	2	AH0175	probable membrane
258	53.5	13.0	299	2	B95149	heat shock protein	331	52.5	12.8	183	1	QOBPGL	git protein - phag
259	53.5	13.0	313	2	A45774	odorant receptor 8	332	52.5	12.8	195	2	E71000	hypothetical prote
260	53.5	13.0	350	2	C56118	vetispiradiene syn	333	52.5	12.8	261	2	T11306	cytochrome-c oxida
261	53.5	13.0	354	2	B86650	protein C09G12.4 [	334	52.5	12.8	263	2	T22536	hypothetical prote
262	53.5	13.0	355	2	A80426	two-component syst	335	52.5	12.8	268	2	AI1175	hypothetical prote
263	53.5	13.0	362	2	E71637	hypothetical prote	336	52.5	12.8	268	2	AG1532	spermidine/putresc
264	53.5	13.0	362	2	G97849	hypothetical prote	337	52.5	12.8	278	2	D83080	hypothetical prote
265	53.5	13.0	379	2	PC4180	thiazide-sensitive	338	52.5	12.8	285	2	E97144	probable permease
266	53.5	13.0	400	2	T39792	multidrug-efflux t	339	52.5	12.8	289	2	F88539	protein C05E4.5 [i
267	53.5	13.0	429	2	T28950	hypothetical prote	340	52.5	12.8	299	2	S59144	NADH2 dehydrogenas
268	53.5	13.0	452	2	G64894	probable membrane	341	52.5	12.8	321	2	T02236	NBS-LRR type resis
269	53.5	13.0	476	2	AF0765	undecaprenyl-phosp	342	52.5	12.8	356	2	S37356	spas protein - Sal
270	53.5	13.0	523	2	T11916	NADH2 dehydrogenas	343	52.5	12.8	360	2	G02064	G protein-coupled
271	53.5	13.0	578	2	G82950	conserved hypothet	344	52.5	12.8	364	2	S67855	GumF protein - Xan
272	53.5	13.0	603	2	T11843	NADH2 dehydrogenas	345	52.5	12.8	374	2	T10349	very-late factor 1
273	53.5	13.0	627	2	S37994	RNA polymerase I t	346	52.5	12.8	395	2	E90896	probable transport
274	53.5	13.0	706	2	D81236	nitrogen regulatio	347	52.5	12.8	395	2	B85721	probable transport
275	53.5	13.0	706	2	E82009	probable two-compo	348	52.5	12.8	395	2	A64908	membrane protein y
276	53.5	13.0	770	2	S76883	nitric-oxide reduc	349	52.5	12.8	436	2	T36320	hypothetical prote
277	53.5	13.0	927	2	A48085	transcription fact	350	52.5	12.8	441	2	G75306	drug transport pro
278	53.5	13.0	1021	2	G01202	NaCl electroneutra	351	52.5	12.8	452	2	G85847	hypothetical prote
279	53.5	13.0	1083	2	H86921	probable membrane	352	52.5	12.8	452	2	G90787	hypothetical prote
280	53.5	13.0	1488	2	T02856	hypothetical prote	353	52.5	12.8	487	2	G90496	transporter [impor
281	53	12.9	119	2	B90198	hypothetical prote	354	52.5	12.8	489	2	I51532	potassium channel
282	53	12.9	174	2	A54853	anastigote surface	355	52.5	12.8	513	2	C69809	spore germination
283	53	12.9	174	2	C54853	anastigote surface	356	52.5	12.8	597	2	AE2780	conserved hypothet
284	53	12.9	228	2	D90553	hypothetical prote	357	52.5	12.8	646	2	G97559	probable cyclic be
285	53	12.9	229	2	A05198	hypothetical prote	358	52.5	12.8	691	2	H71405	hypothetical prote
286	53	12.9	255	2	AC3368	diguanylate cyclas	359	52.5	12.8	717	2	S31034	retrovirus-related
287	53	12.9	288	2	A83040	hypothetical prote	360	52.5	12.8	717	2	S31035	retrovirus-related
288	53	12.9	297	2	AG0143	probable LysR-fami	361	52.5	12.8	735	2	AD0341	probable membrane
289	53	12.9	301	2	H70505	hypothetical prote	362	52.5	12.8	836	2	C82726	DNA uptake protein
290	53	12.9	330	2	S55595	G protein-coupled	363	52.5	12.8	848	1	T02053	S-receptor kinase
291	53	12.9	337	2	AE3216	ABC transporter, m	364	52.5	12.8	902	2	S49931	SYG1 protein - yea
292	53	12.9	338	2	T21161	hypothetical prote	365	52.5	12.8	1082	2	T45096	probable arabinosy
293	53	12.9	343	2	T27798	hypothetical prote	366	52	12.7	184	2	F82270	probable type IV p
294	53	12.9	350	2	A39445	interleukin-8 rece	367	52	12.7	208	2	T24065	hypothetical prote
295	53	12.9	353	2	B96767	unknown protein F2	368	52	12.7	213	2	AI3280	hypothetical prote
296	53	12.9	360	2	S36750	cannabinoid recept	369	52	12.7	252	2	F87575	ABC transporter, p
297	53	12.9	361	2	T39784	hypothetical prote	370	52	12.7	260	2	G81290	probable capsule p
298	53	12.9	415	2	B81373	transmembrane tran	371	52	12.7	261	2	T11460	cytochrome-c oxida
299	53	12.9	429	2	S41537	citrate (si)-synth	372	52	12.7	282	2	D72771	probable bacterioc
300	53	12.9	429	2	G71937	hypothetical prote	373	52	12.7	301	2	E97972	conserved hypothet
301	53	12.9	431	2	T11911	NADH2 dehydrogenas	374	52	12.7	311	2	F95374	probable ABC trans
302	53	12.9	440	2	C82410	conserved hypothet	375	52	12.7	313	2	F90884	probable transport
303	53	12.9	458	2	D97799	NADH2 dehydrogenas	376	52	12.7	333	2	A85734	hypothetical prote
304	53	12.9	469	2	S73404	MG061 homolog R02	377	52	12.7	329	2	C75122	hypothetical prote
305	53	12.9	490	1	G69282	hypothetical prote	378	52	12.7	340	2	C72851	AcOrf-11 protein -
306	53	12.9	501	2	B89135	protein F25G6.7 [i	379	52	12.7	345	2	T34998	probable transmemb
307	53	12.9	509	2	D86146	F22L4.11 protein -	380	52	12.7	352	2	T27298	hypothetical prote
308	53	12.9	512	2	B83060	iron (III)-transpo	381	52	12.7	377	2	T27316	hypothetical prote
309	53	12.9	520	2	T26201	hypothetical prote	382	52	12.7	398	2	T20901	hypothetical prote
310	53	12.9	537	2	JC1127	frizzled protein 4	383	52	12.7	404	2	T32998	hypothetical prote
311	53	12.9	553	2	C81024	hypothetical prote	384	52	12.7	447	2	G89917	branched-chain ami
312	53	12.9	555	2	S69671	hypothetical prote	385	52	12.7	477	2	E95158	hypothetical prote
313	53	12.9	555	2	E70409	carbon starvation	386	52	12.7	477	2	E98024	hypothetical prote
314	53	12.9	558	2	F81967	probable inner mem	387	52	12.7	502	2	T25263	hypothetical prote
315	53	12.9	590	1	S34960	NADH2 dehydrogenas	388	52	12.7	545	2	E90460	hypothetical prote
316	53	12.9	611	2	C58893	NADH2 dehydrogenas	389	52	12.7	574	2	S46178	phosphate-repressi
317	53	12.9	655	2	A86153	hypothetical prote	390	52	12.7	590	1	QOUTC5	NADH2 dehydrogenas
318	53	12.9	666	2	JC7312	frizzled-3 protein	391	52	12.7	763	2	AD0170	probable membrane
319	53	12.9	692	2	T05111	hypothetical prote	392	52	12.7	866	2	I79267	traB protein - Esc
320	53	12.9	717	2	AD0627	probable membrane	393	52	12.7	990	2	T01896	probable Na+/K+/Cl
321	53	12.9	746	2	AD1622	probable integral	394	52	12.7	1450	2	A84780	probable ABC trans

395	52	12.7	1505	2	T31418	synaptonemal compl	468	51	12.4	312	2	D90198	transposase ISC123
396	52	12.7	1977	2	S54771	sodium channel alp	469	51	12.4	314	2	T05993	probable peroxidase
397	52	12.7	2005	2	A46269	sodium channel alp	470	51	12.4	319	2	D90342	transposase ISC123
398	51.5	12.6	39	2	T03344	gene e23 protein -	471	51	12.4	321	2	D90370	conserved hypochet
399	51.5	12.6	93	2	T28322	ORF MSV161 probabl	472	51	12.4	323	2	G81312	protein-export mem
400	51.5	12.6	113	2	A32995	t complex atelilit	473	51	12.4	328	2	I55450	G protein-coupled
401	51.5	12.6	137	2	R83892	protein-diulfide	474	51	12.4	336	2	T23902	hypothetical prote
402	51.5	12.6	203	2	A36886	surface protein PA	475	51	12.4	346	2	T11390	NADH2 dehydrogenas
403	51.5	12.6	204	1	F0HUGL	granulocyte colony	476	51	12.4	348	2	T12290	NADH2 dehydrogenas
404	51.5	12.6	209	1	OBUTMB	cytochrome-c oxida	477	51	12.4	359	2	A39008	histamine H2 recep
405	51.5	12.6	252	2	F85017	hypothetical prote	478	51	12.4	360	2	T14084	hypothetical prote
406	51.5	12.6	262	2	S75891	hypothetical prote	479	51	12.4	380	2	A83458	hypothetical prote
407	51.5	12.6	271	2	T11590	hypothetical prote	480	51	12.4	385	2	G72569	hypothetical prote
408	51.5	12.6	281	2	S60477	1-acylglycerol-3-p	481	51	12.4	389	2	E96516	P1693.13 [imported
409	51.5	12.6	293	2	T27270	hypothetical prote	482	51	12.4	393	2	AH0184	probable multidrug
410	51.5	12.6	296	2	S76512	hypothetical prote	483	51	12.4	394	2	AH0020	conserved integral
411	51.5	12.6	302	2	A99017	heat shock protein	484	51	12.4	407	2	A83479	sensory transducti
412	51.5	12.6	317	2	T47551	nuclear envelope m	485	51	12.4	418	2	S38125	hypothetical prote
413	51.5	12.6	317	2	H95143	conserved hypochet	486	51	12.4	421	2	C82305	ubiquinol-cytochro
414	51.5	12.6	317	2	F98011	conserved hypochet	487	51	12.4	433	2	F70968	hypothetical prote
415	51.5	12.6	318	2	T21589	hypothetical prote	488	51	12.4	435	2	A84824	probable nematode-
416	51.5	12.6	320	2	A86439	protein T19E23.9 [	489	51	12.4	443	2	H96542	transporter (Pho87
417	51.5	12.6	321	2	AC0658	peptide transport	490	51	12.4	446	2	F70302	cellulase (EC 3.2.
418	51.5	12.6	375	2	F78572	hypothetical prote	491	51	12.4	505	2	T07883	hypothetical prote
419	51.5	12.6	379	2	F72859	very late expressi	492	51	12.4	513	2	T21887	hypothetical prote
420	51.5	12.6	383	2	F82871	conserved hypochet	493	51	12.4	528	2	T43919	yfub protein limpo
421	51.5	12.6	383	2	T38194	hypothetical prote	494	51	12.4	528	2	A12321	hypothetical prote
422	51.5	12.6	387	2	S64082	probable membrane	495	51	12.4	546	2	S48932	hypothetical prote
423	51.5	12.6	395	2	AD0678	probable membrane	496	51	12.4	546	2	G86440	hypothetical prote
424	51.5	12.6	411	2	PC2168	phosphoenolpyruvat	497	51	12.4	566	1	HMITV2	hemagglutinin prec
425	51.5	12.6	418	2	A64763	probable transport	498	51	12.4	597	2	T15324	hypothetical prote
426	51.5	12.6	418	2	D85530	probable transport	499	51	12.4	600	2	S36736	hypothetical prote
427	51.5	12.6	418	2	H90679	probable transport	500	51	12.4	600	2	E48951	nist protein - Lac
428	51.5	12.6	420	2	T28827	hypothetical prote	501	51	12.4	606	2	T11334	nisin transport pr
429	51.5	12.6	446	2	G86645	damage-inducible p	502	51	12.4	628	2	F81277	NADH2 dehydrogenas
430	51.5	12.6	461	2	H64636	proline/betaine tr	503	51	12.4	634	2	T32324	hypothetical prote
431	51.5	12.6	467	2	T10025	hypothetical prote	504	51	12.4	646	2	T28868	hypothetical prote
432	51.5	12.6	469	2	B83368	hypothetical prote	505	51	12.4	766	2	H83141	probable two-compo
433	51.5	12.6	474	2	S75464	hypothetical prote	506	51	12.4	840	2	T32217	hypothetical prote
434	51.5	12.6	477	2	S61891	undecaprenyl-phosp	507	51	12.4	870	2	T25338	hypothetical prote
435	51.5	12.6	492	2	AD2993	succinoglycan bios	508	51	12.4	967	2	JH0440	RAD54 protein - ye
436	51.5	12.6	493	2	F98290	exot protein limpo	509	51	12.4	967	2	G96637	hypothetical prote
437	51.5	12.6	499	2	JH0313	potassium channel	510	51	12.4	1013	2	T04740	hypothetical prote
438	51.5	12.6	549	1	ODUTMB	cytochrome-c oxida	511	51	12.4	1125	2	S67794	probable membrane
439	51.5	12.6	550	2	T03714	5-epi-aristolochen	512	51	12.4	1187	2	T18355	hypothetical prote
440	51.5	12.6	559	2	T08174	sesquiterpene cycl	513	51	12.4	1216	2	T09224	spindle assembly c
441	51.5	12.6	605	2	H71562	probable flagellar	514	51	12.4	1293	2	B40025	maleless protein, c
442	51.5	12.6	612	2	T11830	NADH2 dehydrogenas	515	51	12.4	1528	2	T37308	ATPase homolog - C
443	51.5	12.6	612	2	AE3091	conserved hypochet	516	51	12.4	2039	2	S64540	probable calcium c
444	51.5	12.6	648	2	E98195	hypothetical prote	517	51	12.4	4085	2	S28600	hypothetical prote
445	51.5	12.6	683	2	T05149	protein kinase hom	518	50.5	12.3	102	2	S49642	probable membrane
446	51.5	12.6	696	2	B87265	Kup system potassi	519	50.5	12.3	114	2	AC3033	hypothetical prote
447	51.5	12.6	705	2	T48464	hypothetical prote	520	50.5	12.3	119	2	H90513	hypothetical prote
448	51.5	12.6	707	1	LEBBBV	hemolysin secretio	521	50.5	12.3	140	2	A99253	hypothetical prote
449	51.5	12.6	787	2	H70374	NADH2 dehydrogenas	522	50.5	12.3	141	2	G85799	hypothetical prote
450	51.5	12.6	824	2	A86783	glycosyl transfera	523	50.5	12.3	141	2	C90951	hypothetical prote
451	51.5	12.6	827	1	F0MSIA	retrovirus-related	524	50.5	12.3	141	2	E64949	probable membrane
452	51.5	12.6	1023	2	A47296	thiazide-sensitive	525	50.5	12.3	171	2	T25696	hypothetical prote
453	51.5	12.6	1111	2	T05646	hypothetical prote	526	50.5	12.3	173	2	H82141	disulfide bond for
454	51.5	12.6	2610	2	T20968	hypothetical prote	527	50.5	12.3	176	2	S58618	NADH2 dehydrogenas
455	51	12.4	56	2	AH1492	probable secreted	528	50.5	12.3	179	2	D90361	hypothetical prote
456	51	12.4	81	1	WSWJ35	Es protein - human	529	50.5	12.3	184	2	S10125	alpha-2u-globulin
457	51	12.4	101	2	S60434	probable membrane	530	50.5	12.3	203	2	AF1995	hypothetical prote
458	51	12.4	109	2	T33239	synaptobrevin SNB-	531	50.5	12.3	222	2	JC7697	beta-casein-like p
459	51	12.4	143	2	H82385	conserved hypochet	532	50.5	12.3	224	2	AD0743	probable membrane
460	51	12.4	208	1	B69066	conserved hypochet	533	50.5	12.3	261	2	S55010	cytochrome-c oxida
461	51	12.4	225	1	J73641	hypothetical prote	534	50.5	12.3	270	2	C62760	cytochrome-c oxida
462	51	12.4	226	1	JQ1571	major surface anti	535	50.5	12.3	277	2	C82128	4-amino-4-deoxycho
463	51	12.4	226	1	JQ1572	hemolysin III (yp)	536	50.5	12.3	277	2	T31089	probable ABC trans
464	51	12.4	233	2	E70114	ABC-2 transporter,	537	50.5	12.3	278	2	S64317	hypothetical prote
465	51	12.4	266	2	H95122	hypothetical prote	538	50.5	12.3	280	2	T19362	hypothetical prote
466	51	12.4	285	2	G83934	probable membrane	539	50.5	12.3	283	2	T18678	hypothetical prote
467	51	12.4	301	2	AH1503		540	50.5	12.3	285	2	H69369	branched-chain ami

541	50.5	12.3	286	2	146855	voltage-gated pota	614	50	12.2	175	2	AB0185	probable membrane
542	50.5	12.3	286	2	C81147	sulfate ABC transp	615	50	12.2	274	2	T05509	hypothetical prote
543	50.5	12.3	286	2	G81875	sulfate ABC transp	616	50	12.2	286	2	H89003	protein T2A6.5 [i
544	50.5	12.3	298	2	E90172	hypothetical prote	617	50	12.2	287	2	E82546	pre-pilin leader p
545	50.5	12.3	306	2	H86695	ABC transporter pe	618	50	12.2	291	2	B72284	oligopeptide ABC t
546	50.5	12.3	309	2	AB0343	probable phosphati	619	50	12.2	301	2	E95104	conserved hypothe
547	50.5	12.3	310	2	G40808	polynucleotide ade	620	50	12.2	306	1	QREBOB	oligopeptide trans
548	50.5	12.3	310	2	G86073	probable endonucle	621	50	12.2	306	2	AH0650	oligopeptide trans
549	50.5	12.3	310	2	A91227	probable endonucle	622	50	12.2	308	2	T20043	hypothetical prote
550	50.5	12.3	317	2	T33861	hypothetical prote	623	50	12.2	325	2	B87234	conserved membrane
551	50.5	12.3	335	2	AC1343	hypothetical prote	624	50	12.2	328	2	T44931	mocr protein [impo
552	50.5	12.3	335	2	AG1713	hypothetical prote	625	50	12.2	338	1	S44207	hypothetical prote
553	50.5	12.3	345	2	T16498	hypothetical prote	626	50	12.2	340	2	T24615	hypothetical prote
554	50.5	12.3	346	2	T11194	NADH2 dehydrogenas	627	50	12.2	342	2	S51891	probable membrane
555	50.5	12.3	353	2	S28787	neuropeptide Y/pep	628	50	12.2	349	2	A75612	phosphate ABC tran
556	50.5	12.3	368	2	S01651	probable RNA-direc	629	50	12.2	349	2	I55601	Na/taurocholate co
557	50.5	12.3	383	2	C71683	rod shape-determin	630	50	12.2	357	2	A45619	ubiquinol-cytochro
558	50.5	12.3	401	2	AD0969	glutamate permease	631	50	12.2	380	2	T43016	DNA mismatch repai
559	50.5	12.3	401	2	D91082	probable transport	632	50	12.2	381	2	T02589	hypothetical prote
560	50.5	12.3	401	2	E85927	partial transport t	633	50	12.2	388	2	C40605	hmc 3'-region hypo
561	50.5	12.3	402	2	G96642	hypothetical prote	634	50	12.2	396	1	E64143	chloramphenicol re
562	50.5	12.3	403	2	A90925	probable transport	635	50	12.2	419	2	T19260	hypothetical prote
563	50.5	12.3	403	2	E85773	probable transport	636	50	12.2	427	2	G70936	hypothetical prote
564	50.5	12.3	417	2	AB0682	probable membrane	637	50	12.2	436	2	G70058	hypothetical prote
565	50.5	12.3	417	2	F90916	probable transport	638	50	12.2	440	2	D87076	probable conserved
566	50.5	12.3	417	2	F64915	membrane protein Y	639	50	12.2	443	1	BVECTC	threonine-serine p
567	50.5	12.3	417	2	C85765	probable transport	640	50	12.2	443	2	C85973	threonine-serine p
568	50.5	12.3	418	2	S56369	hypothetical 44.8K	641	50	12.2	443	2	D91128	threonine-serine p
569	50.5	12.3	418	2	H86109	probable transport	642	50	12.2	443	2	F89426	protein M162.5 [im
570	50.5	12.3	418	2	B98269	probable transport	643	50	12.2	451	2	A95379	HYPOPHETICAL 50.8
571	50.5	12.3	446	2	S22614	hypothetical prote	644	50	12.2	467	2	AB2493	hypothetical prote
572	50.5	12.3	449	2	T50555	delta-8 sphingolip	645	50	12.2	483	2	T20895	hypothetical prote
573	50.5	12.3	459	2	F81914	probable transmemb	646	50	12.2	487	2	T23776	hypothetical prote
574	50.5	12.3	470	2	AE1930	ammonium transport	647	50	12.2	494	2	AE1372	proteins involved
575	50.5	12.3	471	2	B64099	undecaprenyl-phosp	648	50	12.2	495	2	T20885	hypothetical prote
576	50.5	12.3	473	2	T04218	hypothetical prote	649	50	12.2	496	2	G71693	apolipoprotein n-a
577	50.5	12.3	483	2	A81352	integral membrane	650	50	12.2	504	2	T29338	hypothetical prote
578	50.5	12.3	483	2	S69894	major DNA-binding	651	50	12.2	507	2	F97765	hypothetical prote
579	50.5	12.3	564	2	AC2893	adenylate cyclase	652	50	12.2	528	2	A10359	iron(III)-transpor
580	50.5	12.3	564	2	F97668	probable electron	653	50	12.2	529	2	E84813	hypothetical prote
581	50.5	12.3	572	2	S46051	probable resistanc	654	50	12.2	547	2	AE1022	probable membrane
582	50.5	12.3	575	2	B83586	probable permease	655	50	12.2	553	2	T40438	hypothetical prote
583	50.5	12.3	603	2	H90061	hypothetical prote	656	50	12.2	555	2	S56946	probable membrane
584	50.5	12.3	604	2	C90619	NADH dehydrogenase	657	50	12.2	575	2	H69450	prolyl-CRNA synthe
585	50.5	12.3	604	2	T38017	hypothetical prote	658	50	12.2	575	2	F71360	probable K+ transp
586	50.5	12.3	608	2	T35755	probable branched	659	50	12.2	607	2	AH0381	probable ATP trans
587	50.5	12.3	634	2	E96927	probable permease	660	50	12.2	611	2	S68138	NADH2 dehydrogenas
588	50.5	12.3	677	2	A71406	hypothetical prote	661	50	12.2	616	2	T19873	hypothetical prote
589	50.5	12.3	719	2	T45845	hypothetical prote	662	50	12.2	720	1	G64836	probable membrane
590	50.5	12.3	721	2	D82496	conserved hypothe	663	50	12.2	720	2	D90759	hypothetical prote
591	50.5	12.3	742	2	I37225	leucocyte antigen	664	50	12.2	720	2	B85623	hypothetical prote
592	50.5	12.3	771	2	H84845	hypothetical prote	665	50	12.2	729	2	G70539	hypothetical prote
593	50.5	12.3	772	2	T26313	hypothetical prote	666	50	12.2	752	2	E82146	Rec2-related prote
594	50.5	12.3	779	2	T49717	related to BCS1 pr	667	50	12.2	820	2	C81252	probable NADH2 deh
595	50.5	12.3	788	2	I64045	recombination prot	668	50	12.2	952	2	H84583	hypothetical prote
596	50.5	12.3	792	2	T00487	probable potassium	669	50	12.2	1020	2	A34474	Na+/K+-exchanging
597	50.5	12.3	830	2	T01058	hypothetical prote	670	50	12.2	1020	2	B24639	major acidic nucle
598	50.5	12.3	847	2	G85666	hypothetical prote	671	50	12.2	1023	2	JC4013	probable membrane
599	50.5	12.3	847	2	AH0636	periplasmic glucan	672	50	12.2	1029	2	S56229	transmembrane effl
600	50.5	12.3	847	2	F64847	glucan biosynthesi	673	50	12.2	1040	2	D81379	hypothetical prote
601	50.5	12.3	857	2	C90807	membrane glycosylt	674	50	12.2	1130	2	T20288	probable potassium
602	50.5	12.3	974	1	PXLNPD	H+-exporting ATPas	675	50	12.2	1284	2	T13168	multidrug resistanc
603	50.5	12.3	1098	2	G70697	probable arabinosy	676	50	12.2	1302	2	S30327	protein-tyrosine k
604	50.5	12.3	1099	2	T16283	hypothetical prote	677	50	12.2	1400	1	I38185	sodium channel alp
605	50.5	12.3	1143	4	B84547	dynein beta heavy	678	50	12.2	1835	2	I54323	sodium channel alp
606	50.5	12.3	4568	2	T08030	photosystem I 8K p	679	50	12.2	1836	2	J50648	sodium channel alp
607	50	12.2	83	2	S22207	photosystem I 8K p	680	50	12.2	1836	2	JS0648	sodium channel pro
608	50	12.2	87	2	T26867	hypothetical prote	681	50	12.2	1840	1	CHRTM1	ES protein - human
609	50	12.2	98	2	T17091	NADH2 dehydrogenas	682	49.5	12.1	84	1	WSML51	hypothetical membr
610	50	12.2	115	2	T17082	NADH2 dehydrogenas	683	49.5	12.1	107	2	AC3315	hypothetical prote
611	50	12.2	121	2	AH2497	hypothetical prote	684	49.5	12.1	110	2	F90830	integral membrane
612	50	12.2	133	2	S61662	dolichyl-diphospho	685	49.5	12.1	110	2	C85688	hypothetical prote
613	50	12.2	133	2	B70027	hypothetical prote	686	49.5	12.1	110	2	JN0329	ethidium efflux pr

687	49.5	12.1	131	2	AD0744	probable membrane	760	49	12.0	157	2	H95891	hypothetical prote
688	49.5	12.1	154	2	D70387	hypothetical prote	761	49	12.0	158	2	S39770	seminal vesicle au
689	49.5	12.1	160	2	AB1185	B. subtilis Yds p	762	49	12.0	178	2	A71730	ubiquinone biosynt
690	49.5	12.1	214	2	A40721	hypothetical prote	763	49	12.0	179	2	JC1151	hypothetical prote
691	49.5	12.1	219	2	A75628	response regulator	764	49	12.0	185	2	H83296	hypothetical prote
692	49.5	12.1	236	2	S42069	TEGT protein - rat	765	49	12.0	202	2	AF0604	probable permease
693	49.5	12.1	238	1	DEEC51	succinate dehydrog	766	49	12.0	222	2	T18587	hypothetical prote
694	49.5	12.1	238	2	E90722	succinate dehydrog	767	49	12.0	229	2	F64398	hypothetical prote
695	49.5	12.1	238	2	D85573	succinate dehydrog	768	49	12.0	235	2	C89949	hypothetical prote
696	49.5	12.1	239	2	AC0591	succinate dehydrog	769	49	12.0	246	2	A69013	conserved hypotet
697	49.5	12.1	242	2	T14791	hypothetical prote	770	49	12.0	259	2	S50337	cytochrome-c oxida
698	49.5	12.1	261	2	T11770	cytochrome-c oxida	771	49	12.0	261	2	T11540	cytochrome-c oxida
699	49.5	12.1	265	2	B84468	hypothetical prote	772	49	12.0	263	2	A95865	probable protein l
700	49.5	12.1	266	2	C45164	cytochrome-c oxida	773	49	12.0	267	2	F75377	conserved hypotet
701	49.5	12.1	276	2	H83568	probable permease	774	49	12.0	294	2	T11379	NADH2 dehydrogenas
702	49.5	12.1	281	2	JQ2226	middle surface pro	775	49	12.0	300	2	F81799	hypothetical integ
703	49.5	12.1	292	2	A60547	hypothetical prote	776	49	12.0	301	2	AH1144	probable membrane
704	49.5	12.1	302	2	B84421	probable phosphati	777	49	12.0	302	2	B81696	4-hydroxybenzoate
705	49.5	12.1	310	2	H82138	probable phosphati	778	49	12.0	302	2	G86920	probable integral
706	49.5	12.1	311	2	T44610	cytochrome a3 con	779	49	12.0	320	2	T26259	hypothetical prote
707	49.5	12.1	313	2	T24994	hypothetical prote	780	49	12.0	332	2	T19649	hypothetical prote
708	49.5	12.1	318	1	QO7R1M	NADH2 dehydrogenas	781	49	12.0	332	2	S03871	spherulin 4 precur
709	49.5	12.1	328	2	T32210	hypothetical prote	782	49	12.0	348	2	T12281	NADH2 dehydrogenas
710	49.5	12.1	339	2	T21473	hypothetical prote	783	49	12.0	356	2	S13221	GTP-binding regula
711	49.5	12.1	343	2	B84129	hypothetical prote	784	49	12.0	357	2	T25499	hypothetical prote
712	49.5	12.1	344	2	JC5942	chemokine receptor	785	49	12.0	368	2	AF1992	hypothetical prote
713	49.5	12.1	362	2	C81453	flagellar biosynth	786	49	12.0	378	2	C83465	flagellar biosynth
714	49.5	12.1	366	2	S53898	probable membrane	787	49	12.0	381	2	T29927	hypothetical prote
715	49.5	12.1	368	2	A85768	partial beta-D-glu	788	49	12.0	386	2	AD2649	ABC transporter, m
716	49.5	12.1	370	2	D90919	beta-D-glucuronida	789	49	12.0	386	2	C97431	alpha-glucosides t
717	49.5	12.1	394	2	S48522	cell division cont	790	49	12.0	391	2	AC0326	probable potassium
718	49.5	12.1	400	2	JQ2230	large surface prot	791	49	12.0	398	2	T44331	hypothetical prote
719	49.5	12.1	423	2	C82763	cell division prot	792	49	12.0	399	2	A87392	conserved hypotet
720	49.5	12.1	428	2	T00731	hypothetical prote	793	49	12.0	403	2	C83825	multidrug resistan
721	49.5	12.1	431	2	B97277	probable O-antigen	794	49	12.0	405	2	T21188	hypothetical prote
722	49.5	12.1	435	2	AC0104	proline/sugar tra	795	49	12.0	408	2	T34467	hypothetical prote
723	49.5	12.1	452	2	A71877	hypothetical prote	796	49	12.0	414	2	D81387	probable integral
724	49.5	12.1	452	2	C72295	hypothetical prote	797	49	12.0	415	2	T22760	hypothetical prote
725	49.5	12.1	458	2	S10196	NADH2 dehydrogenas	798	49	12.0	439	2	F96499	hypothetical prote
726	49.5	12.1	489	2	C86183	hypothetical prote	799	49	12.0	439	2	AF0551	branched chain ami
727	49.5	12.1	494	2	AC1742	protein involved i	800	49	12.0	443	2	JQ0007	branched-chain ami
728	49.5	12.1	506	1	D64048	iron (III) ABC tra	801	49	12.0	443	2	E96956	CBS-domain contain
729	49.5	12.1	521	2	B85088	hypothetical prote	802	49	12.0	459	2	C65212	DNA-damage-inducib
730	49.5	12.1	542	2	A81662	apolipoprotein N-a	803	49	12.0	460	2	AH0968	sodium galactoside
731	49.5	12.1	565	1	HMVGM	hemagglutinin prec	804	49	12.0	462	2	T11136	NADH2 dehydrogenas
732	49.5	12.1	575	2	A11996	hypothetical prote	805	49	12.0	463	2	E83242	probable adenylate
733	49.5	12.1	579	2	A11789	ABC transporter (A	806	49	12.0	478	2	T11318	NADH2 dehydrogenas
734	49.5	12.1	592	2	D64044	hypothetical prote	807	49	12.0	480	2	G86285	hypothetical prote
735	49.5	12.1	603	1	GBEGC	beta-glucuronidase	808	49	12.0	516	2	H70935	hypothetical prote
736	49.5	12.1	603	2	T11284	NADH2 dehydrogenas	809	49	12.0	520	2	C89980	hypothetical prote
737	49.5	12.1	604	2	I36917	glycoprotein lib -	810	49	12.0	521	2	T41621	hypothetical prote
738	49.5	12.1	615	2	AH2248	proteinase [improt	811	49	12.0	523	2	A11970	hypothetical prote
739	49.5	12.1	645	2	A12963	cellulose synthase	812	49	12.0	541	2	AC2392	hypothetical prote
740	49.5	12.1	645	2	D98319	hypothetical prote	813	49	12.0	546	2	T71348	probable apolipop
741	49.5	12.1	647	2	A83908	bo-type ubiquinol	814	49	12.0	547	2	A40656	hypothetical prote
742	49.5	12.1	669	2	S64795	suppressor protein	815	49	12.0	553	2	B83714	iron (III) transpo
743	49.5	12.1	669	2	E71127	hypothetical prote	816	49	12.0	559	2	G71327	probable apolipop
744	49.5	12.1	724	2	A82538	cation transportin	817	49	12.0	569	2	S74053	probable acylamino
745	49.5	12.1	745	2	T46178	hypothetical prote	818	49	12.0	599	2	T18831	hypothetical prote
746	49.5	12.1	791	2	A99514	hypothetical prote	819	49	12.0	618	2	G86288	probable adenine n
747	49.5	12.1	808	2	T04459	hypothetical prote	820	49	12.0	624	2	E96834	adenine nucleotide
748	49.5	12.1	834	2	A97178	probable permease	821	49	12.0	662	2	T47649	ABC transporter-li
749	49.5	12.1	944	2	S56936	vacuolar protein-s	822	49	12.0	693	2	H86214	protein T6022.6 [i
750	49.5	12.1	1051	2	R83330	RND divalent metal	823	49	12.0	706	2	J80164	frizzled-6 protein
751	49	12.0	62	2	H81337	probable periplasm	824	49	12.0	772	2	G02860	carnitine O-palmit
752	49	12.0	98	2	S14206	NADH2 dehydrogenas	825	49	12.0	772	2	S65532	carnitine palmitoy
753	49	12.0	101	2	A26696	NADH2 dehydrogenas	826	49	12.0	780	2	T29580	hypothetical prote
754	49	12.0	104	2	S60405	hypothetical prote	827	49	12.0	787	2	G86436	hypothetical prote
755	49	12.0	110	2	AG0137	conserved hypotet	828	49	12.0	842	2	S18462	glycoprotein H pre
756	49	12.0	114	2	T11513	NADH2 dehydrogenas	829	49	12.0	853	2	AC2079	ferrichrome-iron r
757	49	12.0	136	2	AD2309	hypothetical prote	830	49	12.0	854	2	T23155	hypothetical prote
758	49	12.0	151	2	E71051	hypothetical prote	831	49	12.0	871	2	A46742	metabotropic gluta
759	49	12.0	155	2	S59155	NADH2 dehydrogenas	832	49	12.0	927	2	A45039	CTF4 protein - yea

833	49	12.0	939	2	A57487	inositol-polyphosp	906	48.5	11.8	480	2	A83487	probable MFS trans
834	49	12.0	976	2	C71248	hypothetical prote	907	48.5	11.8	481	2	C95920	hypothetical membr
835	49	12.0	1502	2	S53602	carbamoyl-phosphat	908	48.5	11.8	507	2	T47785	hypothetical prote
836	49	12.0	1515	2	T52081	MFP-like ABC trans	909	48.5	11.8	512	2	B90050	hypothetical prote
837	48.5	11.8	113	2	JC6573	outer-arm dynein 1	910	48.5	11.8	529	1	S71774	calcium-dependent
838	48.5	11.8	118	1	B64248	hypothetical prote	911	48.5	11.8	544	2	B75541	probable multidrug
839	48.5	11.8	137	2	AC2739	conserved hypoteth	912	48.5	11.8	576	2	T25375	hypothetical prote
840	48.5	11.8	138	2	AD0368	probable membrane	913	48.5	11.8	582	2	H82393	probable L-lactate
841	48.5	11.8	139	2	A87036	probable conserved	914	48.5	11.8	588	2	G82118	succinate dehydrog
842	48.5	11.8	148	2	H70531	hypothetical prote	915	48.5	11.8	588	2	T48766	probable sugar tra
843	48.5	11.8	152	2	A97320	hypothetical prote	916	48.5	11.8	592	2	D84431	probable endosomal
844	48.5	11.8	162	2	F71319	hypothetical prote	917	48.5	11.8	606	2	S41830	NADH2 dehydrogenas
845	48.5	11.8	169	2	E96510	hypothetical prote	918	48.5	11.8	644	2	A25684	hypothetical prote
846	48.5	11.8	174	2	B30020	NADH2 dehydrogenas	919	48.5	11.8	685	2	S65974	conserved hypoteth
847	48.5	11.8	179	2	S70898	intracellular sept	920	48.5	11.8	692	2	H71494	probable thiol-dis
848	48.5	11.8	206	2	H84165	hypothetical prote	921	48.5	11.8	711	2	C49219	toxin apxIII secre
849	48.5	11.8	206	2	S76279	hypothetical prote	922	48.5	11.8	748	2	T47250	complex I intermed
850	48.5	11.8	226	1	JQ1579	major surface anti	923	48.5	11.8	792	2	G84830	probable potassium
851	48.5	11.8	226	1	JQ1580	major surface anti	924	48.5	11.8	809	1	IJBODD	desmocolin 2b pre
852	48.5	11.8	226	2	T41063	surface antigen -	925	48.5	11.8	863	1	IJBODD	desmocolin 2a pre
853	48.5	11.8	226	2	JQ2225	small surface prot	926	48.5	11.8	886	2	A57172	probable hormone r
854	48.5	11.8	230	2	S05118	hypothetical prote	927	48.5	11.8	1065	2	B69795	acri flavin resista
855	48.5	11.8	230	2	S58563	cema protein - mai	928	48.5	11.8	1333	2	S65812	RNA-directed DNA p
856	48.5	11.8	237	2	I38334	TEGT (testis enhan	929	48.5	11.8	2098	2	T13166	rough deal protein
857	48.5	11.8	238	2	T41063	hypothetical prote	930	48.5	11.8	2386	2	T39511	rad3 checkpoint pr
858	48.5	11.8	245	2	T30127	hypothetical prote	931	48.5	11.8	3149	1	QOBE8	BPLF1 protein - hu
859	48.5	11.8	249	2	B84147	ABC transporter (p	932	48	11.7	82	2	T10148	sugar transport pr
860	48.5	11.8	252	2	AH1482	hypothetical prote	933	48	11.7	115	2	T11057	NADH2 dehydrogenas
861	48.5	11.8	259	2	H97708	hypothetical prote	934	48	11.7	115	2	T17173	NADH2 dehydrogenas
862	48.5	11.8	260	2	A00099	conserved hypoteth	935	48	11.7	115	2	S60397	hypothetical prote
863	48.5	11.8	264	2	T50011	hypothetical prote	936	48	11.7	115	2	A10332	probable membrane
864	48.5	11.8	265	2	T07747	hypothetical prote	937	48	11.7	118	1	GLYC	gene 1 protein - S
865	48.5	11.8	267	2	B81431	ABC transporter in	938	48	11.7	126	2	B83265	hypothetical prote
866	48.5	11.8	269	2	D82001	probable integral	939	48	11.7	129	2	T04230	hypothetical prote
867	48.5	11.8	269	2	G81230	conserved hypoteth	940	48	11.7	139	2	S72841	probable ABC-type
868	48.5	11.8	275	2	AH1924	hypothetical prote	941	48	11.7	145	2	F81338	probable periplasm
869	48.5	11.8	280	2	AD0099	prepilin peptidase	942	48	11.7	171	2	S72489	hypothetical prote
870	48.5	11.8	283	2	S19420	hypothetical prote	943	48	11.7	180	2	B97242	hypothetical prote
871	48.5	11.8	299	2	G90386	conserved hypoteth	944	48	11.7	197	2	I39723	ORF13 - Agrobacter
872	48.5	11.8	300	2	E71534	probable pnp2b met	945	48	11.7	198	2	J70356	Cop protein - Clos
873	48.5	11.8	308	2	H64153	hypothetical prote	946	48	11.7	200	2	F70900	hypothetical prote
874	48.5	11.8	318	2	T11402	NADH2 dehydrogenas	947	48	11.7	200	2	B90933	hypothetical prote
875	48.5	11.8	322	2	AD3134	hypothetical prote	948	48	11.7	200	2	F85781	hypothetical prote
876	48.5	11.8	326	2	H71884	iron (III) dicitra	949	48	11.7	202	2	H64931	hypothetical prote
877	48.5	11.8	326	2	A64631	iron(III) dicitrat	950	48	11.7	211	2	D69529	conserved hypoteth
878	48.5	11.8	327	2	B83636	hypothetical prote	951	48	11.7	230	2	E71315	conserved hypoteth
879	48.5	11.8	332	2	H98153	peptide ABC transp	952	48	11.7	251	2	AH0732	probable bacteriop
880	48.5	11.8	334	2	T34124	hypothetical prote	953	48	11.7	261	2	S47876	cytochrome-c oxida
881	48.5	11.8	334	2	A97643	exopolysaccharide	954	48	11.7	261	2	T11293	cytochrome-c oxida
882	48.5	11.8	334	2	AD2866	acetyltransferase	955	48	11.7	264	2	E95410	probable ABC trans
883	48.5	11.8	338	2	A83389	probable permease	956	48	11.7	266	2	G82386	amino acid ABC tra
884	48.5	11.8	340	2	E69544	hypothetical prote	957	48	11.7	277	2	T29611	hypothetical prote
885	48.5	11.8	350	2	D75272	hypothetical prote	958	48	11.7	293	2	AD3438	CDPdiacylglycerol-
886	48.5	11.8	351	2	T21855	hypothetical prote	959	48	11.7	294	2	E97671	thuf protein (Ar17
887	48.5	11.8	361	2	B81402	probable integral	960	48	11.7	294	2	AB2896	hypothetical prote
888	48.5	11.8	363	2	A82567	GumF protein Xp236	961	48	11.7	296	2	E69025	conserved hypoteth
889	48.5	11.8	382	1	S33573	ubiquinol-cytochro	962	48	11.7	300	2	G81069	conserved hypoteth
890	48.5	11.8	389	2	B96522	hypothetical prote	963	48	11.7	302	2	H82045	conserved hypoteth
891	48.5	11.8	389	2	H69048	conserved hypoteth	964	48	11.7	303	2	JQ1382	hypothetical 34K p
892	48.5	11.8	393	2	B96780	hypothetical prote	965	48	11.7	306	2	T23686	hypothetical prote
893	48.5	11.8	403	2	C83422	nitrate transporte	966	48	11.7	309	1	S51356	olfactory receptor
894	48.5	11.8	404	2	T20453	hypothetical prote	967	48	11.7	317	2	C82411	hypothetical prote
895	48.5	11.8	413	2	C71971	saraine transport p	968	48	11.7	319	1	S73290	cytochrome c-type
896	48.5	11.8	418	2	A81394	probable sugar tra	969	48	11.7	321	2	T06932	plastoquinol-plast
897	48.5	11.8	419	2	F97133	phage-related, hea	970	48	11.7	321	2	D90353	conserved hypoteth
898	48.5	11.8	439	2	T32470	hypothetical prote	971	48	11.7	327	2	T34720	probable lipoprote
899	48.5	11.8	444	2	AH3597	glycerol-3-phospha	972	48	11.7	333	2	C82888	phenylalanine-tRNA
900	48.5	11.8	445	2	B82219	pN <sup>5</sup> system, cellob	973	48	11.7	340	2	T41757	AcMNPV orf11 - Bom
901	48.5	11.8	459	2	G81187	Na+/H+ antiporter	974	48	11.7	341	2	AF1319	ferrichrome ABC tr
902	48.5	11.8	461	2	H85087	hypothetical prote	975	48	11.7	341	2	AF1691	ferrichrome ABC tr
903	48.5	11.8	462	2	B88613	protein T27E9.5 [i	976	48	11.7	345	2	T25561	hypothetical prote
904	48.5	11.8	470	2	B82943	probable ABC subst	977	48	11.7	348	2	T12287	NADH2 dehydrogenas
905	48.5	11.8	473	2	T31717	hypothetical prote	978	48	11.7	348	2	T12285	NADH2 dehydrogenas

979	48	11.7	348	2	B83869	hypothetical prote	1052	48	11.7	2005	2	B25019	sodium channel pro
980	48	11.7	349	2	T09858	NADH2 dehydrogenas	1053	48	11.7	2163	2	S50675	pre-mRNA splicing
981	48	11.7	349	2	T09948	NADH2 dehydrogenas	1054	48	11.7	3014	1	JC5620	genome polyprotein
982	48	11.7	354	1	RGXLOA	GTP-binding regula	1055	47.5	11.6	50	2	H90537	hypothetical prote
983	48	11.7	357	2	E71708	hypothetical prote	1056	47.5	11.6	83	2	T18122	hypothetical prote
984	48	11.7	363	1	CBUTB	ubiquinol-cytochro	1057	47.5	11.6	132	2	F82246	conserved hypotet
985	48	11.7	367	2	S01431	modulation protei	1058	47.5	11.6	138	2	F81355	probable integral
986	48	11.7	367	2	T23273	hypothetical prote	1059	47.5	11.6	140	2	E86283	hypothetical prote
987	48	11.7	369	2	AE2345	phospho-N-acetylmu	1060	47.5	11.6	146	2	C84113	acetobutylicum pho
988	48	11.7	371	2	H88208	protein K02A2.1 [i	1061	47.5	11.6	148	2	T33937	hypothetical prote
989	48	11.7	374	2	F81357	probable membrane-	1062	47.5	11.6	151	2	H65017	hypothetical prote
990	48	11.7	379	2	E58889	ubiquinol-cytochro	1063	47.5	11.6	151	2	C85886	hypothetical prote
991	48	11.7	379	2	T24814	hypothetical prote	1064	47.5	11.6	151	2	H91041	hypothetical prote
992	48	11.7	383	2	F70752	hypothetical prote	1065	47.5	11.6	163	2	D64025	hypothetical prote
993	48	11.7	387	2	L69202	G protein-coupled	1066	47.5	11.6	168	2	AF2802	conserved hypotet
994	48	11.7	388	2	S59860	hypothetical prote	1067	47.5	11.6	168	2	G97581	hypothetical prote
995	48	11.7	389	2	S71336	mesotocin receptor	1068	47.5	11.6	171	2	AD0554	phosphatidylglycer
996	48	11.7	391	2	S07743	ubiquinol-cytochro	1069	47.5	11.6	174	2	S01189	NADH2 dehydrogenas
997	48	11.7	392	2	G85076	probable reverse t	1070	47.5	11.6	179	2	T22143	hypothetical prote
998	48	11.7	408	2	B82507	sodium/glutamate s	1071	47.5	11.6	195	2	B90202	hypothetical prote
999	48	11.7	418	2	S67138	probable membrane	1072	47.5	11.6	196	2	T01982	tumor related prot
1000	48	11.7	419	2	D72357	hypothetical prote	1073	47.5	11.6	201	2	A86636	hypothetical prote
1001	48	11.7	428	2	S38461	ubiquinol-cytochro	1074	47.5	11.6	204	2	AG1466	serine O-acetyltra
1002	48	11.7	428	2	PC4163	toxin-co-regulated	1075	47.5	11.6	220	2	T41562	hypothetical wtf p
1003	48	11.7	428	2	JC4601	hypothetical 48.2k	1076	47.5	11.6	243	2	AD1983	hypothetical prote
1004	48	11.7	429	2	G97528	citrate synthase [	1077	47.5	11.6	247	2	T16061	hypothetical prote
1005	48	11.7	439	2	AH2747	citrate synthase [	1078	47.5	11.6	247	2	E89994	conserved hypotet
1006	48	11.7	436	2	H87793	protein C27A12.8 [	1079	47.5	11.6	249	1	SYBCDG	phosphatidate cyti
1007	48	11.7	439	2	AB0389	branched-chain ami	1080	47.5	11.6	249	2	A99651	CDP-diglyceride sy
1008	48	11.7	447	2	F82619	proton glutamate s	1081	47.5	11.6	249	2	A85502	CDP-diglyceride sy
1009	48	11.7	452	1	JNECGT	glycerol-3-phospha	1082	47.5	11.6	261	2	JQ1513	H+-transporting tw
1010	48	11.7	452	2	E91019	sn-glycerol-3-phos	1083	47.5	11.6	261	2	B34167	H+-transporting tw
1011	48	11.7	452	2	G85863	sn-glycerol-3-phos	1084	47.5	11.6	265	2	T14645	hypothetical prote
1012	48	11.7	452	2	AC3184	efflux protein [im	1085	47.5	11.6	272	2	E64182	cys2 protein - Hae
1013	48	11.7	454	1	T25203	probable membrane-	1086	47.5	11.6	275	2	E75548	conserved hypotet
1014	48	11.7	458	2	H71657	NADH2 dehydrogenas	1087	47.5	11.6	275	2	T28869	hypothetical prote
1015	48	11.7	462	2	D81251	NADH2 dehydrogenas	1088	47.5	11.6	278	2	AI2517	hypothetical prote
1016	48	11.7	465	2	E69825	amino acid transpo	1089	47.5	11.6	280	2	T25829	hypothetical prote
1017	48	11.7	474	2	AH0226	D-serine/D-alanine	1090	47.5	11.6	284	2	AB0680	probable dimethyl
1018	48	11.7	488	2	F96724	hypothetical prote	1091	47.5	11.6	305	2	B84187	hypothetical prote
1019	48	11.7	493	2	A71875	hypothetical prote	1092	47.5	11.6	311	2	H82541	conserved hypotet
1020	48	11.7	497	2	G87793	protein C27A12.7 [	1093	47.5	11.6	313	2	T11160	NADH2 dehydrogenas
1021	48	11.7	500	2	AD1047	probable amino aci	1094	47.5	11.6	313	2	D96793	hypothetical prote
1022	48	11.7	509	2	F71526	hypothetical prote	1095	47.5	11.6	317	2	T11337	NADH2 dehydrogenas
1023	48	11.7	523	2	JQ1926	polyprotein - hepa	1096	47.5	11.6	319	1	F69777	conserved hypotet
1024	48	11.7	528	2	D85048	hypothetical prote	1097	47.5	11.6	323	2	A58892	NADH2 dehydrogenas
1025	48	11.7	532	2	S46831	probable membrane	1098	47.5	11.6	325	2	T32174	hypothetical prote
1026	48	11.7	535	2	T41384	hypothetical prote	1099	47.5	11.6	326	2	AC2953	hypothetical ABC t
1027	48	11.7	537	2	AE2454	two-component sens	1100	47.5	11.6	326	2	B98330	hypothetical ABC t
1028	48	11.7	557	2	T27130	hypothetical prote	1101	47.5	11.6	329	2	AG2951	probable oligopept
1029	48	11.7	584	2	AH2321	hypothetical prote	1102	47.5	11.6	329	2	F98331	probable oligopept
1030	48	11.7	581	2	JC7086	FZD10 protein - hu	1103	47.5	11.6	332	2	A49879	alpha-2,3-sialyltr
1031	48	11.7	586	2	S64779	probable membrane	1104	47.5	11.6	333	2	I65989	G protein-coupled
1032	48	11.7	615	2	G82658	periplasmic glucan	1105	47.5	11.6	346	2	T14133	NADH2 dehydrogenas
1033	48	11.7	627	2	D90452	hypothetical prote	1106	47.5	11.6	346	2	T33309	hypothetical prote
1034	48	11.7	644	2	T37692	probable transport	1107	47.5	11.6	354	2	T32319	hypothetical prote
1035	48	11.7	705	2	T19595	hypothetical prote	1108	47.5	11.6	358	2	F71897	flagellar biosynth
1036	48	11.7	727	2	S27043	neurotransmitter t	1109	47.5	11.6	366	2	T33462	hypothetical prote
1037	48	11.7	744	2	T34116	voltage-gated pota	1110	47.5	11.6	367	2	T28892	hypothetical prote
1038	48	11.7	790	2	A82200	cation transport A	1111	47.5	11.6	370	2	AB0602	probable membrane
1039	48	11.7	840	2	T02164	hypothetical prote	1112	47.5	11.6	372	2	B64819	probable membrane
1040	48	11.7	848	2	T34823	probable turgor pr	1113	47.5	11.6	379	2	H86364	hypothetical prote
1041	48	11.7	881	2	T25786	hypothetical prote	1114	47.5	11.6	387	2	F82692	conserved hypotet
1042	48	11.7	908	2	AH0055	probable cation-tr	1115	47.5	11.6	394	2	AB0713	probable membrane
1043	48	11.7	921	2	T51804	respiratory burst	1116	47.5	11.6	403	2	F64923	probable glutamate s
1044	48	11.7	928	2	T01191	RNA-directed DNA p	1117	47.5	11.6	404	2	AD0005	sodium/glutamate s
1045	48	11.7	1149	2	T18515	adenosinetriphosph	1118	47.5	11.6	404	2	H81699	conserved hypotet
1046	48	11.7	1206	2	E86445	hypothetical prote	1119	47.5	11.6	418	2	AB2308	hypothetical prote
1047	48	11.7	1245	1	VHW82	structural polypro	1120	47.5	11.6	423	2	AH1407	PTS system galacti
1048	48	11.7	1337	2	T38949	hypothetical prote	1121	47.5	11.6	423	2	AH1783	PTS system galacti
1049	48	11.7	1355	2	T22522	hypothetical prote	1122	47.5	11.6	425	2	E86737	malate transport
1050	48	11.7	1687	2	T30176	EGF repeat transme	1123	47.5	11.6	427	2	S42658	H+-transporting tw
1051	48	11.7	1765	2	T42388	sodium channel alp	1124	47.5	11.6	443	2	D83106	hypothetical prote

1125	47.5	11.6	449	2	S76839	hypothetical prote	1198	47	11.5	187	2	T49684	hypothetical prote
1126	47.5	11.6	457	2	D83867	hypothetical prote	1199	47	11.5	192	2	G71920	hypothetical prote
1127	47.5	11.6	463	2	G69829	hypothetical prote	1200	47	11.5	200	2	F84708	probable integral
1128	47.5	11.6	465	2	A83192	two component sens	1201	47	11.5	203	2	B83606	hypothetical prote
1129	47.5	11.6	474	2	D83396	conserved hypotet	1202	47	11.5	206	2	S56059	probable membrane
1130	47.5	11.6	480	2	G70008	NADH dehydrogenase	1203	47	11.5	212	2	AF1644	hypothetical prote
1131	47.5	11.6	482	2	T01762	hypothetical prote	1204	47	11.5	219	2	T47881	hypothetical prote
1132	47.5	11.6	483	2	F75360	hypothetical prote	1205	47	11.5	223	2	B96927	response regulator
1133	47.5	11.6	485	2	G82037	potassium uptake p	1206	47	11.5	224	2	T21101	hypothetical prote
1134	47.5	11.6	486	2	H84805	hypothetical prote	1207	47	11.5	234	2	T35312	probable integral
1135	47.5	11.6	488	2	T11230	NADH2 dehydrogenas	1208	47	11.5	235	1	QOBY1M	mRNA maturase-rela
1136	47.5	11.6	492	2	AC0768	probable transmemb	1209	47	11.5	235	2	G81138	hypothetical prote
1137	47.5	11.6	497	2	G86878	arginine/ornitine	1210	47	11.5	254	2	B83286	hypothetical prote
1138	47.5	11.6	515	2	D95924	probable phosphogl	1211	47	11.5	260	1	OTXL3	cytochrome-c oxida
1139	47.5	11.6	516	2	G86243	hypothetical prote	1212	47	11.5	260	2	S22850	ERS1 protein - yea
1140	47.5	11.6	520	2	AC6118	vetispiradiene syn	1213	47	11.5	262	2	H71390	cytochrome-C oxida
1141	47.5	11.6	529	2	A56119	virulence factor M	1214	47	11.5	264	2	H81720	conserved hypotet
1142	47.5	11.6	546	2	A69890	hypothetical prote	1215	47	11.5	272	2	H87075	probable conserved
1143	47.5	11.6	557	2	C97401	virulence factor m	1216	47	11.5	272	2	D86482	protein F5J5.3 lim
1144	47.5	11.6	557	2	B86106	YidB protein [simi	1217	47	11.5	286	2	B70614	probable mmaA1 pro
1145	47.5	11.6	557	2	S56342	YidB protein - Esc	1218	47	11.5	297	2	T36786	probable integral
1146	47.5	11.6	557	2	H91265	hypothetical prote	1219	47	11.5	300	1	A32566	ubiquinol-cytochro
1147	47.5	11.6	559	2	S62503	inorganic phosphat	1220	47	11.5	300	2	S40858	hypothetical 32.9K
1148	47.5	11.6	575	2	T08964	hypothetical prote	1221	47	11.5	300	2	H91233	probable transport
1149	47.5	11.6	594	2	T45842	calcium dependent	1222	47	11.5	300	2	H86080	probable transport
1150	47.5	11.6	595	2	JC8012	G protein-coupled	1223	47	11.5	301	2	S50737	probable membrane
1151	47.5	11.6	598	2	B90589	sugar ABC transpor	1224	47	11.5	306	2	G85704	oligopeptide trans
1152	47.5	11.6	603	2	C90621	NADH dehydrogenase	1225	47	11.5	306	2	H90846	oligopeptide trans
1153	47.5	11.6	606	2	T11909	NADH2 dehydrogenas	1226	47	11.5	306	2	B36263	oligopeptide trans
1154	47.5	11.6	620	2	A96668	probable endo-beta	1227	47	11.5	306	2	D70409	hypothetical prote
1155	47.5	11.6	623	2	T16167	hypothetical prote	1228	47	11.5	308	2	AC1053	probable membrane
1156	47.5	11.6	626	2	E90079	hypothetical prote	1229	47	11.5	313	2	D69336	conserved hypotet
1157	47.5	11.6	643	2	B69373	conserved hypotet	1230	47	11.5	319	2	D90344	transposase ISC123
1158	47.5	11.6	657	2	B83041	probable chemotaxi	1231	47	11.5	319	2	E90466	transposase ISC123
1159	47.5	11.6	708	2	C30169	leukotoxin express	1232	47	11.5	319	2	H90321	transposase ISC123
1160	47.5	11.6	715	2	A34408	peroxidase (EC 1.1	1233	47	11.5	319	2	T51280	hypothetical prote
1161	47.5	11.6	737	2	AE0819	probable membrane	1234	47	11.5	321	2	F90862	peptide transport
1162	47.5	11.6	749	2	A69861	conserved hypotet	1235	47	11.5	321	2	C85756	peptide transport
1163	47.5	11.6	778	2	T16111	hypothetical prote	1236	47	11.5	321	2	H64877	peptide transport
1164	47.5	11.6	782	2	T39696	methionyl tRNA syn	1237	47	11.5	322	2	S68128	NADH2 dehydrogenas
1165	47.5	11.6	802	2	T05596	probable potassium	1238	47	11.5	325	2	F82558	lipopolysaccharide
1166	47.5	11.6	832	2	S76815	hypothetical prote	1239	47	11.5	328	2	T20582	hypothetical prote
1167	47.5	11.6	857	2	TC7716	prominin - rat	1240	47	11.5	330	2	E64826	YbJX protein - Esc
1168	47.5	11.6	858	2	J08881	prominin - mouse	1241	47	11.5	330	2	C71009	hypothetical prote
1169	47.5	11.6	919	2	T21663	hypothetical prote	1242	47	11.5	336	2	T19498	hypothetical prote
1170	47.5	11.6	932	2	H86325	hypothetical prote	1243	47	11.5	340	2	T25677	hypothetical prote
1171	47.5	11.6	958	2	AC0204	probable integral	1244	47	11.5	344	2	T25567	hypothetical prote
1172	47.5	11.6	1094	2	T05472	hypothetical prote	1245	47	11.5	345	2	T24533	hypothetical prote
1173	47.5	11.6	1165	2	T15279	hypothetical prote	1246	47	11.5	348	2	T11301	NADH2 dehydrogenas
1174	47.5	11.6	1174	2	A40853	potassium channel	1247	47	11.5	348	2	T12291	NADH2 dehydrogenas
1175	47.5	11.6	1493	2	H71445	hypothetical prote	1248	47	11.5	352	2	AF3073	hypothetical prote
1176	47.5	11.6	1876	2	S50235	1,3-beta-glucan sy	1249	47	11.5	356	2	C40656	regulatory protein
1177	47.5	11.6	2055	2	T31617	hypothetical prote	1250	47	11.5	357	2	AB1176	spermidine/putresc
1178	47.5	11.6	2223	2	A47447	calcium channel pr	1251	47	11.5	357	2	AH1532	spermidine/putresc
1179	47.5	11.6	2242	2	A57541	pyrimidine synthe	1252	47	11.5	358	2	T11165	ubiquinol-cytochro
1180	47	11.5	61	2	S78741	protein YP170w-a	1253	47	11.5	358	2	H83554	ubiquinol-cytochro
1181	47	11.5	82	2	H84046	hypothetical prote	1254	47	11.5	359	2	JC4120	histamine H2 recep
1182	47	11.5	84	1	W5ML31	E5 protein - human	1255	47	11.5	360	2	AE0068	phospho-N-acetylmu
1183	47	11.5	92	2	B81100	conserved hypotet	1256	47	11.5	365	2	F95857	probable sugar ABC
1184	47	11.5	92	2	JN0095	hypothetical 10.6K	1257	47	11.5	371	2	C98213	sugar ABC transpor
1185	47	11.5	105	2	E71132	hypothetical prote	1258	47	11.5	378	2	S51591	chitinase (EC 3.2.
1186	47	11.5	116	2	G82398	conserved hypotet	1259	47	11.5	380	2	D84295	hypothetical prote
1187	47	11.5	121	2	A24272	Ig heavy chain pre	1260	47	11.5	390	2	T12421	NADH2 dehydrogenas
1188	47	11.5	122	2	C82926	hypothetical prote	1261	47	11.5	390	2	S66497	isotocin receptor
1189	47	11.5	125	2	D85595	probable membrane	1262	47	11.5	394	2	C64185	cell division prot
1190	47	11.5	125	2	H90744	probable membrane	1263	47	11.5	394	2	D65167	probable membrane
1191	47	11.5	125	2	H64822	probable membrane	1264	47	11.5	395	2	S76793	hypothetical prote
1192	47	11.5	131	2	S65197	probable membrane	1265	47	11.5	396	2	S54999	ubiquinol-cytochro
1193	47	11.5	137	1	B64239	hypothetical prote	1266	47	11.5	401	2	D83873	hypothetical prote
1194	47	11.5	149	2	T11066	NADH2 dehydrogenas	1267	47	11.5	411	2	H72084	chs domain protein
1195	47	11.5	162	2	G98046	conserved hypotet	1268	47	11.5	419	2	T25565	hypothetical prote
1196	47	11.5	167	2	B71518	probable signal pe	1269	47	11.5	431	2	D86433	hypothetical prote
1197	47	11.5	167	2	B64904	fimbrial protein p	1270	47	11.5	433	2	T30807	TRAF interacting p

1271	47	11.5	438	2	H64713	Na+/H+-exchanging
1272	47	11.5	440	1	B29413	ubiquinol-cytochro
1273	47	11.5	440	2	JL0144	interleukin-6 rece
1274	47	11.5	440	2	JC5520	serotonin receptor
1275	47	11.5	440	2	H90253	NADH-Ubiquinone/pl
1276	47	11.5	443	2	F95243	sensor histidine k
1277	47	11.5	443	2	C98108	histidine kinase (
1278	47	11.5	446	2	E81367	probable transmemb
1279	47	11.5	446	2	B83033	probable MFS trans
1280	47	11.5	458	2	I49480	alpha-2 adrenergic
1281	47	11.5	458	2	A37869	alpha-2-adrenergic
1282	47	11.5	458	2	A40392	alpha-2-adrenergic
1283	47	11.5	459	2	T11202	NADH2 dehydrogenas
1284	47	11.5	461	2	AP1079	amino acid transpo
1285	47	11.5	465	2	G96855	unknown protein, 2
1286	47	11.5	470	2	F96806	probable AUX1-like
1287	47	11.5	476	2	T23728	hypothetical prote
1288	47	11.5	481	2	T15657	hypothetical prote
1289	47	11.5	482	2	G83142	probable transport
1290	47	11.5	483	2	T16443	hypothetical prote
1291	47	11.5	487	2	D86285	hypothetical prote
1292	47	11.5	488	2	T16402	hypothetical prote
1293	47	11.5	491	2	AG0557	AmpG protein (impo
1294	47	11.5	494	2	S67314	regulatory protein
1295	47	11.5	499	2	T46923	hypothetical prote
1296	47	11.5	500	2	A10963	two-component syst
1297	47	11.5	500	2	B41853	hexose phosphate t
1298	47	11.5	500	2	A11913	apolipoprotein N-a
1299	47	11.5	501	1	DELVN2	NADH2 dehydrogenas
1300	47	11.5	505	2	E87021	probable integral-
1301	47	11.5	505	2	T23398	hypothetical prote
1302	47	11.5	531	2	A35343	glucuronosyltransf
1303	47	11.5	532	2	T27235	hypothetical prote
1304	47	11.5	548	2	B25542	probable cytochrom
1305	47	11.5	559	2	F88392	protein M01G5.5 [i
1306	47	11.5	559	2	T33425	hypothetical prote
1307	47	11.5	582	2	A70755	hypothetical prote
1308	47	11.5	600	2	S73366	carnitine O-palmit
1309	47	11.5	609	2	E97442	probable ABC trans
1310	47	11.5	631	2	T07420	ATP/ADP-transporte
1311	47	11.5	637	2	S78171	heme lyase yelJr -
1312	47	11.5	637	2	H85043	hypothetical prote
1313	47	11.5	657	2	T52460	hypothetical prote
1314	47	11.5	689	1	JW0107	very-long-chain ac
1315	47	11.5	718	2	A41663	Na+/myo-inositol c
1316	47	11.5	720	2	T47648	ABC transporter-li
1317	47	11.5	742	2	H81088	ABC transporter fa
1318	47	11.5	742	2	H81855	probable cytolysin
1319	47	11.5	858	2	B64656	cell division prot
1320	47	11.5	888	2	H88085	protein T11P1.8 [i
1321	47	11.5	909	1	A54809	disease resistance
1322	47	11.5	924	1	S13913	hexokinase (EC 2.7
1323	47	11.5	980	2	T32381	hypothetical prote
1324	47	11.5	983	2	A87063	conserved large me
1325	47	11.5	1004	2	T38074	hypothetical prote
1326	47	11.5	1008	2	S72898	transport protein
1327	47	11.5	1010	2	T33372	hypothetical prote
1328	47	11.5	1021	2	B42862	Na+/K+-exchangin
1329	47	11.5	1191	2	A53491	bumetanide-sensiti
1330	47	11.5	1198	2	D96723	hypothetical prote
1331	47	11.5	1375	2	S48375	hypothetical prote
1332	47	11.5	1718	2	T14603	hypothetical prote
1333	47	11.5	1836	2	I51964	sodium channel alp
1334	47	11.5	1938	2	A37361	probable integral
1335	47	11.5	1972	2	S68176	TOG protein - huma
1336	47	11.5	2262	2	T30890	calcium channel al
1337	46.5	11.3	52	2	S23285	light-harvesting p
1338	46.5	11.3	102	2	S12809	hypothetical prote
1339	46.5	11.3	115	2	T17176	NADH2 dehydrogenas
1340	46.5	11.3	121	2	S69859	hypothetical prote
1341	46.5	11.3	132	2	H86846	hypothetical prote
1342	46.5	11.3	141	2	T11270	NADH2 dehydrogenas
1343	46.5	11.3	144	2	D81508	Conserved hypothet

1344	46.5	11.3	148	2	A86593	CT568 hypothetical
1345	46.5	11.3	148	2	H72032	ct568 hypothetical
1346	46.5	11.3	160	2	A11542	B. subtilis YdbS p
1347	46.5	11.3	164	2	C35216	Fp18 protein - low
1348	46.5	11.3	164	2	T22102	hypothetical prote
1349	46.5	11.3	165	2	D86761	hypothetical prote
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1351	46.5	11.3	177	2	T31499	hypothetical prote
1352	46.5	11.3	180	2	AG0267	probable intracell
1353	46.5	11.3	183	2	E72459	hypothetical prote
1354	46.5	11.3	194	2	G71698	lipoprotein signal
1355	46.5	11.3	199	1	JQ2137	NADH2 dehydrogenas
1356	46.5	11.3	220	2	E64169	conserved hypothet
1357	46.5	11.3	225	2	G83371	probable amino aci
1358	46.5	11.3	226	2	FJ2120	surface antigen -
1359	46.5	11.3	235	2	E83448	succinate dehydrog
1360	46.5	11.3	243	2	B41191	B. subtilis YhfI p
1361	46.5	11.3	245	2	B42600	OccM protein - Agr
1362	46.5	11.3	246	2	B41044	octopine permease
1363	46.5	11.3	247	2	E64040	hypothetical prote
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1367	46.5	11.3	295	2	AB0462	sn-glycerol-3-phos
1368	46.5	11.3	300	2	D70018	sugar permease hom
1369	46.5	11.3	302	2	B70888	hypothetical prote
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1372	46.5	11.3	315	2	AB0677	probable membrane
1373	46.5	11.3	318	2	T11833	NADH2 dehydrogenas
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1375	46.5	11.3	319	2	D43680	J319 protein - Afr
1376	46.5	11.3	319	2	D83848	cobalamin biosynth
1377	46.5	11.3	322	2	H90600	prolipoprotein dia
1378	46.5	11.3	323	2	AE0324	probable membrane
1379	46.5	11.3	323	2	G90487	maltoase ABC transp
1380	46.5	11.3	325	2	T26350	hypothetical prote
1381	46.5	11.3	330	2	A88990	protein C36C5.10 [
1382	46.5	11.3	341	2	T31826	hypothetical prote
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1386	46.5	11.3	343	2	T32051	hypothetical prote
1387	46.5	11.3	346	2	T29003	hypothetical prote
1388	46.5	11.3	351	2	G71983	hypothetical prote
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1391	46.5	11.3	356	2	D88979	protein F37B4.9 [i
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1394	46.5	11.3	372	2	AB0276	probable membrane
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1396	46.5	11.3	379	2	T41820	VLF-1 oxfr77 - Bomb
1397	46.5	11.3	382	2	T13474	large surface anti
1398	46.5	11.3	383	2	H83205	hypothetical prote
1399	46.5	11.3	386	2	H70821	probable integral
1400	46.5	11.3	395	2	F81343	hypothetical prote
1401	46.5	11.3	396	2	T01201	hypothetical prote
1402	46.5	11.3	397	2	C83470	hypothetical prote
1403	46.5	11.3	401	1	YOECNQ	sodium-glutamate s
1404	46.5	11.3	401	2	A98195	glutamate transpor
1405	46.5	11.3	401	2	B86042	glutamate transpor
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1407	46.5	11.3	405	2	B36340	conserved hypothet
1408	46.5	11.3	405	2	A13148	hypothetical prote
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1412	46.5	11.3	421	2	F72213	hypothetical prote
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ALIGNMENTS

RESULT 1  
 T19408  
 hypothetical protein C18E9.10 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T19408; T25046  
 R/Sims, M.  
 submitted to the EMBL Data Library, March 1996  
 A/Reference number: Z19120  
 A/Accession: T19408  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-235 <WT>  
 A/Cross-references: UNIPROT:Q9XTH1; EMBL:Z70034; PIDN:CAA93859.1; GSPDB:GN00020; CESP:C1  
 R/Baynes, C.  
 submitted to the EMBL Data Library, December 1995  
 A/Reference number: Z19973  
 A/Accession: T25046  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-235 <WI2>  
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 A/Experimental source: clone T21B10  
 C/Genetics:  
 A/Gene: CESP:C18E9.10  
 A/Map position: 2  
 A/Introns: 39/2; 72/2; 112/3; 141/2; 180/3; 200/2  
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 Db 146 LGPKSVLTHMASPQRRLVTVSYLSALFATLYSSILWLKSTFTTLIAAIFQGFLLVWVLSY 205  
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 Db 206 VP 207  
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 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C/Accession: T05049  
 R/Bevan, M.; Vandenberg, M.; Jallet, C.; Portetalle, D.; Hoheisel, J.; Mewes, H.W.; Mayer  
 submitted to the Protein Sequence Database, March 1999  
 A/Reference number: Z15396  
 A/Accession: T05049  
 A/Molecule type: DNA  
 A/Residues: 1-385 <BEV>  
 A/Cross-references: UNIPROT:O65579; EMBL:AL022223  
 A/Experimental source: cultivar Columbia; BAC clone M3E9  
 C/Genetics:

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A;Map position: 4
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A;Note: M3E9.20

Query Match
Best Local Similarity 27.3%; Score 79; DB 2; Length 385;
Matches 21; Conservative 13; Mismatches 27; Indels 16; Gaps 1;

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DB 286 GPNKQLAHSSMEVCVTVLLCVCHALNPRPLPSTGLFIATWGTIVYVMVLSYLSVLP 345
QY 46 CILQSLATWYSLSFIP 62
DB 346 SVLQVLALVYICISYFP 362

RESULT 3
S45393
probable membrane protein YBL102w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBL0812
C;Species: Saccharomyces cerevisiae
C;Date: 09-Jun-1994 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A;Description: Sequence analysis of a 78,6 kb segment of the left end of Saccharomyces cerevisiae chromosome III
A;Reference number: S45387
A;Accession: S45393
A;Molecule type: DNA
A;Residues: 1-215 <OB>
A;Cross-references: UNIPROT:P38166; EMBL:X79489; NID:g496661; PID:g496667
A;Experimental source: strain S288C
R;Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45816
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A;Cross-references: EMBL:X79489; NID:g536171; PID:g536172; MIPS:YBL102w
A;Experimental source: strain S288C
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
Yeast 11, 1103-1112, 1995
A;Title: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevisiae chromosome III
A;Reference number: S59184; MUID:96076635; PMID:7502586
A;Accession: S59190
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <OBW>
A;Cross-references: EMBL:X79489; NID:g496661; PIDN:CRA55993.1; PID:g496667
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C;Genetics:
A;Gene: SGD:SFT2
A;Cross-references: SGD:S0000198; MIPS:YBL102w
A;Map position: 2L
C;Keywords: transmembrane protein
F;79-107/Domain: transmembrane #status predicted <TM1>
F;111-138/Domain: transmembrane #status predicted <TM2>
F;148-166/Domain: transmembrane #status predicted <TM3>
F;168-193/Domain: transmembrane #status predicted <TM4>

Query Match
Best Local Similarity 27.3%; Score 75; DB 2; Length 215;
Matches 19; Conservative 17; Mismatches 32; Indels 2; Gaps 2;

QY 1 MGPKVKQLKRMFEPTFLIATIVLLCFALTLCSAFWHKNKGLALIFCILQSLATWYSLS 59
DB 131 MGFLAYLKHLTARELPFSNFFATCF-WTIYFAFSKNTVLTITCALLELVAVIYALS 189
QY 60 FIFPARDAVK 69
DB 190 YFPFGATGLR 199
```

```
RESULT 4
T02324
hypothetical protein At2g34360 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F13P17.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02324; F84755
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.
A;Reference number: Z14657
A;Accession: T02324
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-466 <ROU>
A;Cross-references: UNIPROT:O80785; EMBL:AC004481; NID:G3337347; PID:G3337367
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84755
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-466 <STO>
A;Cross-references: GB:AE002093; NID:G3337367; PIDN:AAC27412.1; GSPDB:GN00139
C;Genetics:
A;Gene: F13P17.20; At2g34360
A;Map position: 2
A;Introns: 82/3; 264/2; 292/1; 306/2; 386/1; 425/3
C;Superfamily: conserved hypothetical protein H11612

Query Match
Best Local Similarity 25.6%; Score 66.5; DB 2; Length 466;
Matches 20; Conservative 13; Mismatches 22; Indels 23; Gaps 4;

QY 19 TMVLVLCFALTLCSAF-----WNNKGLALIFCILQ---SLATWYSLS---- 59
DB 189 SLHVIICVWLKSLGIFRGAANAISYLN--VILLSCYKFPSPSCSLTWTGFSKEAR 246
QY 60 --FIFPARDAVKKCPAVC 75
DB 247 RDIIPFKLVIPSAFWVC 264

RESULT 5
F58930
cytochrome-c oxidase (EC 1.9.3.1) chain III - Cyanidioschyzon merolae mitochondrion
C;Species: mitochondrion Cyanidioschyzon merolae
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: F58930
R;Ohta, N.; Sato, N.; Kuroiwa, T.
Nucleic Acids Res. 26, 5190-5198, 1998
A;Title: Structure and organization of the mitochondrial genome of the unicellular red alga
A;Reference number: A58930; MUID:99030526; PMID:9801318
A;Accession: F58930
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <ARN>
A;Cross-references: UNIPROT:Q9ZZQ8; GB:D89861; NID:g4115781; PIDN:BAA34657.1; PID:G3927861
C;Genetics:
A;Gene: cox3
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane;

Query Match
Best Local Similarity 32.4%; Score 65; DB 2; Length 272;
Matches 22; Conservative 13; Mismatches 15; Indels 18; Gaps 5;
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C:Genetics:  
A:Gene: yhdk

Query Match 15.6%; Score 64; DB 2; Length 96;  
Best Local Similarity 36.6%; Pred. No. 3;  
Matches 15; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 32 SAFWVHNKGLALIFCIIQSLAL-----TWISLSFIPFARDAY 68  
Db 11 NVFGWISVGTAVLSLLLLNLAIISNVTFSYQMLPFAMAAY 51

RESULT 8  
A38908  
spa40 protein - Shigella flexneri plasmid pMYSH6000  
C:Species: Shigella flexneri  
C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 09-Jul-2004  
C:Accession: A38908  
R:Sasaakawa, C.; Komatsu, K.; Tobe, T.; Suzuki, T.; Yoshikawa, M.  
J. Bacteriol. 175, 2334-2346, 1993  
A:Title: Eight genes in region 5 that form an operon are essential for invasion of epithelial cells  
A:Reference number: A49846; MUID:93224456; PMID:8385666  
A:Accession: A38908  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-342 <SAS>  
A:Cross-references: UNIPROT:P40707; GB:D13663; NID:G287439; PIDN:BAA02832.1; PID:G303896  
C:Genetics:  
C:Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology  
C:Keywords: transmembrane protein

Query Match 15.6%; Score 64; DB 2; Length 342;  
Best Local Similarity 31.7%; Pred. No. 8.6;  
Matches 20; Conservative 9; Mismatches 22; Indels 12; Gaps 3;

Qy 1 MGPKVQLKRMPEPTLLIATI-----WVLLCFALTLCSAFWHNKG---LALIFCIIQSLA 52  
Db 116 LNPVKGLKKIFS-----IKTIKEFFKSILLIILITLTYFFWINDRKIIFSQVFSVDGLY 171

Qy 53 LTW 55  
Db 172 LIW 174

RESULT 9  
T26918  
hypothetical protein Y45F10B.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26918  
R:McMurray, A.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z20286  
A:Accession: T26918  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-351 <WIL>  
A:Cross-references: UNIPROT:O62470; EMBL:AL021487; PIDN:CAA16356.1; GSPDB:GNO0022; CESP:  
A:Experimental source: clone Y45F10B  
C:Genetics:  
A:Gene: CESP:Y45F10B.5  
A:Map position: 4  
A:Introns: 94/3; 164/3; 217/3; 283/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b

Query Match 15.6%; Score 64; DB 2; Length 351;  
Best Local Similarity 35.1%; Pred. No. 8.8;  
Matches 20; Conservative 10; Mismatches 21; Indels 6; Gaps 4;

Qy 17 IATINVLICFALTLCSAFWHNKGLALIFCIIQSLALTWISLSFIPFARDAYKKCF 72  
Db 267 ITAUSMLJLSFVTLICARF--HAKIFQLFIPIPTWAV--YFIALRPFNGDC-EICF 318

Qy 12 EPTRIATIMVLLCFALT--LCSAFWNNKGLALI 44  
          :|: :||| | | | | | | | |  
Db 345 DPGRAVLAIILLCTLTAFIAQRFWLSGKNFATV 379

T16599  
hypothetical protein K09F5.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*

Search completed: April 7, 2005, 03:30:23  
Job time : 76 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 7, 2005, 03:17:03 ; Search time 184 Seconds  
(without alignments)  
214.294 Million cell updates/sec

Title: US-10-063-563-56

Perfect score: 410

Sequence: 1 MGPVKOLKRMFEPTRIAT.....LSFIPFARDAVKCFACVLA 77

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	410	100.0	77	2	Q6UWR8
2	410	100.0	160	2	Q95562
3	366.5	89.4	159	2	Q8VD57
4	324	79.0	161	2	Q7T375
5	306	74.6	159	2	Q8WV19
6	298	72.7	178	2	Q9UIC7
7	240	58.5	163	2	Q9VFD4
8	225.5	55.0	113	2	Q86F94
9	167	40.7	162	2	Q7YTP0
10	159	38.8	163	2	Q9NEC2
11	157	38.3	175	2	Q9LRT0
12	147	35.9	163	2	Q6GKX4
13	144	35.1	171	2	Q6Z7B9
14	142	34.6	218	2	Q9N6J5
15	140	34.1	136	2	Q922U5
16	129	31.5	155	2	Q7YVB3
17	106	25.9	235	2	Q9XTH1
18	97	23.7	138	2	Q9FIP2
19	97	23.7	214	2	Q6BPR2
20	96	23.4	198	2	Q6C220
21	84.5	20.6	231	2	Q69V58
22	83	20.2	212	2	Q75A53
23	83	20.2	227	2	Q6IDC5
24	83	20.2	230	2	Q9FKD4
25	81.5	19.9	1169	2	Q7N4N7
26	80.5	19.6	486	2	Q9FHB6
27	79	19.3	385	2	Q65579
28	77	18.8	213	2	Q6FJ40
29	76.5	18.7	1769	2	Q8WQJ2
30	76	18.5	199	2	Q6II06
31	75	18.3	210	2	Q6BHX8

32	75	18.3	215	1	SFT2 YEAST
33	74	18.0	213	2	Q6CEP97
34	73.5	17.9	353	2	Q8GAP9
35	72.5	17.7	675	2	Q6AX77
36	70	17.1	389	2	Q6D311
37	69.5	17.0	312	2	Q7TRN8
38	69.5	17.0	313	2	Q7TRN9
39	69.5	17.0	319	2	Q8VGV1
40	68	16.6	1033	2	Q9VCM4
41	67	16.3	171	2	Q8SQN0
42	67	16.3	191	2	Q6AS37
43	67	16.3	309	2	Q8VFT9
44	67	16.3	309	2	Q7TRM3
45	67	16.3	335	2	Q9M6Q6
46	66.5	16.2	466	2	Q80785
47	66	16.1	228	2	Q7Z0P6
48	66	16.1	259	2	Q642V4
49	66	16.1	282	2	Q6CY96
50	66	16.1	482	2	Q64C53
51	66	16.1	529	2	Q6HMP1
52	66	16.1	546	1	FVR2 RAT
53	66	16.1	619	2	Q74ZK5
54	66	16.1	1441	2	Q9LK63
55	66	16.1	1466	2	Q8VZZ4
56	65	15.9	136	2	Q7Q051
57	65	15.9	272	2	Q9ZZQ8
58	65	15.9	342	2	Q6XWV1
59	65	15.9	484	2	Q630H5
60	65	15.9	484	2	Q81JM7
61	64.5	15.7	217	2	Q89ZB3
62	64.5	15.7	356	2	Q6LN82
63	64.5	15.7	379	2	Q7CQ09
64	64.5	15.7	379	2	Q9E224
65	64.5	15.7	557	2	Q6Q3H3
66	64.5	15.7	626	2	Q88KQ0
67	64.5	15.7	1253	2	Q729R3
68	64	15.6	96	1	YHDK_BACSU
69	64	15.6	96	2	Q7X2K9
70	64	15.6	231	2	Q64B46
71	64	15.6	342	1	SPAS SHIFL
72	64	15.6	390	2	Q758M8
73	64	15.6	403	2	Q9HYV5
74	64	15.6	452	2	Q83C47
75	64	15.6	494	2	Q83DA1
76	64	15.6	529	2	Q81UF4
77	64	15.6	538	2	Q81H85
78	64	15.6	570	2	Q62K30
79	64	15.6	570	2	Q63TT9
80	64	15.6	681	2	Q92W19
81	64	15.6	685	1	FZD8 MOUSE
82	64	15.6	694	1	FZD8 HUMAN
83	63.5	15.5	388	2	Q6AAQ0
84	63	15.4	148	2	Q6CC06
85	63	15.4	255	2	Q8DLR5
86	63	15.4	258	1	Y256 MYCPN
87	63	15.4	260	2	Q9MNJ0
88	63	15.4	330	2	Q8TEJ8
89	63	15.4	387	2	P72672
90	63	15.4	442	2	Q07845
91	63	15.4	529	2	Q73CQ5
92	63	15.4	662	2	Q7Q4B8
93	63	15.4	802	2	Q95QC9
94	63	15.4	1022	2	Q17943
95	63	15.4	1683	2	Q86KV1
96	62.5	15.2	310	2	Q65269
97	62.5	15.2	316	2	Q8KPR7
98	62.5	15.2	347	2	Q9ZDJ0
99	62.5	15.2	379	1	HCAT ECOLI
100	62.5	15.2	379	2	Q8FF40
101	62.5	15.2	379	2	Q8XA77
102	62.5	15.2	438	2	Q8Z430
103	62.5	15.2	2379	2	Q6UN13
104	62	15.1	97	2	Q6IE38

P38166	saccharomyc
Q6cp97	kluyveromyc
Q8gap9	lyngbya maj
Q6ax77	xenopus lae
Q6d311	erwinia car
Q7trn8	mus musculu
Q7trn9	mus musculu
Q8vgv1	mus musculu
Q9vcm4	drosophila
Q8sgn0	encephalito
Q6as37	desulfotale
Q8vft9	mus musculu
Q7trm3	mus musculu
Q9m6q6	gallus gall
Q80785	arabidopsis
Q7z0p6	paramecium
Q642v4	iftia pach
Q6cy96	kluyveromyc
Q64c53	uncultured
Q6hmp1	bacillus th
F60815	rattus norv
Q74zk5	ashbya goss
Q9lk63	arabidopsis
Q8vzz4	arabidopsis
Q7qq51	giardia lam
Q9zzq8	canididosec
Q6xwv1	shigella fl
Q630h5	bacillus ce
Q81jm7	bacillus an
Q89zb3	bacteroides
Q6ln82	photobacter
Q7cq09	salmonella
Q9ez24	salmonella
Q6q3h3	vitis vinif
Q88kq0	pseudomonas
Q82kq0	desulfovibr
Q729r3	bacillus su
Q7x2k9	bacillus su
Q64b46	uncultured
P40707	shigella fl
Q758m8	ashbya goss
Q9hyv5	pseudomonas
Q83c47	coxiella bu
Q83da1	coxiella bu
Q81uf4	bacillus an
Q81h85	bacillus ce
Q62k30	burkholderi
Q63tt9	burkholderi
Q92w19	rhizobium m
Q61091	mus musculu
Q9h461	homo sapien
Q6aaq0	propionibac
Q6cc06	varrowia li
Q8dlr5	synecococc
Q9mnj0	mycoplasma
Q9m110	helobdella
Q8tpj8	methanosarc
P72672	synecocyst
Q07845	raistonia s
Q73cq5	bacillus ce
Q7q4b8	anopheles g
Q95qc9	caenorhabdi
Q17943	caenorhabdi
Q86kv1	dictyosteli
Q65269	african swi
Q8kpr7	synecococc
Q9zdj0	rickettsia
Q47142	escherichia
Q8ff40	escherichia
Q8xa77	escherichia
Q8z430	salmonella
Q6un13	porcine rep
Q6ie38	homo sapien

105	62	15.1	126	2	Q63P27	O63pz7 burkholderi	178	60	14.6	143	2	Q6SRP0	Q6srp0 sars corona
106	62	15.1	354	1	YA94_BIFLO	O85c0 bifidobacte	179	60	14.6	143	2	Q6SRP4	Q6srp4 sars corona
107	62	15.1	481	2	Q6PH58	O6ph58 brachydanio	180	60	14.6	143	2	Q6SRP8	Q6srp8 sars corona
108	62	15.1	498	2	Q7VU08	O7vu08 bordetella	181	60	14.6	151	2	Q7NCL4	Q7ncl4 gloebacter
109	62	15.1	501	2	Q9BU25	O9bu25 homo sapien	182	60	14.6	185	2	Q90444	Q90444 brachydanio
110	62	15.1	504	2	Q9KZP1	O9kzf1 streptomyc	183	60	14.6	221	1	VME1_CVHSA	P59596 human coron
111	62	15.1	551	1	FVR2_MOUSE	O91x85 mus musculu	184	60	14.6	221	2	Q66VB9	Q66vb9 sars corona
112	62	15.1	551	2	Q96S66	O96s66 homo sapien	185	60	14.6	221	2	Q6GVO7	Q6gv07 sars corona
113	62	15.1	1015	2	Q97925	O97925 thermoplasm	186	60	14.6	221	2	Q6JH34	Q6jh34 sars corona
114	61.5	15.0	93	2	Q98238	O98238 molluscum c	187	60	14.6	221	2	Q6JH42	Q6jh42 sars corona
115	61.5	15.0	222	2	Q7QBD3	O7qbd3 anopheles g	188	60	14.6	221	2	Q6R7Y2	Q6r7y2 sars corona
116	61.5	15.0	259	2	Q6P924	O6p924 acinetobact	189	60	14.6	221	2	Q6RCW1	Q6rcw1 sars corona
117	61.5	15.0	263	2	Q6CS38	O6cs38 kluyveromyc	190	60	14.6	221	2	Q6RCX2	Q6rcx2 sars corona
118	61.5	15.0	326	2	Q9WVD9	O9wvd9 mus musculu	191	60	14.6	221	2	Q6RCY3	Q6rcy3 sars corona
119	61.5	15.0	340	2	O18689	O18689 caenorhabdi	192	60	14.6	221	2	Q6RCZ4	Q6rcz4 sars corona
120	61.5	15.0	379	2	Q83MK7	O83mk7 shigella fl	193	60	14.6	221	2	Q6RD05	Q6rd05 sars corona
121	61.5	15.0	386	2	Q6D247	O6d247 erwinia car	194	60	14.6	221	2	Q6RD16	Q6rd16 sars corona
122	61.5	15.0	420	1	FTSW_LACLA	P58119 lactococcus	195	60	14.6	221	2	Q6RD27	Q6rd27 sars corona
123	61.5	15.0	539	2	Q99L12	O99li2 mus musculu	196	60	14.6	221	2	Q6RD38	Q6rd38 sars corona
124	61.5	15.0	1000	1	YG44_STRCO	O9fcia4 streptomyc	197	60	14.6	221	2	Q6RD49	Q6rd49 sars corona
125	61.5	15.0	3859	1	RPOA_PRRSV	O04561 porcine rep	198	60	14.6	221	2	Q6RD60	Q6rd60 sars corona
126	61.5	15.0	230	1	CYBH_WOLSU	P31875 wolinnella s	199	60	14.6	221	2	Q6SDD3	Q6sdd3 sars corona
127	61	14.9	306	2	Q7UEJ1	O7uej1 rhodopirell	200	60	14.6	221	2	Q6T1D8	Q6t1d8 sars corona
128	61	14.9	373	2	Q8XGf9	O8xgf9 escherichia	201	60	14.6	221	2	Q6TPE4	Q6tpe4 sars corona
129	61	14.9	376	2	Q7NB16	O7nb16 mycoplasma	202	60	14.6	221	2	Q6UZE9	Q6uze9 sars corona
130	61	14.9	383	2	Q8BXJ5	O8bxj5 mus musculu	203	60	14.6	221	2	Q6UZP3	Q6uzp3 sars corona
131	61	14.9	392	2	Q45173	O45173 caenorhabdi	204	60	14.6	221	2	Q6V584	Q6v584 sars corona
132	61	14.9	459	2	Q7PP97	O7pp97 anopheles g	205	60	14.6	221	2	Q6VA74	Q6va74 sars corona
133	61	14.9	491	2	Q8OVZ6	O8ovz6 mus musculu	206	60	14.6	221	2	Q6VA85	Q6va85 sars corona
134	61	14.9	554	2	Q87OV7	O87ov7 neurospora	207	60	14.6	221	2	Q6VA96	Q6va96 sars corona
135	60.5	14.8	59	1	YAMS_CAEEL	O17638 caenorhabdi	208	60	14.6	226	2	Q8QGX4	Q8qgx4 hepatitis b
136	60.5	14.8	152	2	O05277	O05277 chlorante-a	209	60	14.6	243	2	Q93RC4	Q93rc4 escherichia
137	60.5	14.8	159	2	Q47946	O47946 lumbricus r	210	60	14.6	285	2	Q6BD87	Q6bdb7 erwinia car
138	60.5	14.8	168	2	Q7EN6	O7en6 callinectes	211	60	14.6	313	1	YDCU_ECOLI	P77156 escherichia
139	60.5	14.8	180	1	Y1B2_CLOAB	O04352 clostridium	212	60	14.6	346	2	Q6ECB6	Q6ecb6 acanthiza a
140	60.5	14.8	223	2	Q6AMP6	O6amp6 desulfotale	213	60	14.6	346	2	Q6ECC0	Q6ecc0 timeliopsis
141	60.5	14.8	339	2	O8NX81	O8nx81 staphylococ	214	60	14.6	380	2	Q8HEH4	Q8heh4 monochirus
142	60.5	14.8	339	2	Q99V11	O99v11 staphylococ	215	60	14.6	387	2	Q96FK6	Q96fk6 homo sapien
143	60.5	14.8	339	2	Q7A684	O7a684 staphylococ	216	60	14.6	424	2	Q93440	Q93440 caenorhabdi
144	60.5	14.8	339	2	Q6GAC7	O6gac7 staphylococ	217	60	14.6	435	2	Q8XS70	Q8xs70 ralstonia b
145	60.5	14.8	339	2	Q6GHZ8	O6ghz8 staphylococ	218	60	14.6	491	2	Q9U622	Q9u622 drosophila
146	60.5	14.8	360	2	Q8VIF0	O8vif0 rattus norv	219	60	14.6	498	2	Q7WFB2	Q7wfb2 bordetella
147	60.5	14.8	385	2	Q667X4	O667x4 yersinia ps	220	60	14.6	526	1	FVR2_HUMAN	Q9up13 homo sapien
148	60.5	14.8	385	2	Q8ZCR4	O8zcr4 yersinia pe	221	60	14.6	540	2	Q8C16	Q8c16 pseudomonas
149	60.5	14.8	394	2	Q6KCB7	O6kcb7 saccharomyc	222	60	14.6	585	1	FZD5_HUMAN	Q13467 homo sapien
150	60.5	14.8	394	2	Q6KCB8	O6kcb8 saccharomyc	223	60	14.6	895	2	Q6CY55	Q6cy55 kluyveromyc
151	60.5	14.8	394	2	Q6KCB9	O6kcb9 saccharomyc	224	60	14.6	994	2	Q8PD78	Q8pd78 xanthomonas
152	60.5	14.8	394	2	Q8VIE8	O8vie8 rattus norv	225	60	14.6	1007	2	Q6KZ39	Q6kz39 picrophilus
153	60.5	14.8	395	2	Q8VIE9	O8vie9 rattus norv	226	60	14.6	1918	2	Q7QO48	Q7qq48 giardia lam
154	60.5	14.8	401	2	Q9RMD3	O9rmd3 acinetobact	227	59.5	14.5	142	2	Q8CBJ2	Q8cbj2 mus musculu
155	60.5	14.8	443	2	Q7N0H9	Q7n0h9 photorhabdu	228	59.5	14.5	221	2	Q9JWY7	Q9jw7 neisseria m
156	60.5	14.8	451	2	Q82CB2	O82cb2 streptomyc	229	59.5	14.5	221	2	Q9K1K8	Q9k1k8 neisseria m
157	60.5	14.8	507	2	Q8VIF1	O8vif1 rattus norv	230	59.5	14.5	244	1	YML6_MARPO	P38459 marchantia
158	60.5	14.8	540	2	Q6CPQ7	O6cpq7 kluyveromyc	231	59.5	14.5	256	2	Q83GU8	Q83gu8 tropheryma
159	60.5	14.8	541	2	Q66HQ5	O66hq5 rattus norv	232	59.5	14.5	256	2	Q83NS6	Q83ns6 tropheryma
160	60.5	14.8	541	2	Q9WU61	O9wu61 rattus norv	233	59.5	14.5	259	2	Q7NCV4	Q7ncv4 gloebacter
161	60.5	14.8	1063	2	Q6F7C5	O6f7c5 acinetobact	234	59.5	14.5	274	2	Q6FCHO	Q6fch0 acinetobact
162	60.5	14.8	2304	2	Q9BMQ4	O9bmq4 blattella g	235	59.5	14.5	308	2	Q697F7	Q697f7 neomaskelli
163	60	14.6	143	2	Q6SR10	O6sr10 sars corona	236	59.5	14.5	320	2	Q729W0	Q729w0 desulfovibr
164	60	14.6	143	2	Q6SR14	O6sr14 sars corona	237	59.5	14.5	325	2	Q72K20	Q72k20 thermus the
165	60	14.6	143	2	Q6SR18	O6sr18 sars corona	238	59.5	14.5	351	2	Q9VFG7	Q9vfg7 drosophila
166	60	14.6	143	2	Q6SRJ2	O6srj2 sars corona	239	59.5	14.5	362	2	Q705X0	Q705x0 scyllorhinu
167	60	14.6	143	2	Q6SRJ6	O6srj6 sars corona	240	59.5	14.5	400	2	Q7NZ17	Q7nz17 chromobacte
168	60	14.6	143	2	Q6SRK0	O6srk0 sars corona	241	59.5	14.5	403	2	Q8GJG4	Q8gjg4 leptospira
169	60	14.6	143	2	Q6SRK4	O6srk4 sars corona	242	59.5	14.5	412	2	Q72R73	Q72r73 leptospira
170	60	14.6	143	2	Q6SRK8	O6srk8 sars corona	243	59.5	14.5	412	2	Q8F4K6	Q8f4k6 leptospira
171	60	14.6	143	2	Q6SRL2	O6srl2 sars corona	244	59.5	14.5	414	2	Q7PL30	Q7pl30 drosophila
172	60	14.6	143	2	Q6SRU6	O6sru6 sars corona	245	59.5	14.5	414	2	Q7ME69	Q7me69 vibrio vuln
173	60	14.6	143	2	Q6SRM0	O6srm0 sars corona	246	59.5	14.5	414	2	Q8D747	Q8d747 vibrio vuln
174	60	14.6	143	2	Q6SRM4	O6srm4 sars corona	247	59.5	14.5	515	2	Q6PDN5	Q6pdn5 acinetobact
175	60	14.6	143	2	Q6SRM8	O6srm8 sars corona	248	59.5	14.5	577	2	Q88XR1	Q88xr1 lactobacill
176	60	14.6	143	2	Q6SRN2	O6srn2 sars corona	249	59.5	14.5	692	2	Q98HS3	Q98hs3 rhizobium 1
177	60	14.6	143	2	Q6SRN6	O6srn6 sars corona	250	59.5	14.5	749	2	Q8PFD1	Q8pfd1 escherichia

251	59.5	14.5	760	2	Q9N6L2	Q9N6L2 leishmania	324	58	14.1	170	2	Q8T9C6	Q8T9C6 drosophila
252	59.5	14.5	858	2	Q741E5	Q741E5 lactobacilli	325	58	14.1	216	2	Q6G597	Q6G597 bartonella
253	59.5	14.5	998	2	P735I9	P735I9 synechocyst	326	58	14.1	217	1	FZD8 CHICK	Q91A07 gallus gall
254	59.5	14.5	1031	2	Q9ULF42	Q9ULF42 homo sapien	327	58	14.1	222	2	Q6G1C5	Q6G1C5 brachydanio
255	59.5	14.5	1777	2	Q9UHF40	Q9UHF40 homo sapien	328	58	14.1	226	2	Q6NWF9	Q6NWF9 brachydanio
256	59	14.4	113	2	Q744T2	Q744T2 mycobacteri	329	58	14.1	227	2	Q06498	Q06498 lactate deh
257	59	14.4	141	2	Q6PER5	Q6PER5 acinetobact	330	58	14.1	230	1	COBS_PYRO	Q58111 pyrococcus
258	59	14.4	141	2	Q9Z8U1	Q9Z8U1 chlamydia p	331	58	14.1	232	1	COBS_PYRAB	Q9V2N1 pyrococcus
259	59	14.4	205	2	Q6F8F8	Q6F8F8 acinetobact	332	58	14.1	239	2	Q90447	Q90447 brachydanio
260	59	14.4	221	2	Q692E0	Q692E0 sars corona	333	58	14.1	256	2	Q6NOK7	Q6NOK7 rhodopseudo
261	59	14.4	221	2	Q6QJ38	Q6QJ38 sars corona	334	58	14.1	259	2	Q8IE98	Q8IE98 plasmodium
262	59	14.4	233	1	YSR3_CABEL	Q09951 caenorhabdi	335	58	14.1	259	2	Q9TB55	Q9TB55 platynereis
263	59	14.4	237	2	Q647V2	Q647V2 uncultured	336	58	14.1	264	2	Q832N8	Q832N8 enterococcu
264	59	14.4	239	2	Q64D59	Q64D59 uncultured	337	58	14.1	264	2	Q923Z9	Q923Z9 mus muscucu
265	59	14.4	244	2	Q6QLQ4	Q6QLQ4 mus muscucu	338	58	14.1	273	1	CIK2 RABIT	Q90901 oryctolagus
266	59	14.4	244	2	Q9J150	Q9J150 mus muscucu	339	58	14.1	293	2	Q7N9Z0	Q7N9Z0 photorhabdu
267	59	14.4	244	2	Q8K1L4	Q8K1L4 mus muscucu	340	58	14.1	293	2	Q88DH2	Q88DH2 pseudomonas
268	59	14.4	260	2	Q63593	Q63593 florometra	341	58	14.1	314	2	Q8VOK4	Q8VOK4 brucella ab
269	59	14.4	260	2	Q9ZHX3	Q9ZHX3 brucella me	342	58	14.1	314	2	Q8VUX0	Q8VUX0 brucella su
270	59	14.4	260	2	Q8G221	Q8G221 brucella su	343	58	14.1	315	2	Q8YDG7	Q8YDG7 campylobact
271	59	14.4	263	2	Q8U0R0	Q8U0R0 pyrococcus	344	58	14.1	334	2	Q9PHS9	Q9PHS9 pseudomonas
272	59	14.4	265	2	Q8YFV2	Q8YFV2 brucella me	345	58	14.1	335	2	Q88PJ8	Q88PJ8 pseudomonas
273	59	14.4	268	2	Q8GST6	Q8GST6 arabidopsis	346	58	14.1	341	2	Q7N4Z0	Q7N4Z0 photorhabdu
274	59	14.4	269	2	Q7MEQ4	Q7MEQ4 vibrio vuln	347	58	14.1	346	2	Q6ECB3	Q6ECB3 gerygone ch
275	59	14.4	299	2	Q47578	Q47578 onchocerca	348	58	14.1	353	1	IL8E_MACMU	Q28519 macaca mula
276	59	14.4	301	2	Q8H3H8	Q8H3H8 oryza sativ	349	58	14.1	359	1	IL8B_RAT	F35407 rattus norv
277	59	14.4	328	1	P2Y6_HUMAN	Q15077 homo sapien	350	58	14.1	370	2	Q9X8K5	Q9X8K5 streptomyce
278	59	14.4	359	1	IL8B_MOUSE	P35343 mus muscucu	351	58	14.1	383	1	FLHB_YEREN	Q56886 yersinia en
279	59	14.4	386	2	Q8ZFC4	Q8ZFC4 yersinia pe	352	58	14.1	414	2	Q6CA15	Q6CA15 yarrowia li
280	59	14.4	403	2	Q20067	Q20067 caenorhabdi	353	58	14.1	417	2	Q9V6Q3	Q9V6Q3 drosophila
281	59	14.4	471	2	P72122	P72122 pseudomonas	354	58	14.1	460	1	Y1C1_ECOLI	Q3V644 drosophila
282	59	14.4	483	2	Q6BW26	Q6BW26 debaryomyce	355	58	14.1	476	2	Q8XQE9	Q8XQE9 ralstonia s
283	59	14.4	489	2	Q6YXZ6	Q6YXZ6 oryza sativ	356	58	14.1	479	2	Q6CPY8	Q6CPY8 kluyveromye
284	59	14.4	564	2	Q7R692	Q7R692 giardia lam	357	58	14.1	479	2	Q93SE8	Q93SE8 escherichia
285	59	14.4	624	2	Q7XMU9	Q7XMU9 oryza sativ	358	58	14.1	479	2	Q8FC70	Q8FC70 escherichia
286	59	14.4	629	2	Q86H95	Q86H95 dictyosteli	359	58	14.1	479	2	Q8XCA5	Q8XCA5 escherichia
287	59	14.4	680	2	Q6BSW5	Q6BSW5 debaryomyce	360	58	14.1	551	1	FZD2_XENLA	Q9PNU6 xenopus lae
288	59	14.4	683	2	Q84L74	Q84L74 arabidopsis	361	58	14.1	553	2	Q66KA3	Q66KA3 xenopus tro
289	59	14.4	763	2	Q8RW70	Q8RW70 arabidopsis	362	58	14.1	558	2	Q6WJ01	Q6WJ01 gallus gall
290	59	14.4	780	2	Q8XEA2	Q8XEA2 escherichia	363	58	14.1	565	1	FZD2_HUMAN	Q14332 homo sapien
291	59	14.4	795	2	Q64552	Q64552 arabidopsis	364	58	14.1	523	2	Q9VLY4	Q9VLY4 drosophila
292	59	14.4	815	2	Q44385	Q44385 caenorhabdi	365	58	14.1	523	2	Q90YL7	Q90YL7 brachydanio
293	59	14.4	1028	2	Q67J93	Q67J93 synechocyst	366	58	14.1	550	2	FZD2_MOUSE	Q9PNU6 xenopus lae
294	59	14.4	1089	2	Q7JK70	Q7JK70 caenorhabdi	367	58	14.1	551	1	FZD2_MOUSE	Q9PNU6 xenopus lae
295	59	14.4	1139	2	Q9U280	Q9U280 caenorhabdi	368	58	14.1	553	2	Q9VLY4	Q9VLY4 drosophila
296	59	14.4	1591	2	Q7QRS0	Q7QRS0 giardia lam	369	58	14.1	553	2	Q90YL7	Q90YL7 brachydanio
297	58.5	14.3	147	2	Q8HNS0	Q8HNS0 schistosoma	370	58	14.1	551	1	FZD2_XENLA	Q9PNU6 xenopus lae
298	58.5	14.3	237	2	Q82L92	Q82L92 streptomyce	371	58	14.1	551	1	FZD2_XENLA	Q9PNU6 xenopus lae
299	58.5	14.3	250	2	Q72115	Q72115 listeria mo	372	58	14.1	553	2	Q66KA3	Q66KA3 xenopus tro
300	58.5	14.3	261	2	Q87P44	Q87P44 vibrio para	373	58	14.1	558	2	Q6WJ01	Q6WJ01 gallus gall
301	58.5	14.3	282	2	Q9Y682	Q9Y682 homo sapien	374	58	14.1	558	2	FZD2_HUMAN	Q14332 homo sapien
302	58.5	14.3	311	2	Q8R2A3	Q8R2A3 mus muscucu	375	58	14.1	565	1	FZD2_MOUSE	Q9J1P6 mus muscucu
303	58.5	14.3	333	2	Q757U1	Q757U1 ashbya goss	376	58	14.1	570	1	FZD2_MOUSE	Q832K0 enterococcu
304	58.5	14.3	356	2	Q6XG66	Q6XG66 homo sapien	377	58	14.1	575	2	Q9PWK6	Q9PWK6 brachydanio
305	58.5	14.3	358	1	FLHB_HELPY	P56416 helicobacte	378	58	14.1	576	2	Q9PWN8	Q9PWN8 brachydanio
306	58.5	14.3	365	2	Q7MJ81	Q7MJ81 vibrio vuln	379	58	14.1	576	2	Q9YI49	Q9YI49 brachydanio
307	58.5	14.3	387	2	Q20012	Q20012 caenorhabdi	380	58	14.1	577	1	FZD5_MOUSE	Q9EQ40 mus muscucu
308	58.5	14.3	428	2	Q6C482	Q6C482 yarrowia li	381	58	14.1	577	1	FZD5_MOUSE	Q9EQ40 mus muscucu
309	58.5	14.3	433	2	Q6ULN6	Q6ULN6 biophalari	382	58	14.1	585	2	Q8CHL0	Q8CHL0 rattus norv
310	58.5	14.3	476	2	Q8B635	Q8B635 bos taurus	383	58	14.1	600	2	Q617Z0	Q617Z0 sceloporos
311	58.5	14.3	499	1	CIK2_HUMAN	P16389 homo sapien	384	58	14.1	611	2	FZD1_RAT	Q84633 rattus norv
312	58.5	14.3	518	2	Q6K977	Q6K977 legionella	385	58	14.1	611	2	FZD1_MOUSE	Q84633 rattus norv
313	58.5	14.3	538	2	Q6K977	Q6K977 oryza sativ	386	58	14.1	641	2	FZD1_MOUSE	Q84633 rattus norv
314	58.5	14.3	718	2	Q9XXF4	Q9XXF4 caenorhabdi	387	58	14.1	642	1	FZD1_MOUSE	Q84633 rattus norv
315	58.5	14.3	843	2	Q923J8	Q923J8 mus muscucu	388	58	14.1	642	1	FZD1_MOUSE	Q84633 rattus norv
316	58.5	14.3	843	2	Q92514	Q92514 mus muscucu	389	58	14.1	642	1	FZD1_MOUSE	Q84633 rattus norv
317	58.5	14.3	1170	2	Q9PNZ5	Q9PNZ5 campylobact	390	58	14.1	642	1	FZD1_MOUSE	Q84633 rattus norv
318	58	14.1	100	2	Q8QG37	Q8QG37 gallus gall	391	58	14.1	648	1	FZD1_HUMAN	Q84633 rattus norv
319	58	14.1	115	2	Q8A1T5	Q8A1T5 bacteroides	392	58	14.1	681	2	Q68D41	Q68D41 homo sapien
320	58	14.1	123	2	Q6A270	Q6A270 haemophilus	393	58	14.1	681	2	Q92CV4	Q92CV4 listeria in
321	58	14.1	126	2	Q62GJ1	Q62GJ1 burkholderi	394	58	14.1	696	2	Q8U6M2	Q8U6M2 agrobacteri
322	58	14.1	144	2	Q89CT2	Q89CT2 bradyrhizob	395	57.5	14.0	743	2	Q8U6M2	Q8U6M2 agrobacteri
323	58	14.1	169	2	Q9PIM9	Q9PIM9 campylobact	396	57.5	14.0	747	2	Q7CVV3	Q7CVV3 agrobacteri

397	57.5	14.0	150	2	Q7S4F1	Q7S4F1	neurospora	470	57	13.9	359	2	Q887B9	Q887B9	pseudomonas
398	57.5	14.0	157	2	Q9VJR2	Q9VJR2	drosofila	471	57	13.9	361	2	Q88S22	Q88S22	lactobacilli
399	57.5	14.0	189	2	Q7YWX1	Q7YWX1	caenorhabdi	472	57	13.9	367	2	Q927F5	Q927F5	listeria in
400	57.5	14.0	230	2	Q6Z1V2	Q6Z1V2	oryza sativ	473	57	13.9	382	2	Q66VY6	Q66VY6	leishmania
401	57.5	14.0	231	2	Q9V4G4	Q9V4G4	drosofila	474	57	13.9	404	2	Q8EJ63	Q8EJ63	shewanella
402	57.5	14.0	250	2	Q8Y8C8	Q8Y8C8	listeria mo	475	57	13.9	415	2	Q8BGZ8	Q8BGZ8	m mus muscu
403	57.5	14.0	222	2	Q7RPF8	Q7RPF8	plasmodium	476	57	13.9	476	2	Q8PU48	Q8PU48	methanosarc
404	57.5	14.0	254	2	Q69LF7	Q69LF7	oryza sativ	477	57	13.9	515	2	Q6TY91	Q6TY91	xiphinoma a
405	57.5	14.0	295	2	Q6CZ32	Q6CZ32	erwinia car	478	57	13.9	548	2	Q7RZG7	Q7RZG7	neurospora
406	57.5	14.0	328	1	LGT BORBU	LGT BORBU	borrelia bu	479	57	13.9	548	2	Q8AVJ9	Q8AVJ9	xenopus lae
407	57.5	14.0	328	1	Q66IQ7	Q66IQ7	borrelia ga	480	57	13.9	581	1	FZDB_XENLA	FZDB_XENLA	xenopus lae
408	57.5	14.0	333	2	Q9WNA4	Q9WNA4	helobdella	481	57	13.9	583	1	HASS_XENLA	HASS_XENLA	xenopus lae
409	57.5	14.0	336	2	Q44697	Q44697	caenorhabdi	482	57	13.9	583	2	Q6AZI0	Q6AZI0	xenopus lae
410	57.5	14.0	333	2	Q93247	Q93247	cyprinus ca	483	57	13.9	598	2	Q8AQU2	Q8AQU2	oryza sativ
411	57.5	14.0	353	2	Q9PTF7	Q9PTF7	brachydanio	484	57	13.9	604	2	Q9FV73	Q9FV73	perilla fru
412	57.5	14.0	372	1	CYB TRYBO	CYB TRYBO	trypanoplas	485	57	13.9	604	2	Q9FV75	Q9FV75	perilla fru
413	57.5	14.0	387	2	Q49632	Q49632	arabidopsis	486	57	13.9	604	2	Q9M5A4	Q9M5A4	perilla cit
414	57.5	14.0	408	2	Q73TQ1	Q73TQ1	mycobacteri	487	57	13.9	654	2	Q8EUQ4	Q8EUQ4	mycoplasma
415	57.5	14.0	410	2	Q7MR99	Q7MR99	wolinella s	488	57	13.9	674	2	Q9HT30	Q9HT30	pseudomonas
416	57.5	14.0	417	2	Q82SM6	Q82SM6	streptomyc	489	57	13.9	710	2	Q6S3B8	Q6S3B8	oryza sativ
417	57.5	14.0	419	2	Q7NQW0	Q7NQW0	chromobacte	490	57	13.9	712	2	Q66CE7	Q66CE7	yersinia ps
418	57.5	14.0	435	2	Q64VY8	Q64VY8	bacteroides	491	57	13.9	712	2	Q8ZG74	Q8ZG74	yersinia pe
419	57.5	14.0	437	2	Q94AL2	Q94AL2	arabidopsis	492	57	13.9	745	1	PERM_HUMAN	PERM_HUMAN	homo sapien
420	57.5	14.0	445	2	Q16548	Q16548	caenorhabdi	493	57	13.9	754	1	YCAI_ECOLI	YCAI_ECOLI	eschericchia
421	57.5	14.0	479	2	Q651L0	Q651L0	oryza sativ	494	57	13.9	756	2	Q8S7X4	Q8S7X4	oryza sativ
422	57.5	14.0	481	2	Q72V77	Q72V77	leptospiro	495	57	13.9	756	2	Q7XHA3	Q7XHA3	oryza sativ
423	57.5	14.0	530	2	Q7ULI7	Q7ULI7	rhodopirell	496	57	13.9	756	2	Q6HM90	Q6HM90	bacillus th
424	57.5	14.0	533	1	MCP4_ECOLI	MCP4_ECOLI	eschericchia	497	57	13.9	923	2	Q9XIM1	Q9XIM1	arabidopsis
425	57.5	14.0	533	2	Q7UAB7	Q7UAB7	shigella fl	498	57	13.9	953	2	Q7PTC2	Q7PTC2	anopheles g
426	57.5	14.0	533	2	Q8XCF7	Q8XCF7	eschericchia	499	57	13.9	991	2	Q6R5N8	Q6R5N8	mus musculu
427	57.5	14.0	534	2	Q83KP5	Q83KP5	shigella fl	500	57	13.9	999	2	Q93JY2	Q93JY2	erwinia chr
428	57.5	14.0	538	2	Q69XM6	Q69XM6	oryza sativ	501	57	13.9	1028	2	Q8MKX5	Q8MKX5	drosofila
429	57.5	14.0	729	1	YFEA_ECOLI	YFEA_ECOLI	eschericchia	502	57	13.9	1043	2	Q9W1G6	Q9W1G6	drosofila
430	57.5	14.0	729	2	Q7ABU5	Q7ABU5	eschericchia	503	57	13.9	1059	2	Q9W1G5	Q9W1G5	drosofila
431	57.5	14.0	742	2	Q8XBN6	Q8XBN6	eschericchia	504	57	13.9	1074	2	Q8MLQ5	Q8MLQ5	drosofila
432	57.5	14.0	750	2	Q8N3U2	Q8N3U2	homo sapien	505	57	13.9	1431	2	Q9XVH6	Q9XVH6	cryptospori
433	57.5	14.0	822	1	NRP6_CAEEL	NRP6_CAEEL	caenorhabdi	506	57	13.9	1526	2	Q9VVK6	Q9VVK6	drosofila
434	57.5	14.0	851	2	Q7QRZ5	Q7QRZ5	giardia lam	507	57	13.9	1567	2	Q6S652	Q6S652	blueberry s
435	57.5	14.0	1002	1	S123_RAT	S123_RAT	rattus norv	508	57	13.9	3471	2	Q91PP5	Q91PP5	rice tungro
436	57.5	14.0	1015	2	Q8MRT3	Q8MRT3	drosofila	509	57	13.9	3473	2	Q83034	Q83034	leishmania
437	57.5	14.0	1057	2	Q9A5Q7	Q9A5Q7	caulobacter	510	56.5	13.8	89	2	Q7M3S6	Q7M3S6	branchiosto
438	57.5	14.0	1077	2	Q62C80	Q62C80	burkholderi	511	56.5	13.8	135	2	Q71BB4	Q71BB4	branchiosto
439	57.5	14.0	1077	2	Q631H4	Q631H4	burkholderi	512	56.5	13.8	156	2	Q880L4	Q880L4	pseudomonas
440	57.5	14.0	2379	2	Q6U9W8	Q6U9W8	porcine rep	513	56.5	13.8	170	2	Q9MR45	Q9MR45	echinococcu
441	57	13.9	96	1	NULM_MYXGL	NULM_MYXGL	myxine glut	514	56.5	13.8	171	2	Q62F52	Q62F52	burkholderi
442	57	13.9	120	2	Q6Q900	Q6Q900	uncultured	515	56.5	13.8	224	2	Q63XT8	Q63XT8	burkholderi
443	57	13.9	120	2	Q6SG60	Q6SG60	uncultured	516	56.5	13.8	224	2	Q6SN52	Q6SN52	callithrix
444	57	13.9	120	2	Q6UCX0	Q6UCX0	uncultured	517	56.5	13.8	229	2	Q53651	Q53651	mycobacteri
445	57	13.9	157	1	VE5_RHPV1	VE5_RHPV1	rhesus papi	518	56.5	13.8	229	2	Q7U2L0	Q7U2L0	mycobacteri
446	57	13.9	159	2	Q6QRH8	Q6QRH8	bos taurus	519	56.5	13.8	250	2	Q92D41	Q92D41	listeria in
447	57	13.9	170	2	Q6A9P8	Q6A9P8	propionibac	520	56.5	13.8	253	1	TNFA_SPAU	TNFA_SPAU	spartus aura
448	57	13.9	173	2	Q66PD3	Q66PD3	rhizobium m	521	56.5	13.8	257	2	Q8CUT4	Q8CUT4	oceanobacil
449	57	13.9	185	2	Q08786	Q08786	saccharomyc	522	56.5	13.8	260	2	Q7RDX0	Q7RDX0	plasmodium m
450	57	13.9	210	2	Q63546	Q63546	bodo saltan	523	56.5	13.8	260	2	Q92M69	Q92M69	rhizobium m
451	57	13.9	231	2	Q6YR58	Q6YR58	onion yello	524	56.5	13.8	308	2	Q7M5M9	Q7M5M9	simian aden
452	57	13.9	242	1	CRTW_ALCSP	CRTW_ALCSP	alcaligenes	525	56.5	13.8	310	2	Q89LK3	Q89LK3	bradyrhizob
453	57	13.9	261	2	Q9MIA3	Q9MIA3	typhlonecte	526	56.5	13.8	328	2	Q9PSY2	Q9PSY2	carassius a
454	57	13.9	264	2	Q8GON2	Q8GON2	bruceella su	527	56.5	13.8	339	2	Q00331	Q00331	salmonella
455	57	13.9	268	2	Q6YN12	Q6YN12	agrobacteri	528	56.5	13.8	339	2	Q7VCR6	Q7VCR6	prochloroco
456	57	13.9	300	2	Q93DS7	Q93DS7	streptococ	529	56.5	13.8	373	2	Q91G14	Q91G14	epiphyas po
457	57	13.9	300	2	Q8E0K2	Q8E0K2	streptococ	530	56.5	13.8	405	2	Q31600	Q31600	bacillus su
458	57	13.9	300	2	Q8E675	Q8E675	streptococ	531	56.5	13.8	437	2	Q26645	Q26645	methanobact
459	57	13.9	305	2	Q8Y5K2	Q8Y5K2	listeria mo	532	56.5	13.8	465	2	Q41793	Q41793	zea mays (m
460	57	13.9	305	2	Q929V9	Q929V9	listeria in	533	56.5	13.8	467	2	Q75C40	Q75C40	ashbya goss
461	57	13.9	305	2	Q71XV6	Q71XV6	listeria mo	534	56.5	13.8	475	2	Q8YM67	Q8YM67	anabaena sp
462	57	13.9	309	2	Q9RJXP	Q9RJXP	arabidopsis	535	56.5	13.8	494	2	Q9I830	Q9I830	oncorhynch
463	57	13.9	311	2	Q9F0G9	Q9F0G9	pseudomonas	536	56.5	13.8	506	2	Q80XM3	Q80XM3	mus musculu
464	57	13.9	311	2	Q8VET7	Q8VET7	mus musculu	537	56.5	13.8	514	2	Q9XAJ9	Q9XAJ9	streptomyc
465	57	13.9	311	2	Q7TRM2	Q7TRM2	mus musculu	538	56.5	13.8	515	2	Q6AB12	Q6AB12	propionibac
466	57	13.9	315	2	Q9WVD8	Q9WVD8	mus musculu	539	56.5	13.8	516	2	Q729L5	Q729L5	desulfovibr
467	57	13.9	316	2	Q9WVD7	Q9WVD7	mus musculu	540	56.5	13.8	519	2	Q9V546	Q9V546	drosofila
468	57	13.9	325	2	Q6D712	Q6D712	erwinia car	541	56.5	13.8	533	2	Q9UT92	Q9UT92	schizosacch
469	57	13.9	356	1	IL8B_CANFA	IL8B_CANFA	canis famil	542	56.5	13.8	541	1	GT10_HUMAN	GT10_HUMAN	homo sapien

543	56.5	13.8	546	2	Q9MA18	Q9ma18 arabidopsis	616	56	13.7	2013	2	Q865W3	Q865w3 canis fam1
544	56.5	13.8	564	2	Q8LMD3	Q8lmd3-oryza sativ	617	56	13.7	2015	2	Q812C9	Q812c9 homo sapien
545	56.5	13.8	596	2	Q66SK2	Q66sk2 bipes bipor	618	56	13.7	2015	2	Q86J69	Q86j69 homo sapien
546	56.5	13.8	607	2	Q7XLD1	Q7xld1 aythya amer	619	56	13.7	2016	2	Q86UR3	Q86ur3 homo sapien
547	56.5	13.8	647	2	Q7QD21	Q7qld1 anopheles g	620	56	13.7	2015	1	CINS_HUMAN	Q14524 homo sapien
548	56.5	13.8	648	2	Q64W70	Q64w70 bacteroides	621	56	13.7	2016	2	Q75RY0	Q75ry0 homo sapien
549	56.5	13.8	653	1	C1K4_HUMAN	Q64wt0 bacteroides	622	56	13.7	2019	1	CINS_RAT	P15389 rattus norv
550	56.5	13.8	654	1	C1K4_MOUSE	Q22459 homo sapien	623	56	13.7	2019	2	Q9JJV9	P15389 rattus norv
551	56.5	13.8	654	1	C1K4_MUSPF	Q61423 mus musculu	624	56	13.7	2022	2	Q8WMP8	Q8wmp8 mus musculu
552	56.5	13.8	654	1	C1K4_MOUSE	Q28527 mustela put	625	55.5	13.5	52	2	Q852F2	Q852f2 phascolopei
553	56.5	13.8	655	1	C1K4_RAT	Q8cbf8 mus musculu	626	55.5	13.5	99	2	Q6AIE9	Q6aie9 desulfotale
554	56.5	13.8	658	2	Q09946	P15385 rattus norv	627	55.5	13.5	100	2	Q92HI4	Q92hi4 rickettsia
555	56.5	13.8	802	2	Q7UW70	Q09946 caenorhabdi	628	55.5	13.5	134	2	Q8CBT0	Q8cbt0 mus musculu
556	56.5	13.8	938	2	Q7RNR9	Q9wt0 rhodopirell	629	55.5	13.5	152	2	Q8EWD2	Q8ewd2 mycoplasma
557	56.5	13.8	955	2	Q7V7J0	Q7rnr9 plasmodium	630	55.5	13.5	155	2	Q85HD3	Q85hd3 austrochilus
558	56.5	13.8	971	2	Q88KR0	Q7v7j0 prochloroco	631	55.5	13.5	186	2	Q7X2T8	Q7x2t8 uncultured
559	56.5	13.8	1051	2	Q9ALR2	Q88kr0 pseudomonas	632	55.5	13.5	191	2	Q82ZK2	Q82zk2 enterococcu
560	56.5	13.8	1202	1	YE01_SCHPO	Q9alr2 pseudomonas	633	55.5	13.5	193	2	Q73MB3	Q73mb3 treponema d
561	56.5	13.8	1247	2	Q8T6H5	O13798 schizosacch	634	55.5	13.5	198	1	FTSW_LACLC	P27174 lactococcus
562	56.5	13.8	1284	2	Q9Y8G2	Q8t6h5 dictyostell	635	55.5	13.5	203	2	P11788	P11788 crithidia f
563	56.5	13.8	1334	2	Q8ST87	Q9y8g2 emericella	636	55.5	13.5	210	1	COX2_TRYCR	P98023 trypanosoma
564	56	13.7	74	2	Q35990	Q8st87 dictyosteli	637	55.5	13.5	223	2	Q6SNH5	Q6snh5 colobus gue
565	56	13.7	98	2	Q6IE46	O6ie46 rattus norv	638	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
566	56	13.7	100	2	Q8ERU0	Q8eh46 rattus norv	639	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
567	56	13.7	122	2	Q8BNC5	Q8bnc5 mus musculu	640	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
568	56	13.7	161	2	Q65Z26	Q8bnc5 mus musculu	641	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
569	56	13.7	172	2	Q6BWE7	Q65z26 caenorhabdi	642	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
570	56	13.7	182	2	Q6GLU5	Q6bwe7 debaryomyce	643	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
571	56	13.7	193	2	Q7LZC6	O6glu5 xenopus lae	644	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
572	56	13.7	198	2	Q8DSR6	Q7lzc6 clarias mac	645	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
573	56	13.7	201	2	Q9P6K1	Q8dsr6 streptococc	646	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
574	56	13.7	242	2	Q7VR92	Q9p6k1 schizosacch	647	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
575	56	13.7	260	2	Q952F1	Q7vr92 candidatus	648	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
576	56	13.7	269	1	RBN_HAEIN	Q952f1 phascolopsi	649	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
577	56	13.7	300	2	Q8PLV3	P44608 haemophilus	650	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
578	56	13.7	300	2	Q9A0X1	Q8ply3 streptococc	651	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
579	56	13.7	300	2	Q7CFC7	Q9a0x1 streptococc	652	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
580	56	13.7	309	2	Q6ZMA1	Q6zma1 rattus norv	653	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
581	56	13.7	315	2	Q7RI45	Q7ri45 plasmodium	654	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
582	56	13.7	321	2	O18046	O18046 caenorhabdi	655	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
583	56	13.7	324	2	Q98526	Q98526 paramecium	656	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
584	56	13.7	346	2	Q6ECA9	Q6eca9 sericornis	657	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
585	56	13.7	347	2	Q9B6G1	Q9b6g1 thryonomys	658	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
586	56	13.7	351	2	O17520	O17520 caenorhabdi	659	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
587	56	13.7	355	2	Q8HZN5	Q8hzn5 macaca mula	660	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
588	56	13.7	360	2	Q6D010	Q6d010 erwania car	661	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
589	56	13.7	363	2	Q8FHX9	Q8fhx9 escherichia	662	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
590	56	13.7	380	2	Q9ZTX3	Q9zyj3 raja radiat	663	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
591	56	13.7	393	2	Q9TKX2	Q9ktx2 vibrio chol	664	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
592	56	13.7	417	2	Q8PN58	Q8pn58 xanthomonas	665	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
593	56	13.7	429	2	O25682	O25682 helicobacte	666	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
594	56	13.7	452	2	Q7QH57	Q7qhx7 anopheles g	667	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
595	56	13.7	454	2	Q87SK7	Q87sk7 coprinus ci	668	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
596	56	13.7	468	2	Q6N0G9	Q6n0g9 rhodopseudo	669	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
597	56	13.7	506	2	Q7QRD6	Q7qrd6 giardia lam	670	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
598	56	13.7	527	2	P73863	P73863 synochocyst	671	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
599	56	13.7	558	2	Q9KB83	Q9kb83 bacillus ha	672	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
600	56	13.7	603	2	Q953H1	Q953h1 vollemys kik	673	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
601	56	13.7	621	2	Q9XWG9	Q9xwg9 caenorhabdi	674	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
602	56	13.7	667	2	O35267	O35267 rattus norv	675	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
603	56	13.7	674	2	O61456	O61456 schistocerc	676	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
604	56	13.7	684	2	Q9UAQ8	Q9uac8 caenorhabdi	677	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
605	56	13.7	694	1	FR22_DROME	Q9vwx3 drosophila	678	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
606	56	13.7	804	2	O6LPK5	O6lpk5 photobacter	679	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
607	56	13.7	815	2	Q9P6R5	Q9p6r5 schizosacch	680	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
608	56	13.7	824	2	Q9P6R5	Q9p6r5 pasteurella	681	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
609	56	13.7	869	2	O63ER5	O63er5 bacillus ce	682	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
610	56	13.7	869	2	O81U13	O81u13 bacillus an	683	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
611	56	13.7	1300	2	O6ZK22	O6zr22 homo sapien	684	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
612	56	13.7	1352	2	O6LUC6	O6luc6 photobacter	685	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
613	56	13.7	1682	1	CIN7_HUMAN	Q01118 homo sapien	686	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
614	56	13.7	1962	2	Q75RX9	Q75rx9 homo sapien	687	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara
615	56	13.7	1966	2	Q925G6	Q925g6 rattus norv	688	55.5	13.5	224	2	Q6SNZ6	Q6snz6 aotus azara

689	55.5	13.5	1002	1	S123 MOUSE	P59158 mus musculus	762	55	13.4	485	2	Q64290	Q64290 bacteroides
690	55.5	13.5	1063	1	CZCA_ALCEU	P13511 alcaligenes	763	55	13.4	496	2	Q68X09	Q68X09 rickettsia
691	55.5	13.5	1063	1	CZCA_ALCSC	P94177 alcaligenes	764	55	13.4	500	2	Q989D1	Q989D1 rhizobium
692	55.5	13.5	1267	2	Q88IA8	Q88IA8 pseudomonas	765	55	13.4	503	1	ALGE_CABEL	Q99226 caenorhabdi
693	55.5	13.5	1275	2	Q668S7	Q668S7 yersinia ps	766	55	13.4	513	2	Q638Z8	Q638Z8 bacillus ce
694	55.5	13.5	1275	2	Q82D68	Q82D68 yersinia pe	767	55	13.4	513	2	Q6HGK6	Q6HGK6 bacillus th
695	55.5	13.5	1380	2	Q84T60	Q84T60 oryza sativ	768	55	13.4	534	2	Q9N571	Q9N571 caenorhabdi
696	55.5	13.5	1403	2	Q751Q7	Q751Q7 oryza sativ	769	55	13.4	567	1	FZD7_CHICK	Q57329 gallus gall
697	55.5	13.5	1605	2	Q6CUF0	Q6CUF0 kluyveromyc	770	55	13.4	576	2	Q84LJ2	Q84LJ2 malus domes
698	55.5	13.5	1618	2	Q8MMW7	Q8MMW7 drosophila	771	55	13.4	581	2	Q84LJ2	Q84LJ2 malus domes
699	55.5	13.5	2327	2	Q9W0Y8	Q9W0Y8 drosophila	772	55	13.4	592	1	FZD3_DROME	Q77328 gallus gall
700	55.5	13.5	3063	2	Q8QXN1	Q8QXN1 sugarcane m	773	55	13.4	600	2	Q6GSU8	Q6GSU8 amphisbaena
701	55	13.4	63	2	Q832S1	Q832S1 enterococcu	774	55	13.4	623	2	Q6CDZ1	Q6CDZ1 yarrowia li
702	55	13.4	71	1	ER11_ASHGO	Q75D30 ashbya goss	775	55	13.4	706	2	Q45283	Q45283 caenorhabdi
703	55	13.4	98	2	Q9XLI0	Q9XLI0 falco pereg	776	55	13.4	761	2	Q6UD08	Q6UD08 uncultured
704	55	13.4	111	2	Q88AW1	Q88AW1 pseudomonas	777	55	13.4	808	2	Q62KR6	Q62KR6 burkholderi
705	55	13.4	117	2	P71212	P71212 escherichia	778	55	13.4	809	2	Q63UK2	Q63UK2 burkholderi
706	55	13.4	128	1	COXE_CABEL	Q20779 caenorhabdi	779	55	13.4	813	2	Q86HP1	Q86HP1 dictyosteli
707	55	13.4	130	2	Q87T25	Q87T25 pseudomonas	780	55	13.4	814	1	GUNE_CLOTM	P10477 clostridium
708	55	13.4	145	2	Q7YCW1	Q7YCW1 arion flag	781	55	13.4	856	2	Q73NF9	Q73NF9 treponema d
709	55	13.4	157	2	Q6HWM2	Q6HWM2 bacillus an	782	55	13.4	883	2	Q9VZY7	Q9VZY7 drosophila
710	55	13.4	161	2	Q8Y196	Q8Y196 raietonia s	783	55	13.4	911	2	Q73C88	Q73C88 bacillus ce
711	55	13.4	167	2	Q9MDD4	Q9MDD4 gallaria r	784	55	13.4	944	2	Q6N7N7	Q6N7N7 rhodopseudo
712	55	13.4	176	2	Q97XE0	Q97XE0 sulfolobus	785	55	13.4	1013	1	PRML_DROME	Q9V0B3 pyrococcus
713	55	13.4	189	2	Q6TUR0	Q6TUR0 yaba monkey	786	55	13.4	1013	1	PRML_DROME	P82295 drosophila
714	55	13.4	221	2	Q6SNF1	Q6SNF1 gorilla gor	787	55	13.4	1017	1	AL12_CHICK	P24797 gallus gall
715	55	13.4	229	2	Q9JRM7	Q9JRM7 actinobacil	788	55	13.4	1030	2	Q788D2	Q788D2 neurospora
716	55	13.4	241	2	Q8XMD6	Q8XMD6 clostridium	789	55	13.4	1091	2	Q6CKH9	Q6CKH9 kluyveromyc
717	55	13.4	242	1	CRTW_AGRAU	P54972 agrobacteri	790	55	13.4	1139	2	Q8ZC91	Q8ZC91 yersinia pe
718	55	13.4	249	2	Q8D479	Q8D479 vibrio vuln	791	55	13.4	1156	2	Q74WP6	Q74WP6 yersinia pe
719	55	13.4	260	2	Q93PP3	Q93PP3 campylobact	792	55	13.4	1445	2	Q75LT9	Q75LT9 oryza sativ
720	55	13.4	261	2	Q94SS9	Q94SS9 danaceticht	793	55	13.4	1554	2	Q80SX9	Q80SX9 mus musculu
721	55	13.4	263	2	Q64ZA5	Q64ZA5 bacteroides	794	55	13.4	1709	2	Q7RH43	Q7RH43 giardia lam
722	55	13.4	292	1	E434_ADE09	P89083 human adeno	795	55	13.4	2134	2	Q6WQ42	Q6WQ42 avian encep
723	55	13.4	294	2	Q8RNV6	Q8RNV6 brevivacill	796	55	13.4	2134	2	Q6WQ42	Q6WQ42 avian encep
724	55	13.4	301	2	Q7TY09	Q7TY09 mycobacteri	797	54.5	13.3	66	2	Q887R7	Q887R7 pseudomonas
725	55	13.4	301	2	Q8DUY3	Q8DUY3 streptococc	798	54.5	13.3	96	2	Q75L86	Q75L86 oryza sativ
726	55	13.4	309	2	Q6MPX0	Q6MPX0 rattus norv	799	54.5	13.3	136	2	Q7U6F0	Q7U6F0 synchococc
727	55	13.4	320	2	Q94346	Q94346 bacillus st	800	54.5	13.3	155	2	Q85CQ7	Q85CQ7 austrochlus
728	55	13.4	321	2	Q54386	Q54386 bruceella ab	801	54.5	13.3	155	2	Q85CQ9	Q85CQ9 austrochlus
729	55	13.4	321	2	Q8YH82	Q8YH82 bruceella me	802	54.5	13.3	162	2	Q8KMC4	Q8KMC4 methylocyst
730	55	13.4	321	2	Q8GOM5	Q8GOM5 bruceella su	803	54.5	13.3	165	2	Q934M2	Q934M2 uncultured
731	55	13.4	340	2	Q8YSR7	Q8YSR7 anabaena sp	804	54.5	13.3	165	2	Q934N4	Q934N4 uncultured
732	55	13.4	346	2	Q6ECB2	Q6ECB2 gerygone ch	805	54.5	13.3	169	1	VG12_SHV21	P24915 salmeline
733	55	13.4	347	1	CE2R_MOUSE	P47936 mus musculu	806	54.5	13.3	170	2	Q953M7	Q953M7 echinococcu
734	55	13.4	347	2	Q8M161	Q8M161 arctocephal	807	54.5	13.3	174	2	Q268S7	Q268S7 trypanosoma
735	55	13.4	347	2	Q678W1	Q678W1 arctocephal	808	54.5	13.3	174	2	Q98PD3	Q98PD3 rhizobium l
736	55	13.4	353	1	IL8B_GORGO	Q28422 gorilla gor	809	54.5	13.3	185	2	Q7MP11	Q7MP11 vibrio vuln
737	55	13.4	353	1	IL8B_PANTR	Q28807 pan troglod	810	54.5	13.3	193	2	Q89PF3	Q89PF3 bradyrhizob
738	55	13.4	355	1	IL8A_RABIT	P21109 oryctolagus	811	54.5	13.3	204	2	Q94QB4	Q94QB4 opisthotent
739	55	13.4	355	2	Q8HZN7	Q8HZN7 gorilla gor	812	54.5	13.3	217	2	Q6SWR7	Q6SWR7 human cytom
740	55	13.4	355	2	Q8HZN8	Q8HZN8 pan troglod	813	54.5	13.3	224	2	Q6SWR7	Q6SWR7 lagotrix l
741	55	13.4	359	2	Q85098	Q85098 pseudomonas	814	54.5	13.3	224	2	Q6SNB0	Q6SNB0 eulemur mon
742	55	13.4	359	2	Q6QOC6	Q6QOC6 pseudomonas	815	54.5	13.3	224	2	Q6SNE6	Q6SNE6 gorilla gor
743	55	13.4	360	1	IL8B_HUMAN	P25025 homo sapien	816	54.5	13.3	224	2	Q6SNK3	Q6SNK3 pan troglod
744	55	13.4	375	2	Q9V2E0	Q9V2E0 pyrococcus	817	54.5	13.3	226	2	Q6WYZ0	Q6WYZ0 hepatitis b
745	55	13.4	383	2	Q81EN5	Q81EN5 bacillus ce	818	54.5	13.3	229	2	Q8KRY3	Q8KRY3 actinobacil
746	55	13.4	383	2	Q6HGJ3	Q6HGJ3 bacillus th	819	54.5	13.3	234	2	Q97LF0	Q97LF0 clostridium
747	55	13.4	395	1	SOTB_ERWCH	Q983J9 erwania chr	820	54.5	13.3	244	2	Q9LWC5	Q9LWC5 oryza sativ
748	55	13.4	411	2	Q6WJ00	Q6WJ00 gallus gall	821	54.5	13.3	245	1	T4S6_HUMAN	Q43657 homo sapien
749	55	13.4	437	2	Q8R8S1	Q8R8S1 thermoaer	822	54.5	13.3	274	2	Q75DJ2	Q75DJ2 ashbya goss
750	55	13.4	439	1	BRNO_ECOLI	P37011 escherichia	823	54.5	13.3	277	2	Q9TUK6	Q9TUK6 oryctolagus
751	55	13.4	439	2	Q7UDK1	Q7UDK1 shigella fl	824	54.5	13.3	284	2	Q6DOP1	Q6DOP1 yersinia car
752	55	13.4	439	2	Q83SH0	Q83SH0 shigella fl	825	54.5	13.3	284	2	Q6DOP1	Q6DOP1 yersinia car
753	55	13.4	439	2	Q8FKC8	Q8FKC8 escherichia	826	54.5	13.3	287	1	OXAL_LISIN	Q926G5 listeria in
754	55	13.4	440	2	Q6NG43	Q6NG43 corynebacte	827	54.5	13.3	287	1	OXAL_LISIN	Q9Y312 listeria mo
755	55	13.4	449	2	Q31658	Q31658 bacillus su	828	54.5	13.3	287	2	Q71VQ8	Q71VQ8 listeria mo
756	55	13.4	459	2	Q7P7A3	Q7P7A3 fusbobacteri	829	54.5	13.3	290	2	Q6MFW9	Q6MFW9 rattus norv
757	55	13.4	459	2	Q8XSV8	Q8XSV8 escherichia	830	54.5	13.3	297	2	Q64SW7	Q64SW7 bacteroides
758	55	13.4	459	2	Q83P84	Q83P84 shigella fl	831	54.5	13.3	300	2	P91076	P91076 caenorhabdi
759	55	13.4	467	2	Q8LBP1	Q8LBP1 arabidopsis	832	54.5	13.3	300	2	Q66GA9	Q66GA9 yersinia ps
760	55	13.4	480	2	Q6KIC9	Q6KIC9 mycoplasma	833	54.5	13.3	302	2	Q8ZJL7	Q8ZJL7 yersinia ps
761	55	13.4	481	2	Q9X153	Q9X153 arabidopsis	834	54.5	13.3	302	2	Q9MAQ8	Q9MAQ8 arabidopsis

835	54.5	13.3	314	1	OZAL_HUMAN	Q8gh55 homo sapien	908	54.5	13.3	602	1	NUSM_DTDMA	P41309 didelphis m
836	54.5	13.3	315	1	NULM_MOUSE	P03888 mus musculus	909	54.5	13.3	608	2	Q72H22	Q72H22 thermus t
837	54.5	13.3	318	2	Q61F10	Q61f10 homo sapien	910	54.5	13.3	612	2	Q8HLZ1	Q8hlz1 melanotaeni
838	54.5	13.3	318	2	Q8SE28	Q8se28 rattus norv	911	54.5	13.3	612	2	Q8HMF9	Q8hmf9 siremba imb
839	54.5	13.3	318	2	Q7JD06	Q7jd06 mus musculus	912	54.5	13.3	616	1	YGO2_YEAST	P30777 saccharomyc
840	54.5	13.3	318	2	Q8H1D1	Q8h1d1 rattus norv	913	54.5	13.3	660	1	CIK4_BOVIN	Q85037 bos taurus
841	54.5	13.3	318	2	Q9G0S6	Q9g0s6 mus musculus	914	54.5	13.3	661	2	Q9GLF1	Q9glf1 bos taurus
842	54.5	13.3	318	2	Q93550	Q93550 carassius a	915	54.5	13.3	662	2	Q9YGX8	Q9ygx8 gallus gall
843	54.5	13.3	331	2	Q67ES4	Q67es4 rattus norv	916	54.5	13.3	672	2	Q6G0V1	Q6g0v1 bartonella
844	54.5	13.3	346	2	Q6N8W0	Q6n8w0 rhodopsuendo	917	54.5	13.3	672	2	Q6G521	Q6g521 bartonella
845	54.5	13.3	348	2	Q99939	Q99939 cyprinella	918	54.5	13.3	686	2	Q84Z01	Q84z01 oryza sativ
846	54.5	13.3	348	2	Q99948	Q99948 notropis at	919	54.5	13.3	697	1	BYN_DROME	P55965 drosophila
847	54.5	13.3	350	1	CSAR_RABIT	Q9tuei oryctolagus	920	54.5	13.3	729	2	Q8ESC5	Q8esc5 oceanobacil
848	54.5	13.3	350	2	Q8F131	Q8f131 leptospira	921	54.5	13.3	799	2	Q8ESC5	Q8esc5 oceanobacil
849	54.5	13.3	362	2	Q83562	Q83562 treponema p	922	54.5	13.3	931	1	EMR1_MOUSE	Q61549 mus musculus
850	54.5	13.3	363	2	Q9KA51	Q9ka51 bacillus ha	923	54.5	13.3	940	2	Q7XQ41	Q7xq41 oryza sativ
851	54.5	13.3	371	2	Q8VZN9	Q8vzn9 arabidopsis	924	54.5	13.3	1012	2	Q84ZK7	Q84zk7 oryza sativ
852	54.5	13.3	377	2	Q92198	P83292 drosophila	925	54.5	13.3	1022	2	Q6ZQ49	Q6zq49 mus musculus
853	54.5	13.3	377	2	Q92198	Q92198 lactobacill	926	54.5	13.3	1274	2	Q9E168	Q9e168 grass carp
854	54.5	13.3	378	2	Q22722	Q22722 caenorhabdi	927	54.5	13.3	1274	2	Q9E168	Q9e168 grass carp
855	54.5	13.3	383	2	Q83CN5	Q83cn5 coxiella bu	928	54.5	13.3	1435	2	Q9DSQ0	P97536 rattus norv
856	54.5	13.3	387	2	Q630M9	Q630m9 bacillus ce	929	54.5	13.3	2820	1	NF1_RAT	Q97536 rattus norv
857	54.5	13.3	387	2	Q72X77	Q72x77 bacillus ce	930	54.5	13.3	2839	1	NF1_MOUSE	P21359 homo sapien
858	54.5	13.3	387	2	Q81JS9	Q81js9 bacillus an	931	54.5	13.3	2841	1	NF1_MOUSE	Q04690 mus musculus
859	54.5	13.3	387	2	Q6HAR4	Q6har4 bacillus th	932	54.5	13.3	3063	2	Q8QXN2	Q8qxn2 sugarcane m
860	54.5	13.3	396	2	Q9LP12	Q9lp12 arabidopsis	933	54.5	13.3	3063	2	Q8QXN3	Q8qxn3 sugarcane m
861	54.5	13.3	397	2	Q81C11	Q81c11 bacillus ce	934	54.5	13.3	3064	2	Q8QXN4	Q8qxn4 sugarcane m
862	54.5	13.3	398	2	Q969F8	Q969f8 homo sapien	935	54	13.2	82	2	Q6LL67	Q6ll67 photobacter
863	54.5	13.3	398	2	Q96GQ0	Q96gq0 homo sapien	936	54	13.2	115	2	Q9G3S9	Q9g3s9 pteropus sc
864	54.5	13.3	403	1	CS5B_HUMAN	Q9nzh0 homo sapien	937	54	13.2	116	2	Q8SC58	Q8sc58 stx2 conver
865	54.5	13.3	413	2	Q24946	Q24946 helicobacte	938	54	13.2	116	2	Q7Y2N5	Q7y2n5 stx1 conver
866	54.5	13.3	414	2	Q9HJ05	Q9hjd5 thermoplas	939	54	13.2	116	2	Q7Y346	Q7y346 stx1 conver
867	54.5	13.3	416	2	Q7QC16	Q7qci6 anopheles g	940	54	13.2	133	2	Q6ZM75	Q6zm75 brachydanio
868	54.5	13.3	416	2	Q65FV1	Q65fv1 bacillus li	941	54	13.2	140	2	Q7PA91	Q7pa91 rickettsia
869	54.5	13.3	419	2	Q9YL87	Q9yl87 drosophila	942	54	13.2	152	2	Q9R1Q7	Q9rlq7 m proteolip
870	54.5	13.3	421	2	Q8YSL9	Q8ysl9 anabaena sp	943	54	13.2	165	2	Q8WGE5	Q8wge5 callichirus
871	54.5	13.3	428	2	Q7MTK8	Q7mtk8 porphyromon	944	54	13.2	167	1	YMW1_YEAST	Q04767 saccharomyc
872	54.5	13.3	435	1	FUCP_ECOLI	P11551 escherichia	945	54	13.2	175	2	Q90448	Q90448 brachydanio
873	54.5	13.3	438	2	Q8FEB8	Q8feb8 escherichia	946	54	13.2	188	2	Q8CAG5	Q8cag5 mus musculus
874	54.5	13.3	438	2	Q83QC8	Q83qc8 shigella fl	947	54	13.2	192	2	Q9BH50	Q9bh50 babesia bov
875	54.5	13.3	438	2	Q8XG87	Q8xg87 escherichia	948	54	13.2	193	2	Q99985	Q99985 porphyra pu
876	54.5	13.3	442	1	PUS3_YEAST	P31115 saccharomyc	949	54	13.2	206	2	Q751Q7	Q751q7 ashbya gos8
877	54.5	13.3	443	2	Q98C40	Q98c40 rhizobium l	950	54	13.2	220	2	Q6LQ66	Q6lq66 photobacter
878	54.5	13.3	450	2	Q67119	Q67119 influenza a	951	54	13.2	223	2	Q8ZW91	Q8zw91 pyrobaculum
879	54.5	13.3	461	1	Y061_MYCGE	P47307 mycoplasma	952	54	13.2	225	2	Q7YIH2	Q7yih2 pemphigus b
880	54.5	13.3	480	2	Q63FH4	Q63fh4 bacillus ce	953	54	13.2	242	2	Q9RLH7	Q9rlh7 paracoccus
881	54.5	13.3	483	1	CLK1_MOUSE	P22518 mus musculus	954	54	13.2	244	2	Q6XYV8	Q6xyv8 spiroplasma
882	54.5	13.3	483	2	Q9PW88	Q9pwm8 gallus gall	955	54	13.2	254	2	Q8MYB2	Q8myb2 ciona intes
883	54.5	13.3	483	2	Q7PQT4	Q7pqt4 anopheles g	956	54	13.2	257	2	Q7YX63	Q7yx63 caenorhabdi
884	54.5	13.3	488	2	Q61865	Q61865 caenorhabdi	957	54	13.2	259	1	COX3_LUMTE	Q34943 lumbricus t
885	54.5	13.3	490	2	Q65116	Q65116 oryza sativ	958	54	13.2	261	2	Q94TA0	Q94ta0 myctophum a
886	54.5	13.3	492	2	Q92ZQ1	Q92zd1 cyanidiosch.	959	54	13.2	261	2	Q64486	Q64486 plethodon p
887	54.5	13.3	493	2	O17395	O17395 caenorhabdi	960	54	13.2	264	2	Q8YUJ0	Q8yu10 anabaena sp
888	54.5	13.3	499	1	CIK3_MOUSE	P63141 mus musculus	961	54	13.2	265	2	Q63LT1	Q63lt1 burkholderi
889	54.5	13.3	499	1	CIK2_RAT	P63142 rattus norv	962	54	13.2	285	2	Q9K018	Q9k018 neisseria m
890	54.5	13.3	499	2	Q28293	Q28293 canis fami	963	54	13.2	277	2	Q82UI3	Q82ui3 nitrosomona
891	54.5	13.3	499	2	Q9MTX3	Q9mrx3 cryotolagus	964	54	13.2	283	2	Q6MEY2	Q6mey2 parachlamyd
892	54.5	13.3	499	2	Q8C9W4	Q8c9w4 mus musculus	965	54	13.2	295	2	Q65V68	Q65v68 manheimia
893	54.5	13.3	499	2	Q7TIA0	Q7tia0 gallus gall	966	54	13.2	304	2	Q6MKC6	Q6mkc6 bdellovibri
894	54.5	13.3	502	2	Q917D0	Q917d0 drosophila	967	54	13.2	308	2	Q7YVE9	Q7yve9 trypanosoma
895	54.5	13.3	510	2	Q87BQ9	Q87bq9 xyliella fas	968	54	13.2	310	2	Q8VG91	Q8vg91 mus musculus
896	54.5	13.3	510	2	Q9PAY3	Q9pay3 xyliella fas	969	54	13.2	315	1	PSTC_METJA	Q58430 methanococc
897	54.5	13.3	533	2	Q6KH10	Q6kh10 mycoplasma	970	54	13.2	325	2	O61969	O61969 caenorhabdi
898	54.5	13.3	548	2	Q84LG0	Q84lg0 nicotiana a	971	54	13.2	325	2	Q8Q0X6	Q8q0x6 pseudomonas
899	54.5	13.3	560	2	Q7K4Y9	Q7k4y9 drosophila	972	54	13.2	330	2	Q8Q0X6	Q8q0x6 pseudomonas
900	54.5	13.3	560	2	Q9VYV7	Q9vyv7 drosophila	973	54	13.2	337	2	Q97EU0	Q97eu0 clostridium
901	54.5	13.3	566	2	Q6FRJ2	Q6frj2 candida gla	974	54	13.2	338	2	Q9SZU0	Q9szu0 arabidopsis
902	54.5	13.3	589	2	Q6LM81	Q6lm81 photobacter	975	54	13.2	339	2	Q8G686	Q8g686 bifidobacte
903	54.5	13.3	593	2	Q14931	Q14931 homo sapien	976	54	13.2	346	2	Q6ECC1	Q6ecc1 timeliopsis
904	54.5	13.3	595	2	Q8WIN8	Q8win8 oryza sativ	977	54	13.2	346	2	Q6SCI3	Q6sci3 thryothorus
905	54.5	13.3	595	2	Q8W5S2	Q8w5s2 oryza sativ	978	54	13.2	347	2	Q9HXJ3	Q9hxj3 pseudomonas
906	54.5	13.3	596	2	Q6AUS3	Q6aus3 oryza sativ	979	54	13.2	348	2	P91860	P91860 caenorhabdi
907	54.5	13.3	598	2	Q66S89	Q66s89 geocalamus	980	54	13.2	358	1	IL8B_RABIT	P35344 oryctolagus

981	54	13.2	360	1	GP15 MACMU	O97663 macaca mulla	1054	54	13.2	779	2	Q7VEF1	Q7vef1 prochloroco
982	54	13.2	360	1	GP15 MACNE	P56412 macaca neme	1055	54	13.2	782	1	POT6 ARATH	Q84i4 arabadopsis
983	54	13.2	378	2	Q884W1	Q884w1 pseudomonas	1056	54	13.2	788	2	Q94KC6	Q94kc6 mesembryant
984	54	13.2	379	2	Q7NP09	Q7hpu9 chroomonas	1057	54	13.2	801	2	Q843B8	Q8y3b8 ralscomia s
985	54	13.2	385	2	Q9GKZ7	Q9gkz7 tenrec ecau	1058	54	13.2	845	2	Q72UY4	Q72uy4 leptospira
986	54	13.2	385	2	Q631D6	Q631d6 bacillus ce	1059	54	13.2	845	2	Q8EZY9	Q8esy9 leptospira
987	54	13.2	387	2	Q8YU77	Q8yu77 anabaena sp	1060	54	13.2	868	2	Q7X7Q3	Q7x7q3 oryza sativ
988	54	13.2	402	2	Q8CMF9	Q8cmf9 shewanella	1061	54	13.2	872	2	Q9NL45	Q9nl45 ciona intes
989	54	13.2	404	2	Q8CLZ2	Q8clz2 shewanella	1062	54	13.2	883	2	Q8A929	Q8a929 bacteroides
990	54	13.2	404	2	Q8E957	Q8e957 shewanella	1063	54	13.2	894	1	YN86 YEAST	P27514 saccharomyc
991	54	13.2	404	2	Q8EBL3	Q8ebl3 shewanella	1064	54	13.2	1018	2	Q9HKX3	Q9hxx3 thermoplas
992	54	13.2	404	2	Q8EHH7	Q8ehh7 shewanella	1065	54	13.2	1040	2	Q64TN7	Q64tn7 bacteroides
993	54	13.2	408	2	Q8DAU1	Q8dau1 vibrio vuln	1066	54	13.2	1046	2	Q72G02	Q72g02 desulfovibr
994	54	13.2	409	2	Q639H1	Q639h1 bacillus ce	1067	54	13.2	1053	2	Q8IAQ8	Q8iaq8 plasmodium
995	54	13.2	416	2	Q6AGK0	Q6agk0 leifsonia x	1068	54	13.2	1085	2	Q8FCG5	Q8fcg5 rattus norv
996	54	13.2	417	2	Q62EV7	Q62ev7 burkholderi	1069	54	13.2	1164	2	Q66EN6	Q66en6 yersinia ps
997	54	13.2	428	2	Q98M33	Q98m33 rhizobium l	1070	54	13.2	1164	2	Q8CKD9	Q8ckd9 yersinia pe
998	54	13.2	430	2	Q63YE0	Q63ye0 burkholderi	1071	54	13.2	1272	2	Q22731	Q22731 arabadopsis
999	54	13.2	435	2	Q6LUN8	Q6lun8 photobacter	1072	54	13.2	1814	1	TSC2 MOUSE	Q61037 mus musculu
1000	54	13.2	438	2	Q8K2A8	Q8ka28 mus musculu	1073	54	13.2	2065	2	Q9PT63	Q9pt63 xenopus lae
1001	54	13.2	447	2	Q755U5	Q755u5 ashbya goss	1074	54	13.2	2298	1	CU05 HUMAN	Q9y3r5 homo sapien
1002	54	13.2	459	2	Q8FB33	Q8fb33 escherichia	1075	53.5	13.0	112	2	Q8LDK7	Q8ldk7 arabadopsis
1003	54	13.2	463	2	Q86AR0	Q86ar0 dictyosteli	1076	53.5	13.0	132	2	Q6ZNG3	Q6zng3 homo sapien
1004	54	13.2	469	2	Q62BK7	Q62bk7 burkholderi	1077	53.5	13.0	149	2	Q8STV0	Q8stv0 enccephalito
1005	54	13.2	473	2	Q94GS8	Q94gs8 oryza sativ	1078	53.5	13.0	149	2	Q6W051	Q6w051 mus musculu
1006	54	13.2	478	2	Q6VSE7	Q6vse7 capsella ru	1079	53.5	13.0	162	2	Q8TNK2	Q8tnk2 methanosarc
1007	54	13.2	480	2	Q6NAJ2	Q6naj2 rhodospseudo	1080	53.5	13.0	165	2	Q954C1	Q954c1 uncultured
1008	54	13.2	482	2	Q8XIN7	Q8xin7 clostridium	1081	53.5	13.0	184	2	Q8SH72	Q8sh72 dasynelelea s
1009	54	13.2	483	2	Q6TWC9	Q6tmc9 coprinus ci	1082	53.5	13.0	184	2	P74727	P74727 synchocyst
1010	54	13.2	483	2	Q8NUZ4	Q8nuz4 staphylococ	1083	53.5	13.0	191	2	Q9DHK4	Q9dhk4 yaba-like d
1011	54	13.2	488	2	Q9ARJ0	Q9arj0 staphylococ	1084	53.5	13.0	195	2	Q8DUQ8	Q8duq8 streptococc
1012	54	13.2	488	2	Q7A3Q5	Q7a3q5 staphylococ	1085	53.5	13.0	219	2	Q8G4H2	Q8g4h2 bifidobacte
1013	54	13.2	488	2	Q6GEM9	Q6gem9 staphylococ	1086	53.5	13.0	226	2	Q6S9S8	Q6s9s8 hepatitis b
1014	54	13.2	499	1	LNT R1CCN	Q921c5 rickettsia	1087	53.5	13.0	226	2	Q6S9S9	Q6s9s9 hepatitis b
1015	54	13.2	500	2	Q7NAT3	Q7nat3 mycoplasma	1088	53.5	13.0	233	2	Q90305	Q90305 bredda virus
1016	54	13.2	504	2	Q9VPD9	Q9vpd9 drosophila	1089	53.5	13.0	263	2	Q8Z8X0	Q8z8x0 salmonella
1017	54	13.2	504	2	Q7PBL4	Q7pbl4 rickettsia	1090	53.5	13.0	264	2	Q7PXC7	Q7pxc7 anopheles g
1018	54	13.2	507	2	Q6EVS3	Q6evs3 yersinia ps	1091	53.5	13.0	265	2	P96065	P96065 salmonella
1019	54	13.2	507	2	Q9VC02	Q9vc02 drosophila	1092	53.5	13.0	273	2	Q6LS89	Q6ls89 photobacter
1020	54	13.2	511	2	Q8WF37	Q8wf37 venerupis (	1093	53.5	13.0	281	2	Q9VK02	Q9vk02 drosophila
1021	54	13.2	541	2	Q9VRM0	Q9vrm0 drosophila	1094	53.5	13.0	284	2	Q87EH8	Q87eh8 xylella fas
1022	54	13.2	542	2	Q813H5	Q8i3h5 plasmodium	1095	53.5	13.0	290	2	Q73E92	Q73e92 bacillus ce
1023	54	13.2	549	1	FZD7 XENLA	Q9pkh8 xenopus lae	1096	53.5	13.0	298	2	Q9KBJ0	Q9kbj0 bacillus ha
1024	54	13.2	554	2	Q6NV44	Q6nv44 brachydanio	1097	53.5	13.0	299	1	HTPX STRPN	Q97qd6 streptococc
1025	54	13.2	554	2	Q7SZK7	Q7szr7 brachydanio	1098	53.5	13.0	301	2	Q8UY66	Q8uy66 simian aden
1026	54	13.2	558	2	Q8YCG4	Q8ygc4 brucella me	1099	53.5	13.0	301	2	Q6QP87	Q6qp87 simian aden
1027	54	13.2	559	1	FZD1 XENLA	Q9i9m5 xenopus lae	1100	53.5	13.0	301	2	Q6QPF9	Q6qpf9 simian aden
1028	54	13.2	559	1	FZD5 XENLA	P58421 xenopus lae	1101	53.5	13.0	301	2	Q6FF49	Q6ff49 acinetobact
1029	54	13.2	559	2	Q90ZT3	Q90zt3 brachydanio	1102	53.5	13.0	305	2	Q6FF49	Q6ff49 acinetobact
1030	54	13.2	559	2	Q98S12	Q98s12 brachydanio	1103	53.5	13.0	309	2	Q6UAG7	Q6uag7 mus musculu
1031	54	13.2	563	2	Q7Y684	Q7y684 venerupis (	1104	53.5	13.0	310	2	Q8WHX9	Q8whx9 psilotum nu
1032	54	13.2	563	2	Q7YF46	Q7yf46 venerupis (	1105	53.5	13.0	310	2	Q8VFE1	Q8vfe1 mus musculu
1033	54	13.2	563	2	Q7YF49	Q7yf49 venerupis (	1106	53.5	13.0	313	2	Q9PSJ5	Q9psj5 ictalurus p
1034	54	13.2	566	1	HEMA IAGU2	P13103 influenza a	1107	53.5	13.0	315	2	Q87WK8	Q87wk8 pseudomonas
1035	54	13.2	567	2	Q6FTB1	Q6ftb1 candida gla	1108	53.5	13.0	319	2	Q82DA1	Q82da1 streptomyc
1036	54	13.2	570	1	FZD2 RAT	Q8464 rattus norv	1109	53.5	13.0	330	2	Q7TN51	Q7tn51 mus musculu
1037	54	13.2	572	1	FZD7 MOUSE	Q61090 mus musculu	1110	53.5	13.0	337	1	R1R2 TRYBB	Q15910 trypanosoma
1038	54	13.2	572	2	Q6PS51	Q6p551 mus musculu	1111	53.5	13.0	338	2	Q8CFN5	Q8cfn5 staphylococ
1039	54	13.2	573	2	Q871A0	Q871a0 neurospora	1112	53.5	13.0	343	2	P91219	P91219 caenorhabdi
1040	54	13.2	574	1	FZD7 HUMAN	Q75084 homo sapien	1113	53.5	13.0	346	2	Q6WR47	Q6wr47 treron sieb
1041	54	13.2	589	2	Q7R219	Q7r219 neurospora	1114	53.5	13.0	350	2	Q39980	Q39980 hyoscyamus
1042	54	13.2	582	2	Q7T5Q9	Q7t5q9 cryptophleb	1115	53.5	13.0	355	2	Q66F72	Q66f72 yersinia ps
1043	54	13.2	594	2	Q9F409	Q9f409 mycobacteri	1116	53.5	13.0	355	2	Q83ZY2	Q83zy2 yersinia ps
1044	54	13.2	598	2	Q8LX55	Q8lx55 mycocephalu	1117	53.5	13.0	355	2	Q8ZBB0	Q8zbb0 yersinia ps
1045	54	13.2	599	2	Q40322	Q40322 mentha spic	1118	53.5	13.0	356	1	RA13 MOUSE	Q8bhl4 mus musculu
1046	54	13.2	599	2	Q9SW76	Q9sw76 mentha long	1119	53.5	13.0	362	2	Q79TH3	Q79th3 halocynthia
1047	54	13.2	604	2	Q6AY92	Q6ay92 rattus norv	1120	53.5	13.0	362	2	Q7P9U4	Q7p9u4 rickettsia
1048	54	13.2	662	2	Q9PEB4	Q9peb4 xylella fas	1121	53.5	13.0	362	2	Q92GC4	Q92gc4 rickettsia
1049	54	13.2	690	2	Q9SJA2	Q9sja2 arabadopsis	1122	53.5	13.0	362	2	Q68VX9	Q68vx9 rickettsia
1050	54	13.2	694	2	Q7XWQ1	Q7xwq1 oryza sativ	1123	53.5	13.0	362	2	Q9ZCH3	Q9zch3 rickettsia
1051	54	13.2	741	2	Q8FVV4	Q8fvv4 brucella su	1124	53.5	13.0	369	2	Q8SU48	Q8sj48 pfiesteria
1052	54	13.2	750	2	Q810L8	Q810l8 mus musculu	1125	53.5	13.0	373	2	Q8M4X4	Q8mx4 pfiesteria
1053	54	13.2	775	2	Q6CTQ2	Q6ctq2 kluyveromyc	1126	53.5	13.0	374	2	Q6FG00	Q6fg00 acinetobact

1127	53.5	13.0	380	2	Q8M4L5	Q8m4l5 gymnocraniu	1200	53	12.9	228	2	Q98RJ6	Q98rj6 mycoplasma
1128	53.5	13.0	381	1	CYB_ISUPA	P34871 isurus pauc	1201	53	12.9	229	1	CEMA_ATRBE	Q8s8w5 atropa bell
1129	53.5	13.0	385	2	Q81WZ9	Q81wz9 bacillus an	1202	53	12.9	229	1	CEMA_TORAC	P12213 nicotiana t
1130	53.5	13.0	385	2	Q6HB69	Q6hb69 bacillus th	1203	53	12.9	231	1	COBS_PYRKO	O52454 pyrococcus
1131	53.5	13.0	385	2	Q6KK53	Q6kk53 bacillus an	1204	53	12.9	235	2	Q8TDV3	Q8tdv3 homo sapien
1132	53.5	13.0	389	2	Q81932	Q81932 herpesvirus	1205	53	12.9	236	2	Q6A9U4	O6a9u4 propionibac
1133	53.5	13.0	395	2	Q6IE78	Q6ie78 paralicthy	1206	53	12.9	242	2	Q74EF1	Q74ef1 geobacter s
1134	53.5	13.0	400	1	BM2_BACSU	P39843 bacillus su	1207	53	12.9	252	2	Q71U75	Q71u75 homo sapien
1135	53.5	13.0	410	2	Q8SQO4	Q8sqo4 encephalito	1208	53	12.9	252	2	Q8WIN7	Q8win7 oryza sativ
1136	53.5	13.0	417	2	Q81AN4	Q81an4 bacillus ce	1209	53	12.9	253	2	Q8ISN8	Q8isn8 chasmagnath
1137	53.5	13.0	419	2	Q8E200	Q8e200 streptococc	1210	53	12.9	255	2	Q8VH75	Q8vh75 brucella me
1138	53.5	13.0	424	2	Q64W69	Q64w69 bacteroides	1211	53	12.9	255	2	Q66SY9	Q66sy9 rhineura fl
1139	53.5	13.0	446	2	Q8E7F8	Q8e7f8 streptococc	1212	53	12.9	261	2	Q8SD01	Q8sdo1 platyrocce
1140	53.5	13.0	452	1	YCDT_ECOLI	P75908 escherichia	1213	53	12.9	261	2	Q8SD66	Q8sd66 dallia pect
1141	53.5	13.0	455	2	Q70EC6	Q70ec6 bufo melano	1214	53	12.9	262	2	Q8KZ64	Q8kz64 uncultured
1142	53.5	13.0	458	2	Q7Y8U9	Q7y8u9 andrias dav	1215	53	12.9	268	2	Q6YN06	Q6yn06 rhizobium e
1143	53.5	13.0	476	2	Q8Z5J2	Q8z5j2 salmonella	1216	53	12.9	268	2	Q6YN08	Q6yn08 rhizobium e
1144	53.5	13.0	478	2	Q8SW72	Q8sw72 encephalito	1217	53	12.9	268	2	Q6YN11	Q6yn11 agrobacteri
1145	53.5	13.0	500	2	Q9DY00	Q9dy00 avian leuko	1218	53	12.9	268	2	Q6YN14	Q6yn14 rhizobium e
1146	53.5	13.0	523	1	NU4M_PROWI	Q37617 prototheca	1219	53	12.9	271	2	Q9TAK6	Q9tak6 caferteria r
1147	53.5	13.0	529	2	Q8U2T6	Q8u2t6 pyrococcus	1220	53	12.9	288	2	Q9HUW4	Q9huw4 pseudomonas
1148	53.5	13.0	537	2	Q8W118	Q8w118 arabidopsis	1221	53	12.9	288	2	Q8HAY2	Q8hay2 pseudomonas
1149	53.5	13.0	537	2	Q8GWB7	Q8gbw7 arabidopsis	1222	53	12.9	292	2	Q8R229	Q8r229 oryza sativ
1150	53.5	13.0	546	2	Q8G6N6	Q8g6n6 bifidobacte	1223	53	12.9	297	2	Q6H663	Q6h663 oryza sativ
1151	53.5	13.0	549	2	Q9VPP9	Q9vpp9 drosophila	1224	53	12.9	297	2	Q6BD50	Q6bd50 yersinia ps
1152	53.5	13.0	571	2	Q9DLK2	Q9dlk2 avian leuko	1225	53	12.9	297	2	Q6ZGV6	Q6zgv6 yersinia pe
1153	53.5	13.0	571	2	Q9DLK2	Q9dlk2 avian leuko	1226	53	12.9	300	2	Q6CZ45	Q6cz45 erwinia car
1154	53.5	13.0	578	1	OXAA_PSEAE	Q9ht06 pseudomonas	1227	53	12.9	300	2	Q8UUP6	Q8uup6 tetracodon n
1155	53.5	13.0	580	2	Q85MD7	Q85md7 harpochytri	1228	53	12.9	301	2	Q7D6P5	Q7d6p5 mycobacteri
1156	53.5	13.0	602	2	Q70XH5	Q70xh5 caenolestes	1229	53	12.9	301	2	Q33234	Q33234 mycobacteri
1157	53.5	13.0	603	1	NU5M_HYLLA	P03919 hylobates l	1230	53	12.9	305	2	Q6BA71	Q6ba71 uncultured
1158	53.5	13.0	603	1	Q9GA20	Q9ga20 tupia glis	1231	53	12.9	305	2	Q7P5R9	Q7p5r9 fusobacteri
1159	53.5	13.0	608	2	Q76HR3	Q76hr3 leionathus	1232	53	12.9	312	2	Q7YZV7	Q7yzv7 caenorhabdi
1160	53.5	13.0	610	2	Q6CKZ6	Q6ckz6 kluyveromyc	1233	53	12.9	316	1	YBA8_SHEON	Q8e8f7 shewanella
1161	53.5	13.0	627	1	RN3_YEAST	P36070 saccharomyc	1234	53	12.9	328	1	P2Y6_MOUSE	Q9erk9 mus musculu
1162	53.5	13.0	628	2	Q6C657	Q6c657 yarrowia li	1235	53	12.9	330	2	Q66673	Q66673 equid herpe
1163	53.5	13.0	706	2	Q9JWZ2	Q9jwz2 neisseria m	1236	53	12.9	332	2	Q83A71	Q83a71 coxiella bu
1164	53.5	13.0	706	2	Q9K1K3	Q9k1k3 neisseria m	1237	53	12.9	335	2	Q87ZQ3	Q87zq3 pseudomonas
1165	53.5	13.0	720	2	Q87BN6	Q87bn6 xylella fas	1238	53	12.9	336	2	Q9FV74	Q9fv74 perilla fru
1166	53.5	13.0	734	2	Q7ULL8	Q7ull8 rhodopirell	1239	53	12.9	337	2	Q8UJL6	Q8ujl6 agrobacteri
1167	53.5	13.0	770	2	P74677	P74677 synchocyst	1240	53	12.9	338	2	Q9XV78	Q9xv78 caenorhabdi
1168	53.5	13.0	772	2	Q62CR6	Q62cr6 burkholderi	1241	53	12.9	346	2	Q6ECG5	Q6ecg5 certionyx
1169	53.5	13.0	926	2	Q9W2L4	Q9w2l4 drosophila	1242	53	12.9	346	2	Q6Y050	Q6y050 amatoxina far
1170	53.5	13.0	1021	1	S123_HUMAN	P55017 homo sapien	1243	53	12.9	346	2	Q644K3	Q644k3 batrachosep
1171	53.5	13.0	1028	2	O18886	O18886 oryctolagus	1244	53	12.9	347	2	O21636	O21636 darevskia c
1172	53.5	13.0	1053	2	Q88RT6	Q88rt6 pseudomonas	1245	53	12.9	348	2	O21636	O21636 limia versi
1173	53.5	13.0	1072	2	Q820K8	Q820k8 nitrosomona	1246	53	12.9	350	1	IL8A_GORGO	P55919 gorilla gor
1174	53.5	13.0	1083	1	EMBB_MYCLE	Q9cda9 mycobacteri	1247	53	12.9	350	1	IL8A_HUMAN	P25024 homo sapien
1175	53.5	13.0	1112	2	Q8CGT8	Q8cgt8 mus musculu	1248	53	12.9	350	1	IL8A_HUMAN	P55920 pan troglod
1176	53.5	13.0	1112	2	O15849	O15849 leishmania	1249	53	12.9	350	2	Q8N6T6	Q8n6t6 homo sapien
1177	53.5	13.0	3064	2	Q8B388	Q8b388 sugarcane m	1250	53	12.9	350	2	Q6IN95	Q6in95 homo sapien
1178	53	12.9	96	2	Q94ZD5	Q94zd5 eptaretus	1251	53	12.9	353	2	Q95P47	Q95p47 epiphyas po
1179	53	12.9	96	2	Q9B980	Q9b980 blastophaga	1252	53	12.9	353	2	Q9C9B6	Q9c9b6 arabidopsis
1180	53	12.9	117	2	Q8HD87	Q8hd87 panulirus j	1253	53	12.9	355	2	Q8HZN3	Q8hzn3 papio hamad
1181	53	12.9	117	2	Q9MNX9	Q9mnx9 pagurus lon	1254	53	12.9	359	2	Q83HX7	Q83hx7 tropheryma
1182	53	12.9	119	2	Q9UMS9	Q9ums9 sulfolobus	1255	53	12.9	360	1	CB2R_HUMAN	P34972 homo sapien
1183	53	12.9	126	2	Q7QV76	Q7qv76 giardia lam	1256	53	12.9	360	2	Q6NSY0	Q6nsy0 homo sapien
1184	53	12.9	141	2	Q6AWG3	Q6awg3 drosophila	1257	53	12.9	360	2	Q6NSY0	Q6nsy0 homo sapien
1185	53	12.9	147	2	Q8AA90	Q8aa90 bacteroides	1258	53	12.9	361	2	Q60150	O60150 echinosacch
1186	53	12.9	158	2	Q7PFM6	Q7pfm6 anopheles g	1259	53	12.9	364	2	Q9AFH7	Q9afh7 streptococc
1187	53	12.9	158	2	Q7R5K3	Q7r5k3 giardia lam	1260	53	12.9	364	2	Q8DZD6	Q8dzd6 streptococc
1188	53	12.9	170	2	Q8ZTG7	Q8ztg7 pyrobaculum	1261	53	12.9	367	2	Q95YAB	Q95yab caenorhabdi
1189	53	12.9	174	2	Q26856	Q26856 trypanosoma	1262	53	12.9	368	2	O69131	O69131 burkholderi
1190	53	12.9	174	2	Q27227	Q27227 trypanosoma	1263	53	12.9	368	2	O62HQ8	O62hq8 burkholderi
1191	53	12.9	175	2	Q7YZV6	Q7yzv6 caenorhabdi	1264	53	12.9	368	2	Q63RK1	Q63rk1 burkholderi
1192	53	12.9	188	2	Q96177	Q96177 eulimnogamm	1265	53	12.9	377	2	Q8E7B8	Q8e7b8 streptococc
1193	53	12.9	192	2	Q6NM06	Q6nm06 arabidopsis	1266	53	12.9	378	2	Q75V45	Q75v45 monochirus
1194	53	12.9	195	2	Q9G727	Q9g727 eulimnogamm	1267	53	12.9	381	2	Q8BKU9	Q8bku9 mus musculu
1195	53	12.9	200	2	Q9WB66	Q9wb6 carassius a	1268	53	12.9	384	2	O6CB93	O6cb93 yarrowia li
1196	53	12.9	206	2	Q8D255	Q8dz55 streptococc	1269	53	12.9	394	2	O7W2B3	O7w2b3 bordetella
1197	53	12.9	213	2	Q8FTP4	Q8ftp4 brucella su	1270	53	12.9	397	2	O7MDA0	O7mda0 vibrio vuln
1198	53	12.9	221	2	Q7P1V8	Q7p1v8 chromobacte	1271	53	12.9	397	2	Q8D6E7	Q8d6e7 vibrio vuln
1199	53	12.9	227	2	Q9G807	Q9g807 triatoma di	1272	53	12.9	398	2	Q83G95	Q83g95 tropheryma

1273	53	12.9	400	2	Q81C85	Q81c85 bacillus ce	1346	53	12.9	673	2	Q9LJP4	Q9Ljp4 arabidopsis
1274	53	12.9	400	2	Q830N1	Q830n1 enterococcus	1347	53	12.9	683	2	Q6ZGM7	Q6Zgm7 oryza sativ
1275	53	12.9	404	2	Q7QDD3	Q7qdd3 anopheles g	1348	53	12.9	688	2	Q6L538	Q6L538 arabidopsis
1276	53	12.9	405	2	Q8G4Q5	Q8g4q5 bifidobacte	1349	53	12.9	692	2	Q9SB75	Q9sb75 arabidopsis
1277	53	12.9	410	1	CB2R_RAT	Q9qzn9 rattus norv	1350	53	12.9	706	2	Q8Y0N1	Q8y0n1 ralstonia s
1278	53	12.9	410	2	Q6DD05	Q6dd05 xenopus lae	1351	53	12.9	706	2	Q75IY3	Q75iy3 oryza sativ
1279	53	12.9	415	2	Q9PNV8	Q9pnv8 campylobact	1352	53	12.9	716	2	Q9BL30	Q9bl30 caenorhabdi
1280	53	12.9	417	2	Q7MCZ4	Q7mcz4 vibrio vuln	1353	53	12.9	717	2	Q8Z7R8	Q8z7r8 salmonella
1281	53	12.9	417	2	Q8DSX7	Q8dsx7 vibrio vuln	1354	53	12.9	743	2	Q90Z26	Q90z26 sternopygus
1282	53	12.9	419	2	Q6QT97	Q6qt97 trypanosoma	1355	53	12.9	746	2	Q92BN1	Q92bn1 listeria in
1283	53	12.9	419	2	Q725X7	Q725x7 desulfovibr	1356	53	12.9	748	2	Q6NG44	Q6ng44 corynebacte
1284	53	12.9	420	2	Q8HN35	Q8hn35 paragonimus	1357	53	12.9	807	2	Q9V5H6	Q9v5h6 drosophila
1285	53	12.9	420	2	Q9MLH8	Q9mlh8 paragonimus	1358	53	12.9	840	2	Q8IGU8	Q8igu8 drosophila
1286	53	12.9	421	2	Q6AUA6	Q6aua6 oryza sativ	1359	53	12.9	880	2	Q8YI21	Q8yi21 pseudomonas
1287	53	12.9	429	1	CISY_RHTR	P51037 rhizobium t	1360	53	12.9	923	2	Q6CIC7	Q6cic7 kluveromyc
1288	53	12.9	429	1	CISZ_RHTR	P51038 rhizobium t	1361	53	12.9	947	2	Q7RDK2	Q7rdk2 plasmodium
1289	53	12.9	429	2	Q9ZM38	Q9zm38 helicobacte	1362	53	12.9	964	2	Q6XGB6	Q6xgb6 escherichia
1290	53	12.9	431	1	Q9OE THETH	Q56229 thelymus the	1363	53	12.9	992	2	Q9V5H7	Q9v5h7 drosophila
1291	53	12.9	433	2	Q8TJF8	Q8tdt8 homo sapien	1364	53	12.9	1010	2	Q75CL2	Q75cl2 ashbya goss
1292	53	12.9	440	2	Q9KL99	Q9kl99 vibrio chol	1365	53	12.9	1026	2	Q6V495	Q6v495 drosophila
1293	53	12.9	458	1	NUON_RICCN	Q92hns rickettsia	1366	53	12.9	1083	2	Q7Q240	Q7q240 anopheles g
1294	53	12.9	458	2	Q7P8U7	Q7pbu7 rickettsia	1367	53	12.9	1091	2	Q9ZIL5	Q9zil5 mus musculu
1295	53	12.9	461	2	Q7P049	Q7p049 chromobacte	1368	53	12.9	1120	2	Q7XQT5	Q7xqt5 oryza sativ
1296	53	12.9	468	2	Q684E6	Q684e6 sulfolobus	1369	53	12.9	1139	2	Q6BDQ6	Q6bdq6 yersinia ps
1297	53	12.9	486	2	Q75A55	Q75a55 ashbya goss	1370	53	12.9	1139	2	Q6B377	Q6b377 uncultured
1298	53	12.9	490	2	Q29376	Q29976 archaeoglob	1371	53	12.9	1321	2	Q950Z2	Q950z2 tetrahymena
1299	53	12.9	492	2	Q8T7W0	Q8t7w0 drosophila	1372	53	12.9	1341	2	Q9GRK2	Q9grk2 leishmania
1300	53	12.9	496	2	Q8FJ30	Q8fj30 escherichia	1373	53	12.9	1348	2	Q7QDJ1	Q7qdj1 anopheles g
1301	53	12.9	497	2	Q6AV67	Q6av67 oryza sativ	1374	53	12.9	1467	2	Q7PDM5	Q7pdm5 plasmodium
1302	53	12.9	500	2	Q800U0	Q800u0 ictalurus p	1375	53	12.9	1502	2	Q756V3	Q756v3 ashbya goss
1303	53	12.9	509	2	Q9LAW4	Q9lma4 arabidopsis	1376	53	12.9	1672	2	Q6AT77	Q6at77 oryza sativ
1304	53	12.9	512	2	Q9HVA7	Q9hva7 pseudomonas	1377	53	12.9	1693	2	Q80TG7	Q80tg7 mus musculu
1305	53	12.9	513	2	Q6A592	Q6a592 caenorhabdi	1378	53	12.9	1717	2	Q905I9	Q905i9 fugu rubrip
1306	53	12.9	517	2	Q6NCW0	Q6njw0 corynebacte	1379	53	12.9	1724	2	Q75IX6	Q75ix6 oryza sativ
1307	53	12.9	520	2	P91840	P91840 caenorhabdi	1380	53	12.9	1949	2	Q9DF53	Q9df53 brachydanio
1308	53	12.9	522	2	Q9BHW0	Q9bhw0 leishmania	1381	52.5	12.8	83	2	Q9SKG6	Q9skg6 arabidopsis
1309	53	12.9	523	1	FZD4_XENLA	Q9pt62 xenopus lae	1382	52.5	12.8	90	1	N36A_SOYBN	Q02918 glycine max
1310	53	12.9	525	1	FZD4_CHICK	Q9ia05 gallus gall	1383	52.5	12.8	104	2	Q6ETG0	Q6etg0 oryza sativ
1311	53	12.9	526	2	Q98C28	Q98c28 rhizobium l	1384	52.5	12.8	107	2	Q705E0	Q705e0 human papil
1312	53	12.9	526	2	Q6P8H8	Q6p8h8 mus musculu	1385	52.5	12.8	111	2	Q80PY4	Q80py4 anaabena sp
1313	53	12.9	527	2	Q16923	Q16923 caenorhabdi	1386	52.5	12.8	113	1	DYIX_BOVIN	Q8yp73 mycoplasma
1314	53	12.9	537	1	FZD4_HUMAN	Q9ulv1 homo sapien	1387	52.5	12.8	113	1	DYIX_HUMAN	P63171 bos taurus
1315	53	12.9	537	1	FZD4_MOUSE	Q61088 mus musculu	1388	52.5	12.8	113	1	DYIX_RAT	Q92336 rattus norv
1316	53	12.9	537	2	Q6S9E4	Q6s9e4 homo sapien	1389	52.5	12.8	125	2	Q870J2	Q870j2 sulfolobus
1317	53	12.9	537	2	Q8BK53	Q8bk53 mus musculu	1390	52.5	12.8	129	2	Q8CAT5	Q8cat5 mus musculu
1318	53	12.9	537	2	Q8BLL2	Q8bll2 mus musculu	1391	52.5	12.8	133	2	Q8UIF8	Q8ulf8 agrobacteri
1319	53	12.9	538	1	FZD4_RAT	Q9qzh0 rattus norv	1392	52.5	12.8	137	2	Q98QT1	Q98qt1 mycoplasma
1320	53	12.9	541	1	BBR1_SCHCO	P78741 schizophyll	1393	52.5	12.8	138	2	Q8TP69	Q8tp69 methanosarc
1321	53	12.9	545	2	Q851J71	Q851j1 oryza sativ	1394	52.5	12.8	138	2	Q9HK88	Q9hk88 thermoplasma
1322	53	12.9	546	1	Y61B_MYCPN	P75040 mycoplasma	1395	52.5	12.8	141	2	Q85H90	Q85h90 austrochilus
1323	53	12.9	546	2	Q7QA61	Q7qa61 anopheles g	1396	52.5	12.8	145	2	Q7YCV9	Q7ycv9 arion irati
1324	53	12.9	553	2	Q9JXN7	Q9jxn7 neisseria m	1397	52.5	12.8	148	2	Q66CE6	Q66ce6 yersinia ps
1325	53	12.9	555	1	CSTA_AQUAE	Q67304 aquifex ae	1398	52.5	12.8	148	2	Q8ZG73	Q8zg73 yersinia pe
1326	53	12.9	555	2	Q04162	Q04162 saccharomyc	1399	52.5	12.8	154	2	Q85H91	Q85h91 austrochilus
1327	53	12.9	556	2	Q7ZU08	Q7zu08 brachydanio	1400	52.5	12.8	155	2	Q85H92	Q85h92 austrochilus
1328	53	12.9	557	2	Q8QPM3	Q8qfm3 brachydanio	1401	52.5	12.8	162	2	Q6SZ03	Q6sz03 megabalanus
1329	53	12.9	558	2	Q9JWB6	Q9jwb6 neisseria m	1402	52.5	12.8	165	2	Q934N3	Q934n3 uncultured
1330	53	12.9	567	2	Q8TEN4	Q8ten4 homo sapien	1403	52.5	12.8	165	2	Q934N5	Q934ns uncultured
1331	53	12.9	571	2	Q93GF4	Q93gf4 staphylococ	1404	52.5	12.8	165	2	Q50283	Q50283 methylocyst
1332	53	12.9	579	2	Q9W6E4	Q9w6e4 brachydanio	1405	52.5	12.8	169	2	Q6VOT5	Q6vot5 uncultured
1333	53	12.9	588	2	Q8H038	Q8h038 oryza sativ	1406	52.5	12.8	170	2	Q9TGJ3	Q9tgj3 taenia cras
1334	53	12.9	590	2	Q34192	Q34192 crithidia o	1407	52.5	12.8	175	2	Q8DKB9	Q8dkb9 synchococc
1335	53	12.9	590	2	Q8L193	Q8l193 salvia offi	1408	52.5	12.8	177	2	Q6RW20	Q6rw20 uncultured
1336	53	12.9	592	2	Q9W6E2	Q9w6e2 brachydanio	1409	52.5	12.8	177	2	Q6RW21	Q6rw21 uncultured
1337	53	12.9	603	2	Q04806	Q04806 perilla fru	1410	52.5	12.8	183	1	SIEB_LAMBD	P03762 bacterioph
1338	53	12.9	603	2	Q9FV72	Q9fv72 perilla fru	1411	52.5	12.8	190	2	Q7NCD9	Q7ncd9 gloeobacter
1339	53	12.9	604	2	Q9AXM7	Q9axm7 perilla fru	1412	52.5	12.8	195	2	Q59004	Q59004 pyrococcus
1340	53	12.9	611	1	NU5M_LATCH	Q03174 latimeria c	1413	52.5	12.8	214	2	Q9GCA6	Q9gca6 litoria pea
1341	53	12.9	643	2	Q8H6J2	Q8h6j2 zea mays (m	1414	52.5	12.8	214	2	Q9GCB0	Q9gcb0 litoria spe
1342	53	12.9	649	2	Q8IT87	Q8it87 drosophila	1415	52.5	12.8	216	2	Q8P901	Q8p901 xanthomonas
1343	53	12.9	655	2	Q23675	Q23675 arabidopsis	1416	52.5	12.8	219	2	Q8VCL0	Q8vcl0 mus musculu
1344	53	12.9	666	1	FZD3_HUMAN	Q9npg1 homo sapien	1417	52.5	12.8	219	2	Q9D7S1	Q9d7s1 mus musculu
1345	53	12.9	667	2	Q757W1	Q757w1 ashbya goss	1418	52.5	12.8	224	2	Q6SMZ5	Q6smz5 actus azara

1419	52.5	12.8	225	2	Q9B0J6	Q9b0j6 limnodynast
1420	52.5	12.8	227	2	Q8NB08	Q8nbp8 homo sapien
1421	52.5	12.8	229	2	Q8NB01	Q8nbq1 homo sapien
1422	52.5	12.8	236	2	Q91254	Q91254 mus musculus
1423	52.5	12.8	237	2	Q72WL3	Q72wl3 xenopus lae
1424	52.5	12.8	247	2	Q8C962	Q8c962 mus musculus
1425	52.5	12.8	258	2	Q8MPN2	Q8mpn2 drepanosiph
1426	52.5	12.8	261	1	COX3_SCYCA	Q79407 scyloirhinu
1427	52.5	12.8	263	2	Q6CG94	Q6cg94 yarrowia li
1428	52.5	12.8	263	2	Q20705	Q20705 caenorhabdi
1429	52.5	12.8	265	2	Q89BC6	Q89bc6 bradyrhizob
1430	52.5	12.8	266	2	Q9GLI6	Q9gli6 cercopagis
1431	52.5	12.8	266	2	Q8CUN6	Q8cun6 staphylococ
1432	52.5	12.8	268	2	Q92DL4	Q92dl4 listeria mo
1433	52.5	12.8	268	2	Q722A9	Q722a9 listeria in
1434	52.5	12.8	268	2	Q7AP20	Q7ap20 streptococ
1435	52.5	12.8	272	2	Q8DVK0	Q8dvk0 listeria in
1436	52.5	12.8	272	2	Q6IO10	Q6io10 brachydania
1437	52.5	12.8	275	2	Q9G790	Q9gt90 aedes trise
1438	52.5	12.8	277	2	Q6N522	Q6n522 rhodopsedo
1439	52.5	12.8	277	2	Q8BD54	Q8bd54 pseudomonas
1440	52.5	12.8	278	2	Q9ZG99	Q9zg99 pseudomonas
1441	52.5	12.8	281	1	PLSC_LJMAL	Q42868 limnanthes
1442	52.5	12.8	281	1	PLSC_LINDO	Q42870 limnanthes
1443	52.5	12.8	285	2	Q97HM6	Q97hme clostridium
1444	52.5	12.8	285	2	Q6DAJ5	Q6daj5 erwania car
1445	52.5	12.8	286	2	Q6BSA9	Q6bsa9 debaryomyce
1446	52.5	12.8	291	2	Q7YX24	Q7yx24 cryptospori
1447	52.5	12.8	293	2	Q6PCX0	Q6pcx0 mus musculus
1448	52.5	12.8	299	1	NULM_ALECO	P48897 albinaria c
1449	52.5	12.8	301	2	Q6ADE5	Q6ades leifsonia x
1450	52.5	12.8	307	2	Q8BH47	Q8bh47 m mus muscu
1451	52.5	12.8	307	2	Q642F4	Q642f4 rattus norv
1452	52.5	12.8	308	2	Q8BRT0	Q8brt0 mus musculus
1453	52.5	12.8	321	2	Q48995	Q48995 oryza sativ
1454	52.5	12.8	322	1	MRGA_HUMAN	Q961a9 homo sapien
1455	52.5	12.8	322	1	SNS5_HUMAN	Q8tdr7 homo sapien
1456	52.5	12.8	322	2	Q9RTB6	Q9rtb6 oncorhynch
1457	52.5	12.8	322	2	Q6IQ08	Q6iq08 brachydanio
1458	52.5	12.8	327	2	Q7PHP6	Q7php6 anopheles g
1459	52.5	12.8	328	2	O17358	O17358 caenorhabdi
1460	52.5	12.8	330	2	Q7Y166	Q7y166 oryza sativ
1461	52.5	12.8	334	1	FX16_MOUSE	Q9qzm9 mus musculus
1462	52.5	12.8	334	2	Q6P5P4	Q6p5p4 rattus norv
1463	52.5	12.8	336	2	Q9LQW5	Q9lqw5 arabidopsis
1464	52.5	12.8	338	2	Q645S5	Q645s5 macaca mula
1465	52.5	12.8	340	2	Q9CWD6	Q9cwd6 mus musculus
1466	52.5	12.8	342	2	Q7RBE5	Q7rbe5 anopheles g
1467	52.5	12.8	345	2	Q68X34	Q68x34 rickettsia
1468	52.5	12.8	346	2	Q8LZA4	Q8lza4 catharus me
1469	52.5	12.8	346	2	Q66SX8	Q66sx8 diplometopo
1470	52.5	12.8	347	2	Q84BA5	Q84ba5 erwania chr
1471	52.5	12.8	348	2	Q9GON3	Q9gon3 campyloform
1472	52.5	12.8	350	2	Q7NEY9	Q7ney9 gloeobacter
1473	52.5	12.8	353	2	Q6DFK1	Q6dfk1 xenopus lae
1474	52.5	12.8	356	1	SPAS_SALT	F40702 salmonella
1475	52.5	12.8	356	2	Q88NH5	Q88nh5 pseudomonas
1476	52.5	12.8	359	2	Q88RM0	Q88rm0 pseudomonas
1477	52.5	12.8	360	1	GP15_HUMAN	P49685 homo sapien
1478	52.5	12.8	360	1	GP15_PANTR	Q9bg77 pan troglod
1479	52.5	12.8	362	1	G89A_DROME	Q9veu0 drosophila
1480	52.5	12.8	364	2	Q56772	Q56772 xanthomonas
1481	52.5	12.8	364	2	Q56803	Q56803 xanthomonas
1482	52.5	12.8	364	2	Q67A35	Q67a35 streptococc
1483	52.5	12.8	364	2	Q8P801	Q8p801 xanthomonas
1484	52.5	12.8	365	2	Q93PY9	Q93py9 pseudomonas
1485	52.5	12.8	372	2	Q83RE7	Q83re7 shigella fl
1486	52.5	12.8	374	1	VLF1_NPVOP	O10330 orgyia pseu
1487	52.5	12.8	374	2	Q7TiS5	O7t1a5 choristoneu
1488	52.5	12.8	380	2	Q8M4W9	O8m4w9 wattleia mos
1489	52.5	12.8	385	2	Q72XP7	Q72xp7 bacillus ce
1490	52.5	12.8	386	2	Q69ZD3	Q69zd3 mus musculus
1491	52.5	12.8	386	2	Q9D0R9	Q9d0r9 m mus muscu

## ALIGNMENTS

## RESULT 1

Q6UWR8	PRELIMINARY;	PRT;	77	AA.
ID	Q6UWR8			
AC	Q6UWR8;			
DT	05-JUL-2004	(TReMBLrel. 27, Created)		
DT	05-JUL-2004	(TReMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TReMBLrel. 27, Last annotation update)		
DE	GPVK512.			
GN	ORFName=UNQ512;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment";			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL; AY358675; AAQ89038.1; -.			
SQ	SEQUENCE 77 AA; 8772 MW; 110CBFCF87CCC4B86 CRC64;			

Query Match 100.0%; Score 410; DB 2; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 1e-37; Mismatches 0; Indels 0; Gaps 0;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGVPKQLKRMFEPTRLIATIMVLLCFALTLCSAFWHNGKALIFCIQLSALTWYLSF	60
Db	1	MGVPKQLKRMFEPTRLIATIMVLLCFALTLCSAFWHNGKALIFCIQLSALTWYLSF	60
Qy	61	IPFADAVKKCFPAVCLA	77
Db	61	IPFADAVKKCFPAVCLA	77

## RESULT 2

Q95562	PRELIMINARY;	PRT;	160	AA.
ID	Q95562			
AC	Q95562;			
DT	01-MAY-1999	(TrEMBLrel. 10, Created)		
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

RA Rhodes S.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg K.H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Diatchenko L., Matsumoto H., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RC "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RC TISSUE=Lymph;  
 RX STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AL035297; CAA22897.1; -;  
 DR ENBL; BC068098; AAH68098.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 160 AA; 17779 MW; F05C57532B7593BD CRC64;  
 Query Match 100.0%; Score 410; DB 2; Length 160;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGVPKQKRMFEPTRIATIMVLLCFAITCSAFWNNKGLALIFCILOSALTWTSLSF 60  
 DB 84 MGVPKQKRMFEPTRIATIMVLLCFAITCSAFWNNKGLALIFCILOSALTWTSLSF 143  
 QY 61 IPPARDVKKCFVAVCLA 77  
 DB 144 IPPARDVKKCFVAVCLA 160  
 RESULT 3  
 Q8VD57 PRELIMINARY; PRT; 159 AA.  
 AC Q8VD57;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE RIKEN cDNA 2010005013 (Mus musculus adult male bone cDNA, RIKEN full-  
 DE length enriched library, clone:9830137K19 product:hypothetical  
 DE protein, full insert sequence).  
 GN Name:2010005013Rik;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg K.H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Diatchenko L., Matsumoto H., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RC "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RC TISSUE=Lymph;  
 RX STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AL035297; CAA22897.1; -;  
 DR ENBL; BC068098; AAH68098.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 160 AA; 17779 MW; F05C57532B7593BD CRC64;

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RC "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RC TISSUE=Salivary gland;  
 RX STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [5]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RA The FANTOM Consortium,  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RL 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [6]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [7]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multichannel sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Bone;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

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RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohtsuo N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sagaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC017549; AAH17549.1; -.
DR EMBL; AK036578; BAC29488.1; -.
DR MGD; MGI:1917362; 201005013rik.
KW Hypothetical protein.
SQ SEQUENCE 159 AA; 17499 MW; B30B7EB5FB82A0B6 CRC64;

Query Match 89.4%; Score 366.5; DB 2; Length 159;
Best Local Similarity 92.4%; Pred. No. 1.2e-32;
Matches 71; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MGPVKQKRMFPEPTRLIATIMVLLCFALTLCSAFWHNGKIALIFCIIQSLALTWYLSF 60
Db 84 MGLPKQKRMFPEPTRLIATIMVLLCFALTLCSAFLW-NKGLALIFCIIQSLALTWYLSY 142
Qy 61 IPFARDAVKKCFACVLA 77
Db 143 IPYARDAVKKCFACVLA 159

RESULT 4
Q7T375 PRELIMINARY; PRT; 161 AA.
AC Q7T375
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Hypothetical protein zgc:64053.
GN CAPName=zgc:64053.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018969; AAH18969.1; -.
SQ SEQUENCE 159 AA; 17804 MW; 0BC8A9CED7EF27E0 CRC64;

Query Match 74.6%; Score 306; DB 2; Length 159;
Best Local Similarity 70.1%; Pred. No. 5.9e-26;
Matches 54; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MGPVKQKRMFPEPTRLIATIMVLLCFALTLCSAFWHNGKIALIFCIIQSLALTWYLSF 60
Db 83 MGPVKQKRMFPEPTRLIATIMVLLCFALTLCALWVHNGKIALIFCIIQSLALTWYLSY 142
Qy 61 IPFARDAVKKCFACVLA 77
Db 143 IPYARDAVKKCSLLS 159

RESULT 6
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Query Match 79.0%; Score 324; DB 2; Length 161;
Best Local Similarity 76.6%; Pred. No. 6.1e-28;
Matches 59; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MGPVKQKRMFPEPTRLIATIMVLLCFALTLCSAFWHNGKIALIFCIIQSLALTWYLSF 60
Db 85 MGPVKQKRMFPEPTRLIATIMVLLCFALTLCVFWHNGKIALIFCIIQSLALTWYLSY 144
Qy 61 IPFARDAVKKCFACVLA 77
Db 145 IPYARDAVKCCTCLS 161

RESULT 5
Q8WV19 PRELIMINARY; PRT; 159 AA.
AC Q8WV19
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Chromosome 6 open reading frame 83.
GN Name=C6orf83;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018969; AAH18969.1; -.
SQ SEQUENCE 159 AA; 17804 MW; 0BC8A9CED7EF27E0 CRC64;

Query Match 74.6%; Score 306; DB 2; Length 159;
Best Local Similarity 70.1%; Pred. No. 5.9e-26;
Matches 54; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MGPVKQKRMFPEPTRLIATIMVLLCFALTLCSAFWHNGKIALIFCIIQSLALTWYLSF 60
Db 83 MGPVKQKRMFPEPTRLIATIMVLLCFITLCAWVHNGKIALIFCIIQSLALTWYLSY 142
Qy 61 IPFARDAVKKCFACVLA 77
Db 143 IPYARDAVKKCSLLS 159

RESULT 6
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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilkinson J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z79695; CAFE1789.1; -
DR WormBase; WBGene00009191; F27D4.7.
DR Wormpep; F27D4.7; CE34829.
KW Hypothetical protein.
SQ SEQUENCE 162 AA; 17849 MW; C540FE86696A9489 CRC64;

Query Match          40.7%; Score 167; DB 2; Length 162;
Best Local Similarity 48.6%; Pred.No.1.3e-10;
Matches 35; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MGPKVKQLKRMFEPRLTIATIMVLLCFALTCSAFWNNKGIALIFCIIQSALMTWYSLSF 60
   |||::|||:::||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 90 MGPIGQIKMFKDSRWIASSMYILFIPLTLLSGVLKNLSLAICTAGVIAMAWYLSLY 149
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy 61 IPFARDAVKKCF 72
   ||::|||::|||
Db 150 IPYAREAVSKIP 161
   |||::|||::|||

RESULT 10
Q9NEC2 PRELIMINARY; PRT; 163 AA.
AC Q9NEC2;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE Possible hypothetical 17.8 Kd protein.
GN Name=L8325.06;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RN Genome Res. 8:135-145(1998).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: ALI57415; CAB75633.1; -
KW Hypothetical protein.
SQ SEQUENCE 163 AA; 17766 MW; CE8464549DEB6AEC CRC64;

Query Match          38.8%; Score 159; DB 2; Length 163;
Best Local Similarity 45.8%; Pred.No.1e-09;
Matches 33; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy 2 GPVKOLKRMFEPRLTIATIMVLLCFALTCSAFWNNKGIALIFCIIQSALMTWYSLSFI 61
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 87 GPAPQPKSMNEGRIASVTYIITVLTLLCAVLLHSGGLTILMSLIQILLALAWYLSYI 146
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Qy 62 PFARDAVKKCPA 73
   |||||::|||
Db 147 PFARDIVKGAFS 158
   |||||::|||

RESULT 11
Q9LT07 PRELIMINARY; PRT; 175 AA.
AC Q9LT07;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

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RT "Leishmania major chromosome 3 contains two long converg



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GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: April 7, 2005, 03:12:32 ; Search time 175 Seconds  
(without alignments)  
170.175 Million cell updates/sec

Title: US-10-063-563-56  
Perfect score: 410  
Sequence: 1 MGPKVQLKMFETRIIAT.....LSFIPFARDAVKKCPAVCLA 77  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A.Geneseq.16Dec04:\*  
1: Genesexp19808:\*  
2: Genesexp19908:\*  
3: Genesexp20008:\*  
4: Genesexp20018:\*  
5: Genesexp20028:\*  
6: Genesexp2003as:\*  
7: Genesexp2003bs:\*  
8: Genesexp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summary

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	RAY66715	standard; protein; 77 AA.				
DE	Membrane-bound protein PRO1027.					
PN	WO9663088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 410;	DB 3;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 2.3e-44;				
RESULT 2						
ID	AAU29130	standard; protein; 77 AA.				
DE	Human PRO polypeptide sequence #107.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 410;	DB 4;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 2.3e-44;				
RESULT 3						
ID	AA87553	standard; protein; 77 AA.				
DE	Human PRO1027.					
PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 410;	DB 4;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 2.3e-44;				
RESULT 4						
ID	AA65238	standard; protein; 77 AA.				
DE	Human PRO1027 (UNQ512) protein sequence SEQ ID NO:283.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 410;	DB 4;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 2.3e-44;				
RESULT 5						
ID	ABG95878	standard; protein; 77 AA.				
DE	Human secreted/transmembrane protein PRO1027.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 410;	DB 5;	Length 77;		
Best Local Similarity	100.0%;	Pred. No. 2.3e-44;				
RESULT 6						
ID	ABU58506	standard; protein; 77 AA.				

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DE Human PRO polypeptide #107.  
PN US2003027272-A1.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 7  
ID ABU89054 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 8  
ID ABU84369 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 9  
ID ABR66243 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 10  
ID ABR65633 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 11  
ID ABU95973 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 12  
ID ABU58053 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 13  
ID ABU59131 standard; protein; 77 AA.  
DE Novel human secreted or transmembrane protein PRO1027.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 14  
ID ABU82643 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 15  
ID ABU82812 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 16  
ID ABU89933 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036147-A1.

PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 17  
ID ABR68182 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 18  
ID ABU60562 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, #115.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 19  
ID ABU96235 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 20  
ID ABU92666 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 21  
ID ABO08743 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 22  
ID ABO02795 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 23  
ID ABR74949 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 24  
ID ABR94711 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 25  
ID ABU13944 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 26  
ID ABU85684 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036140-A1.  
PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 27  
ID ABU98844 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 28  
ID ABU98059 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 29  
ID ABU91765 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 30  
ID ABU89458 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 31  
ID ABU86299 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 32  
ID ABU67512 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 33  
ID ABU80540 standard; protein; 77 AA.  
DE Human PRO protein #107.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 34  
ID ABU72529 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 35  
ID ABU90903 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 36  
ID ABO33962 standard; protein; 77 AA.

DE Human secreted/transmembrane protein PRO1027.  
PN US2003009013-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 37  
ID ABR99458 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 38  
ID ABR98948 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 39  
ID ABO16371 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 40  
ID ABR92271 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 41  
ID ABO18912 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 42  
ID ABR78333 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 43  
ID ABU71979 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 44  
ID ABUS069 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 45  
ID ABO00208 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 46  
ID ABO11540 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040060-A1.

DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 47  
ID ABO02185 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 48  
ID ABR8759 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 49  
ID ABR83454 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 50  
ID ABO06255 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 51  
ID ABR59291 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 52  
ID ABO09353 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 53  
ID ABO19217 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 54  
ID ABO11235 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 55  
ID ABR66853 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 56  
ID ABO16066 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040060-A1.

PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 57  
ID ABO13772 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 58  
ID ABU71533 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 59  
ID ABU65675 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, SEQ ID 214.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 60  
ID ABO07523 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 61  
ID ABO03710 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 62  
ID ABR67158 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 63  
ID ABO15761 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 64  
ID ABU56042 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, PRO1027.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 65  
ID ABU72314 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 66  
ID ABU65370 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032102-A1.

PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 67  
ID ABU95315 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 68  
ID ABU71218 standard; protein; 77 AA.  
DE Human PRO1027 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 69  
ID ABO07828 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 70  
ID ABR70069 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 71  
ID ABR69402 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 72  
ID ABO01543 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 73  
ID ABU81345 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 74  
ID ABR60142 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 75  
ID ABU90987 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 76  
ID ABR67877 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027269-A1.

PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 77  
ID ABR65265 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 78  
ID ABR6487 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 79  
ID ABR71899 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 80  
ID ABUS9278 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein, #115.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 81  
ID ABUS3379 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 82  
ID ABUS9069 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 83  
ID ABUS3149 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 84  
ID ABUS9005 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 85  
ID ABUS0553 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 86  
ID ABUS4064 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 87  
ID ABUS3715 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 88  
ID ABO25975 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 89  
ID ABR64960 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 90  
ID ABO27308 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO1027.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 91  
ID ABR68792 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 92  
ID ABO06608 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 93  
ID ABR99153 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 94  
ID ABUS7037 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 95  
ID ABUS5989 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 96  
ID ABUS2276 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;

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Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 97
ID ABR66548 standard; protein; 77 AA.
DE Human secreted polypeptide #107.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 98
ID ABR90966 standard; protein; 77 AA.
DE Human secreted polypeptide #107.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 99
ID ABO08133 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 100
ID ABR92503 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003045684-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 101
ID ABR81844 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 102
ID ABR66008 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 103
ID ABR81173 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027.
PN US2003027212-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 104
ID ABR59837 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 105
ID ABR94025 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 106
ID ABR99878 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 107
ID ABR66548 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003027281-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 108
ID ABR90966 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 109
ID ABO53288 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003027986-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 110
ID ABR58984 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, #115.
PN US2002142961-A1.
PD 03-OCT-2002.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 111
ID ABR94393 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 112
ID ABR79275 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 113
ID ABR6604 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 114
ID ABR6909 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 115
ID ABR94698 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 116
ID ABO04625 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
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RESULT 117  
ID ABR70374 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 118  
ID ABU92362 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 119  
ID ABU98539 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 120  
ID ABR65938 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 121  
ID ABR64655 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 122  
ID ABU59427 standard; protein; 77 AA.  
DE Novel human secreted or transmembrane protein PRO1107.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 123  
ID ABR79580 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 124  
ID ABU92971 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 125  
ID ABU95930 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 126  
ID ABU91150 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 127  
ID ABU90243 standard; protein; 77 AA.

DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 128  
ID AB009658 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 129  
ID AB010930 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 130  
ID ABR70984 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 131  
ID ABU98290 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 132  
ID ABU87592 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 133  
ID ABU91460 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 134  
ID ABU89295 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 135  
ID ABU84674 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 136  
ID ABR69764 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;  
RESULT 137  
ID ABU80141 standard; protein; 77 AA.  
DE Human PRO protein #107.

PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 138  
ID ABU92502 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 139  
ID ABU92193 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 140  
ID ABU93410 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 141  
ID ABO09963 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 142  
ID ABO09048 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 143  
ID ABU96466 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 144  
ID ABU10899 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 145  
ID ABU10616 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein #107.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 146  
ID ABU81651 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 147

ID ABU72136 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 148  
ID ABU95625 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 149  
ID ABU96834 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 150  
ID ABR70679 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 151  
ID ABO05030 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 152  
ID ABO08438 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 153  
ID ABU88590 standard; protein; 77 AA.  
DE Human secreted and transmembrane polypeptide PRO1027.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 154  
ID ABO34104 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 155  
ID ABO05645 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 156  
ID ABR74034 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 157  
ID ABR95626 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 158  
ID ABR80923 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 159  
ID ABR81228 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 160  
ID ABR80924 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 161  
ID ABR88526 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 162  
ID ABR77347 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 163  
ID ABO28831 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 164  
ID ABO31576 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 165  
ID ABR07993 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 166  
ID ABO40473 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 167  
ID ABO35898 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 168  
ID ABO44037 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 169  
ID ADA77966 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 170  
ID ABR24832 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 171  
ID ABO3100 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 172  
ID ABR90356 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 173  
ID ABR17270 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 174  
ID ABR95016 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 175  
ID ABR95321 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.

RESULT 185  
ID ABM26357 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 186  
ID ABO48139 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
FN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 187  
ID ABR92881 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 188  
ID ABO24642 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
FN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 189  
ID ADA37794 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
FN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 190  
ID ABM11653 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 191  
ID ABM02754 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 192  
ID ABM16050 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 193  
ID ABO27611 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
FN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 194  
ID ABO27611 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
FN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

ID ABM29102 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 195  
ID ABM07078 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 196  
ID ABM21172 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 197  
ID ABM09518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 198  
ID ABO41388 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 199  
ID ABO36203 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 200  
ID ABO43732 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 201  
ID ABM76432 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 202  
ID ABM76128 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 203  
ID ABM25747 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.

PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 204  
ID ABM26052 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 205  
ID ADA21480 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO1027.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 206  
ID ABO03405 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 207  
ID ABO02490 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 208  
ID ABO44266 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO 1027.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 209  
ID ABR90661 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 210  
ID ABR73729 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 211  
ID ABO16981 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 212  
ID ABR94406 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 213  
ID ABR75913 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 214
ID ABR71289 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 215
ID ABR93186 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 216
ID ABR93491 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 217
ID ADA10267 standard; protein; 77 AA.
DE Human secreted/transmembrane protein, PRO1027.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 218
ID ABR87916 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 219
ID ABO27916 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 220
ID ABO30051 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 221
ID ABO33260 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 222
ID ABR04948 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 223
ID ABO08908 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 224
ID ABO36508 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 225
ID ABO35593 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 226
ID ABO39558 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 227
ID ABO10433 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 228
ID ABO11958 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 229
ID ABO52104 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 230
ID ABO52409 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
RESULT 231
ID ADA19918 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 410; DB 6; Length 77;
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Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 232  
ID ABO23727 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 233  
ID ADB17301 standard; protein; 77 AA.  
DE Human transmembrane PRO polypeptide (SeqID 56).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 234  
ID ADA17811 standard; protein; 77 AA.  
DE Human secreted polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 235  
ID ABR97213 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 236  
ID ABR87001 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 237  
ID ABM11043 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 238  
ID ABM28187 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 239  
ID ABO32186 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 240  
ID ABM15313 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 241  
ID ABM06468 standard; protein; 77 AA.

DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 242  
ID ABM04279 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 243  
ID ABM22392 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 244  
ID ABM07688 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 245  
ID ABO40778 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 246  
ID ABM35425 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 247  
ID ABM33188 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 248  
ID ABO52714 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 249  
ID ABO50274 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 250  
ID ABU99268 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040055-A1.

PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 251  
ID ABO04320 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 252  
ID ABO05950 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 253  
ID ABO18490 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 254  
ID ADA27919 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 255  
ID ABR97518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 256  
ID ABR0618 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 257  
ID ABR01229 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 258  
ID ABR8831 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 259  
ID ABR13483 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 260  
ID ABR20867 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 261  
ID ABO41998 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 262  
ID ABO42608 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 263  
ID ABR10128 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 264  
ID ABO38643 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003088773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 265  
ID ABR32883 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 266  
ID ABR22697 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 267  
ID ABR74908 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 268  
ID ADA79758 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 269  
ID ABR96298 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 270  
ID ABM02449 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 271  
ID ABR86391 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 272  
ID ABR86696 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 273  
ID ABM16660 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 274  
ID ABM29712 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 275  
ID ABO29136 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 276  
ID ABM23917 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 277  
ID ABM23307 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 278  
ID ABM22087 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 279  
ID ABO37728 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 280  
ID ABM28492 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 281  
ID ABM28797 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 282  
ID ABM66441 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 283  
ID ABM75923 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 284  
ID ABM34103 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 285  
ID ABM34408 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 286  
ID ABO20339 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 287  
ID ABO21254 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 288  
ID ABO22169 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054477-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 289  
ID ADA20090 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 290  
ID ABO34194 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO 1027.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 291  
ID ABR96603 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 292  
ID ADA94499 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 293  
ID ABR85781 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 294  
ID ABR99763 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 295  
ID ABR00314 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 296  
ID ABR00619 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 297  
ID ABO29746 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 298

ID ABM23612 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 299  
ID ABM29407 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003088679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 300  
ID ABO38338 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 301  
ID ABO45638 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 302  
ID ABM20562 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 303  
ID ADA81485 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 304  
ID ABO16676 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 305  
ID ABO18302 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 306  
ID ABO22729 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 307  
ID ABO23034 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003054461-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 308  
ID ABR92576 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 309  
ID ABR81533 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 310  
ID ABR77957 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 311  
ID ABR89746 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 312  
ID ABR26662 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 313  
ID ABR13788 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 314  
ID ABO28526 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 315  
ID ABO30356 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 316  
ID ABR07383 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

RESULT 317  
ID ABO03974 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 318  
ID ABO37118 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 319  
ID ABO41693 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 320  
ID ABO35288 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 321  
ID ABR25137 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104540-A1.  
PD 03-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 322  
ID ABO47529 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 323  
ID ABO47834 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 324  
ID ABO48444 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 325  
ID ABO51494 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 326  
ID ABO51799 standard; protein; 77 AA.

DE Human PRO polypeptide #107.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 327  
ID ABO50579 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 328  
ID ABR79703 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 329  
ID ABM16965 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 330  
ID ABO17997 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 331  
ID ABO20949 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 332  
ID ABR96908 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 333  
ID ADA38724 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 334  
ID ABM12263 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 335  
ID ABM16355 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 336  
ID ABM24222 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 337  
ID ABM14703 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 338  
ID ABM04584 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 339  
ID ABM06773 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 340  
ID ABM09213 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 341  
ID ABO39253 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 342  
ID ABM75518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 343  
ID ABM25442 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 344  
ID ABM19952 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 345  
ID ABO46858 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.

PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 346  
ID ABO47163 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 347  
ID ADA83283 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 348  
ID ABR71594 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 349  
ID ABR72204 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 350  
ID ABR98543 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 351  
ID ABO06913 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 352  
ID ABR84866 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 353  
ID ABR73424 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 354  
ID ABR76518 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 355  
ID ABR73119 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 356  
ID ABR18185 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 357  
ID ABO20644 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 358  
ID ABO25387 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 359  
ID ABO25692 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 360  
ID ABR94101 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 361  
ID ADA92845 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 362  
ID ABR80008 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 363  
ID ABR11348 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 364  
ID ABO32955 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

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Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 365
ID ABO30661 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US200304466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 366
ID ABO30966 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 367
ID ABM27272 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US200308760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 368
ID ABM30017 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US200308769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 369
ID ABM05553 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 370
ID ABM15618 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US200308698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 371
ID ABM08603 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 372
ID ABO42303 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 373
ID ABO38033 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 374
ID ABO45943 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 375
ID ABM66746 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 376
ID ADB20326 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 377
ID ABM19647 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 378
ID ABO49359 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 379
ID ABO49664 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 380
ID ADA78578 standard; protein; 77 AA.
DE Human secreted/transmembrane protein (PRO) #107.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 381
ID ABR88221 standard; protein; 77 AA.
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.
PN US2003086720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 382
ID ADA00387 standard; protein; 77 AA.
DE Human secreted/transmembrane polypeptide PRO 1027.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 383
ID ABM26967 standard; protein; 77 AA.
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DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068739-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 384  
ID ABO03364 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 385  
ID ABO39863 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 386  
ID ABO49969 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 387  
ID ABO50884 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 388  
ID ABO05340 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 389  
ID ABR74644 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 390  
ID ABR7123 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 391  
ID ABR17880 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 392  
ID ABR95931 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 393  
ID ABO21864 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 394  
ID ABO20034 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 395  
ID ABO24337 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 396  
ID ABR86086 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 397  
ID ABR10738 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 398  
ID ABR76737 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 399  
ID ABR89441 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 400  
ID ABR12568 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 401  
ID ABR05858 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 402  
ID ABO34983 standard; protein; 77 AA.  
DE Human pro polypeptide #107.

PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 403  
ID ABO4653059 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 404  
ID ABM19037 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 405  
ID ABM19342 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 406  
ID ABO46553 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 407  
ID ABO49054 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 408  
ID ARB69097 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 409  
ID ARB89136 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 410  
ID ARB72509 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 411  
ID ARB74339 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 412  
ID ABO18607 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
FN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 413  
ID ABR80313 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 414  
ID ABR01534 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 415  
ID ABR02144 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 416  
ID ABR87306 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 417  
ID ABR12873 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 418  
ID ABR30627 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 419  
ID ABR24527 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 420  
ID ABO29441 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
FN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 421  
ID ABR87306 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
FN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 422

ID ABO31271 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 422  
ID ABO14398 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 423  
ID ABO09823 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 424  
ID ABO38948 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 425  
ID ABO34713 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 426  
ID ABO51189 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 427  
ID ABO04015 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 428  
ID ABO10485 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 429  
ID ABO53190 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 430  
ID ABR77728 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 431  
ID ABR78938 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 432  
ID ABO24032 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 433  
ID ABR93796 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 434  
ID ABO01839 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 435  
ID ABR78262 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 436  
ID ABR90051 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 437  
ID ADA22406 standard; protein; 77 AA.  
DE Human secreted/transmembrane polypeptide PRO1027.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 438  
ID ABR27577 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 439  
ID ABR13178 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 440  
ID ABO31881 standard; protein; 77 AA.

DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 441  
ID ABR14093 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 442  
ID ABR08298 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003088754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 443  
ID ABO40168 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068691-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 444  
ID ABR74603 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 445  
ID ABR33798 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 446  
ID ABR20257 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 447  
ID ABO48749 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 448  
ID ABO22560 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 449  
ID ABR72814 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 450  
ID ABO15456 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 451  
ID ABR85171 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 452  
ID ABO15151 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 453  
ID ABO17286 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 454  
ID ABR17575 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 455  
ID ADA06572 standard; protein; 77 AA.  
DE Human secreted/transmembrane PRO polypeptide #85.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 456  
ID ADA39265 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 457  
ID ABR85476 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 458  
ID ABR77042 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 459  
ID ABO28221 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 410; DB 7; Length 77;  
RESULT 460  
ID AEM33493 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 461  
ID AEM30322 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 462  
ID AEM21782 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 463  
ID AEM21477 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 464  
ID AEM15008 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 465  
ID ABO41083 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 466  
ID ABO36813 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 467  
ID ABO37423 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 468  
ID AEM75213 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 469  
ID AEM33493 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 470  
ID ABO46248 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 471  
ID ADA82649 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 472  
ID ADB85629 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 473  
ID ADB96291 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 474  
ID AEM31847 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 475  
ID AEM31237 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 476  
ID ADB85957 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 477  
ID AEM32152 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 478  
ID AEM32457 standard; protein; 77 AA.

DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 479  
ID ADB68308 standard; protein; 77 AA.  
DE Human PRO1027 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 480  
ID ADB68115 standard; protein; 77 AA.  
DE Human PRO1027 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 481  
ID ABM31542 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 482  
ID ABM30932 standard; protein; 77 AA.  
DE Human secreted polypeptide PRO1027, SEQ ID NO:214.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 483  
ID ADB90932 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 484  
ID ADC57763 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 485  
ID ADC5127 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 486  
ID ADC11994 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 487  
ID ADC07012 standard; protein; 77 AA.  
DE Human PRO1027 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 488  
ID ADC56416 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 489  
ID ADC17191 standard; protein; 77 AA.  
DE Mammalian PRO polypeptide (SeqID 56).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 490  
ID ADC07471 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 491  
ID ADC11461 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 492  
ID ADC14889 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 493  
ID ADC52384 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 494  
ID ADC14583 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 495  
ID ADD08115 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 496  
ID ADC81940 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 497  
ID ADD07582 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002193299-A1.  
PD 19-DEC-2002.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 498  
ID ADC82473 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 499  
ID ADD05687 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 500  
ID ADD08653 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 501  
ID ADD06902 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 502  
ID ADC83149 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 503  
ID ADD55256 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 504  
ID ADD36060 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 505  
ID ADD56214 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 506  
ID ADD54652 standard; protein; 77 AA.  
DE Human PRO polypeptide #85.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 507  
ID ADE26806 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.

PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 508  
ID ADE26273 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 509  
ID ADF67210 standard; protein; 77 AA.  
DE Human PRO1027 amino acid sequence SEQ ID NO:283.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 510  
ID ADG01061 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 511  
ID ADG08614 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 512  
ID ADG02682 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 513  
ID ADG01389 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 514  
ID ADF95564 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 515  
ID ADF95235 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 516  
ID ADG12379 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 517  
ID ADH24088 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 518  
ID ADH34114 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 519  
ID ADH29947 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 520  
ID ADH23918 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 521  
ID ADH09039 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 522  
ID ADG83322 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 523  
ID ADH24598 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 524  
ID ADH37454 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 525  
ID ADH02043 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 526  
ID ADH37624 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 527  
ID ADG85662 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 528  
ID ADH24258 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 529  
ID ADH38552 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 530  
ID ADG83673 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 531  
ID ADH29481 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 532  
ID ADH27597 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 533  
ID ADH37794 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 534  
ID ADH37971 standard; protein; 77 AA.  
DE Human secreted and transmembrane protein PRO1027.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 535  
ID ADH02043 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

ID ADH57391 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 536  
ID ADH53533 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 537  
ID ADH53703 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 538  
ID ADH52039 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 539  
ID ADH49894 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 540  
ID ADI25404 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 541  
ID ADH90197 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 542  
ID ADI25574 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 543  
ID ADH97748 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 544  
ID ADI35464 standard; protein; 77 AA.

DE Human PRO polypeptide #85.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 545  
ID ADI03596 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 546  
ID ADI11953 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 547  
ID ADH90027 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 548  
ID ADH99956 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 549  
ID ADH98428 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 550  
ID ADI1103 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 551  
ID ADI11613 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 552  
ID ADH98258 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 553  
ID ADH98598 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181708-A1.  
PD 25-SEP-2003.

Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 563  
ID ADH97918 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 564  
ID AD101303 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003190569-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 565  
ID AD101998 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 566  
ID AD103256 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 567  
ID AD111443 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
FN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 568  
ID AD102345 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 569  
ID AD111783 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
FN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 570  
ID AD105420 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 571  
ID ADH79492 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
FN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 572  
ID ADI19449 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 573  
ID ADI05250 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 574  
ID ADH79662 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 575  
ID ADI01488 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 576  
ID ADI01658 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 577  
ID ADI01828 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 578  
ID ADH79832 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 579  
ID ADI04650 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 580  
ID ADI02786 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 581  
ID ADH78105 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 582  
ID ADI25744 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 583  
ID ADI25914 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 584  
ID ADK65426 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 585  
ID ADH98768 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 586  
ID ADH80009 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 587  
ID ADL32820 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 588  
ID ADM30354 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 589  
ID ADL93740 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 7; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 590

ID ADC52194 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 591  
ID ADE74351 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 592  
ID ADE74963 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein (PRO) #107.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 593  
ID ADF35409 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 594  
ID ADG11659 standard; protein; 77 AA.  
DE Human PRO1027 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 595  
ID ADF96176 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 596  
ID ADG04447 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 597  
ID ADG06067 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 598  
ID ADH06626 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 599  
ID ADH06456 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 600  
ID ADG68877 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 601  
ID ADH27767 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 602  
ID ADH3740 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 603  
ID ADH25108 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 604  
ID ADG82863 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 605  
ID ADH02383 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 606  
ID ADH07990 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 607  
ID ADG69387 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 608  
ID ADH39208 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;

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Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 609
ID ADH26144 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 610
ID ADG83948 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 611
ID ADH19529 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US200322866-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 612
ID ADG85492 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003168848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 613
ID ADH06286 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 614
ID ADH30116 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 615
ID ADH24428 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 616
ID ADH3113 standard; protein; 77 AA.
DE Human PRO polypeptide #107.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 617
ID ADG69557 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 618
ID ADH07820 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 619
ID ADG85832 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 620
ID ADH39378 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 621
ID ADH33570 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 622
ID ADH33910 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 623
ID ADH01120 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 624
ID ADG69727 standard; protein; 77 AA.
DE Novel human secreted and transmembrane protein PRO1027.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 625
ID ADH21022 standard; protein; 77 AA.
DE Human secreted/transmembrane protein PRO1027.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 626
ID ADH02213 standard; protein; 77 AA.
DE Human PRO polypeptide #28.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 410; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
RESULT 627
ID ADG69217 standard; protein; 77 AA.
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DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 628  
ID ADG86002 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 629  
ID ADH44938 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 630  
ID ADH39555 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 631  
ID ADH20062 standard; protein; 77 AA.  
DE Human secreted/transmembrane protein PRO1027.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 632  
ID ADH02553 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 633  
ID ADG69047 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 634  
ID ADH07650 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 635  
ID ADG86172 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 636  
ID ADH24768 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.

PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 637  
ID ADH25816 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 638  
ID ADH38382 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 639  
ID ADH57221 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 640  
ID ADH52208 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 641  
ID ADH49575 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 642  
ID ADH90537 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 643  
ID ADI11273 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 644  
ID ADH98938 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 645  
ID ADI02168 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003190699-A1.

PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 646  
ID ADH90707 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 647  
ID ADJ54852 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 648  
ID ADJ98582 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 649  
ID ADJ98752 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 650  
ID ADH78911 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 651  
ID ADJ93145 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 652  
ID ADJ99315 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 653  
ID ADJ98933 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 654  
ID ADH79081 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003181702-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 655  
ID ADK00941 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 656  
ID ADK14462 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 657  
ID ADJ64623 standard; protein; 77 AA.  
DE Human PRO polypeptide #107.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 658  
ID ADM31519 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 659  
ID ADM36566 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 660  
ID ADM40371 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 661  
ID ADM80911 standard; protein; 77 AA.  
DE Human PRO polypeptide #28.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 662  
ID ADN37979 standard; protein; 77 AA.  
DE Novel human secreted and transmembrane protein PRO1027.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 410; DB 8; Length 77;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
RESULT 663  
ID AAB12126 standard; protein; 160 AA.  
DE Hydrophobic domain protein isolated from HT-1080 cells.  
PN WO200029448-A2.  
PD 25-MAY-2000.  
PA (SAGA ) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.  
Query Match 100.0%; Score 410; DB 3; Length 160;  
Best Local Similarity 100.0%; Pred. No. 5.2e-44;  
RESULT 664  
ID ABB11987 standard; peptide; 170 AA.  
DE Human secreted protein homologue, SEQ ID NO:2357.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 100.0%; Score 410; DB 4; Length 170;  
Best Local Similarity 100.0%; Pred. No. 5.5e-44;  
RESULT 665  
ID AAY35997 standard; protein; 160 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 382.  
PN WO9331236-A2.  
PD 24-JUN-1999.  
PA (GEST) GENSET.  
Query Match 98.5%; Score 404; DB 2; Length 160;  
Best Local Similarity 98.7%; Pred. No. 3e-43;  
RESULT 666  
ID ADP19305 standard; protein; 160 AA.  
DE Human secreted polypeptide #156.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST) GENSET SA.  
Query Match 98.5%; Score 404; DB 8; Length 160;  
Best Local Similarity 98.7%; Pred. No. 3e-43;  
RESULT 667  
ID ABP75976 standard; protein; 77 AA.  
DE Human GENSET protein SEQ ID 183.  
PN WO200283898-A1.  
PD 24-OCT-2002.  
PA (GEST) GENSET.  
Query Match 96.1%; Score 394; DB 6; Length 77;  
Best Local Similarity 97.4%; Pred. No. 2.5e-42;  
RESULT 668  
ID ABP76142 standard; protein; 77 AA.  
DE Human GENSET protein SEQ ID 468.  
PN WO200283898-A1.  
PD 24-OCT-2002.  
PA (GEST) GENSET.  
Query Match 96.1%; Score 394; DB 6; Length 77;  
Best Local Similarity 97.4%; Pred. No. 2.5e-42;  
RESULT 669  
ID ABB89647 standard; protein; 124 AA.  
DE Human polypeptide SEQ ID NO 2023.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 74.6%; Score 306; DB 5; Length 124;  
Best Local Similarity 70.1%; Pred. No. 7.1e-31;  
RESULT 670  
ID AAM39275 standard; protein; 159 AA.  
DE Human polypeptide SEQ ID NO 2420.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 74.6%; Score 306; DB 4; Length 159;  
Best Local Similarity 70.1%; Pred. No. 9.4e-31;  
RESULT 671  
ID AAG89299 standard; protein; 159 AA.  
DE Human secreted protein, SEQ ID NO: 419.  
PN WO200142451-A2.  
PD 14-JUN-2001.  
PA (GEST) GENSET.  
Query Match 74.6%; Score 306; DB 4; Length 159;  
Best Local Similarity 70.1%; Pred. No. 9.4e-31;  
RESULT 672  
ID ADP5700 standard; protein; 159 AA.  
DE Human PRO protein sequence SEQ ID NO:1676.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 74.6%; Score 306; DB 8; Length 159;  
Best Local Similarity 70.1%; Pred. No. 9.4e-31;  
RESULT 673  
ID AAM41061 standard; protein; 203 AA.  
DE Human polypeptide SEQ ID NO 5992.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 74.6%; Score 306; DB 4; Length 203;  
Best Local Similarity 70.1%; Pred. No. 1.2e-30;  
RESULT 674  
ID ADP76452 standard; protein; 178 AA.  
DE Novel human secreted and transmembrane protein SeqID 126.  
PN WO2003072035-A2.  
PD 04-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 72.7%; Score 298; DB 7; Length 178;  
Best Local Similarity 68.8%; Pred. No. 1.1e-29;  
RESULT 675  
ID ADP14033 standard; protein; 178 AA.  
DE Human NF-kappaB pathway-associated protein SeqID34.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 72.7%; Score 298; DB 8; Length 178;  
Best Local Similarity 68.8%; Pred. No. 1.1e-29;  
RESULT 676  
ID ABB71351 standard; protein; 163 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40845.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NV.  
Query Match 58.5%; Score 240; DB 4; Length 163;  
Best Local Similarity 61.8%; Pred. No. 2.5e-22;  
RESULT 677  
ID AAY31835 standard; protein; 179 AA.  
DE Human foetal kidney secreted protein pk266\_4.  
PN WO9947555-A1.  
PD 23-SEP-1999.  
PA (GEMY) GENETICS INST INC.  
Query Match 52.7%; Score 216; DB 2; Length 179;  
Best Local Similarity 74.5%; Pred. No. 3.3e-19;  
RESULT 678  
ID AAG41866 standard; protein; 126 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52142.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 35.9%; Score 147; DB 3; Length 126;  
Best Local Similarity 41.4%; Pred. No. 1.4e-10;  
RESULT 679  
ID AAG41865 standard; protein; 163 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52141.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 35.9%; Score 147; DB 3; Length 163;  
Best Local Similarity 41.4%; Pred. No. 1.9e-10;  
RESULT 680  
ID AAG41864 standard; protein; 165 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52140.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 35.9%; Score 147; DB 3; Length 165;  
Best Local Similarity 41.4%; Pred. No. 1.9e-10;  
RESULT 681  
ID AAG52603 standard; protein; 573 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66888.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 21.0%; Score 86; DB 3; Length 573;  
Best Local Similarity 32.8%; Pred. No. 0.046;  
RESULT 682  
ID AAG52602 standard; protein; 663 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66887.

PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 21.0%; Score 86; DB 3; Length 663;  
Best Local Similarity 32.8%; Pred. No. 0.055;  
RESULT 683  
ID AAG52601 standard; protein; 717 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66886.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 21.0%; Score 86; DB 3; Length 717;  
Best Local Similarity 32.8%; Pred. No. 0.06;  
RESULT 684  
ID AAG36124 standard; protein; 135 AA.  
DE Zea mays protein fragment SEQ ID NO: 44225.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 20.6%; Score 84.5; DB 3; Length 135;  
Best Local Similarity 30.5%; Pred. No. 0.014;  
RESULT 685  
ID AAG36123 standard; protein; 225 AA.  
DE Zea mays protein fragment SEQ ID NO: 44224.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 20.6%; Score 84.5; DB 3; Length 225;  
Best Local Similarity 30.5%; Pred. No. 0.025;  
RESULT 686  
ID AAG36122 standard; protein; 252 AA.  
DE Zea mays protein fragment SEQ ID NO: 44223.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 20.6%; Score 84.5; DB 3; Length 252;  
Best Local Similarity 30.5%; Pred. No. 0.028;  
RESULT 687  
ID AAG47038 standard; protein; 220 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59244.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 20.2%; Score 83; DB 3; Length 220;  
Best Local Similarity 30.9%; Pred. No. 0.038;  
RESULT 688  
ID AAG47037 standard; protein; 227 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59243.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 20.2%; Score 83; DB 3; Length 227;  
Best Local Similarity 30.9%; Pred. No. 0.039;  
RESULT 689  
ID AAG47036 standard; protein; 230 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59242.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 20.2%; Score 83; DB 3; Length 230;  
Best Local Similarity 30.9%; Pred. No. 0.04;  
RESULT 690  
ID ABM67329 standard; protein; 1175 AA.  
DE Photobacterium luminescens protein sequence #426.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 19.9%; Score 81.5; DB 6; Length 1175;  
Best Local Similarity 31.6%; Pred. No. 0.39;  
RESULT 691  
ID ABU28937 standard; protein; 1158 AA.  
DE Protein encoded by Prokaryotic essential gene #14464.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 19.8%; Score 81; DB 6; Length 1158;  
Best Local Similarity 32.9%; Pred. No. 0.45;  
RESULT 692  
ID AAG30733 standard; protein; 381 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36795.

PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 19.3%; Score 79; DB 3; Length 381;  
Best Local Similarity 27.3%; Pred. No. 0.23;  
RESULT 693  
ID AAG30732 standard; protein; 383 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36794.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 19.3%; Score 79; DB 3; Length 383;  
Best Local Similarity 27.3%; Pred. No. 0.23;  
RESULT 694  
ID AAG30731 standard; protein; 385 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36793.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 19.3%; Score 79; DB 3; Length 385;  
Best Local Similarity 27.3%; Pred. No. 0.23;  
RESULT 695  
ID ABG30126 standard; protein; 1067 AA.  
DE Novel human diagnostic protein #30117.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 17.6%; Score 72; DB 4; Length 1067;  
Best Local Similarity 31.3%; Pred. No. 5.7;  
RESULT 696  
ID ABG29905 standard; protein; 1222 AA.  
DE Novel human diagnostic protein #29896.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 17.6%; Score 72; DB 4; Length 1222;  
Best Local Similarity 31.3%; Pred. No. 6.7;  
RESULT 697  
ID ABG15851 standard; protein; 1222 AA.  
DE Novel human diagnostic protein #15842.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 17.6%; Score 72; DB 4; Length 1222;  
Best Local Similarity 31.3%; Pred. No. 6.7;  
RESULT 698  
ID ABH68652 standard; protein; 1006 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32748.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 17.2%; Score 70.5; DB 4; Length 1006;  
Best Local Similarity 29.2%; Pred. No. 8.3;  
RESULT 699  
ID AAU10558 standard; protein; 360 AA.  
DE Human interleukin 8 receptor beta (IL8RB) variant polypeptide.  
PN WO200179221-A2.  
PD 25-OCT-2001.  
PA (GENA-) GENAISSANCE PHARM INC.  
Query Match 16.6%; Score 68; DB 5; Length 360;  
Best Local Similarity 22.6%; Pred. No. 5.4;  
RESULT 700  
ID ABO6182 standard; protein; 404 AA.  
DE Klebsiella pneumoniae polypeptide seqid 11699.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 16.2%; Score 66.5; DB 7; Length 404;  
Best Local Similarity 26.3%; Pred. No. 9.6;  
RESULT 701  
ID ABU31563 standard; protein; 263 AA.  
DE Protein encoded by Prokaryotic essential gene #17090.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 16.1%; Score 66; DB 6; Length 263;

Best Local Similarity 37.5%; Pred. No. 6.8;  
RESULT 702  
ID ABO65873 standard; protein; 289 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12390.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 16.1%; Score 66; DB 7; Length 289;  
Best Local Similarity 37.5%; Pred. No. 7.6;  
RESULT 703  
ID AAB41282 standard; protein; 107 AA.  
DE Human ORFX ORF1046 polypeptide sequence SEQ ID NO:2092.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.9%; Score 65; DB 3; Length 107;  
Best Local Similarity 28.8%; Pred. No. 3.3;  
RESULT 704  
ID ABUL8961 standard; protein; 484 AA.  
DE Protein encoded by Prokaryotic essential gene #4488.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.9%; Score 65; DB 6; Length 484;  
Best Local Similarity 33.3%; Pred. No. 18;  
RESULT 705  
ID ADF75261 standard; protein; 575 AA.  
DE Thale cress protein essential for plant growth and development SeqID78.  
PN WO2003074653-A2.  
PD 12-SEP-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 15.7%; Score 64.5; DB 7; Length 575;  
Best Local Similarity 26.0%; Pred. No. 26;  
RESULT 706  
ID ABO59218 standard; protein; 278 AA.  
DE Human genome derived single exon protein #5452.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 15.6%; Score 64; DB 8; Length 278;  
Best Local Similarity 22.1%; Pred. No. 13;  
RESULT 707  
ID ABO75371 standard; protein; 416 AA.  
DE Pseudomonas aeruginosa polypeptide #7546.  
PN US551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 15.6%; Score 64; DB 7; Length 416;  
Best Local Similarity 38.2%; Pred. No. 21;  
RESULT 708  
ID ABG10021 standard; protein; 546 AA.  
DE Novel human diagnostic protein #10012.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.6%; Score 64; DB 4; Length 546;  
Best Local Similarity 22.1%; Pred. No. 28;  
RESULT 709  
ID ADM87619 standard; protein; 546 AA.  
DE Human EST derived amino acid sequence SEQ ID NO:712.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 15.6%; Score 64; DB 8; Length 546;  
Best Local Similarity 22.1%; Pred. No. 28;  
RESULT 710  
ID ADG74252 standard; protein; 599 AA.  
DE Mouse frizzled protein, SEQ ID No 37.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC) UNIV CALIFORNIA.

Query Match 15.6%; Score 64; DB 7; Length 599;  
Best Local Similarity 22.1%; Pred. No. 31;  
RESULT 711  
ID ADC12742 standard; protein; 619 AA.  
DE Human GPCR protein, SEQ ID No 74.  
PN WO2003000893-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 15.6%; Score 64; DB 7; Length 619;  
Best Local Similarity 22.1%; Pred. No. 32;  
RESULT 712  
ID AAW31274 standard; protein; 685 AA.  
DE Mouse frizzled-8 protein Mfz8 (Wnt receptor).  
PN WO9739357-A1.  
PD 23-OCT-1997.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Query Match 15.6%; Score 64; DB 2; Length 685;  
Best Local Similarity 22.1%; Pred. No. 36;  
RESULT 713  
ID ADG74272 standard; protein; 685 AA.  
DE Mouse frizzled protein, SEQ ID No 57.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 15.6%; Score 64; DB 7; Length 685;  
Best Local Similarity 22.1%; Pred. No. 36;  
RESULT 714  
ID ADO29340 standard; protein; 685 AA.  
DE Mouse GPCR FZD8, SEQ ID NO:441.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 15.6%; Score 64; DB 8; Length 685;  
Best Local Similarity 22.1%; Pred. No. 36;  
RESULT 715  
ID AAU74823 standard; protein; 694 AA.  
DE Human RBPTR 6 protein.  
PN WO200198354-A2.  
PD 27-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.6%; Score 64; DB 5; Length 694;  
Best Local Similarity 22.1%; Pred. No. 37;  
RESULT 716  
ID ABUS5903 standard; protein; 694 AA.  
DE Human protein Frizzled-8.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 15.6%; Score 64; DB 6; Length 694;  
Best Local Similarity 22.1%; Pred. No. 37;  
RESULT 717  
ID ADB75320 standard; protein; 694 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 15.6%; Score 64; DB 7; Length 694;  
Best Local Similarity 22.1%; Pred. No. 37;  
RESULT 718  
ID ADG74271 standard; protein; 694 AA.  
DE Human frizzled protein, SEQ ID No 56.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 15.6%; Score 64; DB 7; Length 694;  
Best Local Similarity 22.1%; Pred. No. 37;  
RESULT 719  
ID ADN40026 standard; protein; 694 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C396.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

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Query Match      15.6%; Score 64; DB 7; Length 694;
Best Local Similarity 22.1%; Pred. No. 37;
RESULT 720
ID ADM87157 standard; protein; 694 AA.
DE Human protein SEQ ID NO:250.
PN W02004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match      15.6%; Score 64; DB 8; Length 694;
Best Local Similarity 22.1%; Pred. No. 37;
RESULT 721
ID ADO29339 standard; protein; 694 AA.
DE Human GPCR FZD8, SEQ ID NO:440.
PN W02004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match      15.6%; Score 64; DB 8; Length 694;
Best Local Similarity 22.1%; Pred. No. 37;
RESULT 722
ID ADO22266 standard; protein; 694 AA.
DE Human FZD8 protein (homologue of Drosophila frizzled).
PN W02004042028-A2.
PD 21-MAY-2004.
PA (REGC-) UNIV CALIFORNIA.
Query Match      15.6%; Score 64; DB 8; Length 694;
Best Local Similarity 22.1%; Pred. No. 37;
RESULT 723
ID ADR46693 standard; protein; 694 AA.
DE Cancer-associated protein, SEQ ID 106.
PN W02004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match      15.6%; Score 64; DB 8; Length 694;
Best Local Similarity 22.1%; Pred. No. 37;
RESULT 724
ID ASG24617 standard; protein; 403 AA.
DE Novel human diagnostic protein #24608.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match      15.5%; Score 63.5; DB 4; Length 403;
Best Local Similarity 29.5%; Pred. No. 23;
RESULT 725
ID AAU58372 standard; protein; 409 AA.
DE Propionibacterium acnes immunogenic protein #19268.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match      15.5%; Score 63.5; DB 4; Length 409;
Best Local Similarity 33.3%; Pred. No. 23;
RESULT 726
ID ASM54891 standard; protein; 409 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #19567.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match      15.5%; Score 63.5; DB 6; Length 409;
Best Local Similarity 33.3%; Pred. No. 23;
RESULT 727
ID ABP38658 standard; protein; 74 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3503.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match      15.4%; Score 63; DB 5; Length 74;
Best Local Similarity 36.5%; Pred. No. 3.9;
RESULT 728
ID ADS05168 standard; protein; 74 AA.
DE Staphylococcus epidermidis polypeptide seqid 4463.
PN US2004147734-A1.
PD 23-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.

Query Match      15.4%; Score 63; DB 8; Length 74;
Best Local Similarity 36.5%; Pred. No. 3.9;
RESULT 729
ID AAQ02082 standard; protein; 71 AA.
DE Human polypeptide SEQ ID NO 15974.
PN W0200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match      15.2%; Score 62.5; DB 4; Length 71;
Best Local Similarity 25.0%; Pred. No. 4.4;
RESULT 730
ID ABU45593 standard; protein; 412 AA.
DE Protein encoded by Prokaryotic essential gene #31120.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      15.2%; Score 62.5; DB 6; Length 412;
Best Local Similarity 26.6%; Pred. No. 32;
RESULT 731
ID ABU48248 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #33775.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match      15.2%; Score 62.5; DB 6; Length 438;
Best Local Similarity 26.6%; Pred. No. 34;
RESULT 732
ID AAU07131 standard; protein; 2402 AA.
DE Porcine reproductive and respiratory virus, PRRSV, ORF1a.
PN W0200159077-A1.
PD 16-AUG-2001.
PA (MINU-) UNIV MINNESOTA.
PA (COLL/) COLLINS J E.
PA (FAAB/) FAABERG K S.
PA (ROSS/) ROSSOW K D.
Query Match      15.2%; Score 62.5; DB 4; Length 2402;
Best Local Similarity 30.1%; Pred. No. 2.3e+02;
RESULT 733
ID ADC87597 standard; protein; 280 AA.
DE Human GPCR protein SEQ ID NO:2050.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match      15.1%; Score 62; DB 7; Length 280;
Best Local Similarity 26.1%; Pred. No. 24;
RESULT 734
ID AAW29662 standard; protein; 366 AA.
DE Homo sapiens CN483_2 clone secreted protein.
PN W09830695-A2.
PD 16-JUL-1998.
PA (GEMY-) GENETICS INST INC.
Query Match      15.1%; Score 62; DB 2; Length 366;
Best Local Similarity 24.2%; Pred. No. 32;
RESULT 735
ID AAY02384 standard; protein; 551 AA.
DE Polypeptide identified by the signal sequence trap method.
PN W09918126-A1.
PD 15-APR-1999.
PA (ONCY-) ONO PHARM CO LTD.
Query Match      15.1%; Score 62; DB 2; Length 551;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 736
ID ABP75790 standard; protein; 565 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 974.
PN W0200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match      15.1%; Score 62; DB 6; Length 565;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 737
ID AAB18975 standard; protein; 578 AA.
DE Amino acid sequence of a human transmembrane protein.

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PN WO200056891-A2.  
PD 28-SEP-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 15.1%; Score 62; DB 3; Length 578;  
Best Local Similarity 24.2%; Pred. No. 54;  
RESULT 738  
ID AAE34057 standard; protein; 694 AA.  
DE F2D 8 protein.  
PN WO200209092-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 15.1%; Score 62; DB 6; Length 694;  
Best Local Similarity 22.1%; Pred. No. 66;  
RESULT 739  
ID ABB17549 standard; protein; 92 AA.  
DE Human nervous system related polypeptide SEQ ID NO 6206.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 15.0%; Score 61.5; DB 4; Length 92;  
Best Local Similarity 35.3%; Pred. No. 7.8;  
RESULT 740  
ID AAG72963 standard; protein; 316 AA.  
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2645.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match 15.0%; Score 61.5; DB 4; Length 316;  
Best Local Similarity 21.2%; Pred. No. 32;  
RESULT 741  
ID ABM67481 standard; protein; 320 AA.  
DE Photorhabdus luminescens protein sequence #578.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
PA (INSP) INST PASTEUR.  
Query Match 15.0%; Score 61.5; DB 6; Length 820;  
Best Local Similarity 27.0%; Pred. No. 32;  
RESULT 742  
ID ABO19498 standard; protein; 326 AA.  
DE Mouse GPCR MOR 3' Beta 1.  
PN US2003022237-A1.  
PD 30-JAN-2003.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G A.  
PA (RAMA/) RAMANATHAN C S.  
PA (HAWK/) HAWKEN D R.  
PA (CACA/) CACACE A.  
PA (BARB/) BARBER L.  
PA (KORN/) KORNACKER M G.  
Query Match 15.0%; Score 61.5; DB 6; Length 326;  
Best Local Similarity 21.2%; Pred. No. 33;  
RESULT 743  
ID ADQ98156 standard; protein; 326 AA.  
DE Mouse olfactory receptor 3' beta 1.  
PN US2004121330-A1.  
PD 24-JUN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G A.  
PA (RAMA/) RAMANATHAN C S.  
PA (HAWK/) HAWKEN D R.  
PA (CACA/) CACACE A.  
PA (BARB/) BARBER L E.  
PA (KORN/) KORNACKER M G.  
PA (RYSE/) RYSECK R.  
PA (BENN/) BENNETT K L.  
PA (NELS/) NELSON T C.  
Query Match 15.0%; Score 61.5; DB 8; Length 326;  
Best Local Similarity 21.2%; Pred. No. 33;  
RESULT 744  
ID AAG72618 standard; protein; 339 AA.  
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2299.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match 15.0%; Score 61.5; DB 4; Length 339;  
Best Local Similarity 21.2%; Pred. No. 34;  
RESULT 745  
ID ABU28157 standard; protein; 417 AA.  
DE Protein encoded by Prokaryotic essential gene #13684.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 15.0%; Score 61.5; DB 6; Length 417;  
Best Local Similarity 34.5%; Pred. No. 43;  
RESULT 746  
ID ABB53979 standard; protein; 420 AA.  
DE Lactococcus lactis protein ftsM1.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 15.0%; Score 61.5; DB 5; Length 420;  
Best Local Similarity 25.3%; Pred. No. 44;  
RESULT 747  
ID ABO76137 standard; protein; 464 AA.  
DE Pseudomonas aeruginosa polypeptide #8312.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 15.0%; Score 61.5; DB 7; Length 464;  
Best Local Similarity 25.4%; Pred. No. 49;  
RESULT 748  
ID AAR29939 standard; protein; 2396 AA.  
DE Deduced from Lelystad Agent genome ORF 1A.  
PN WO9221375-A1.  
PD 10-DEC-1992.  
PA (DIER-) STICHTING CENT DIERGENEESKUNDIG INST.  
Query Match 15.0%; Score 61.5; DB 2; Length 2396;  
Best Local Similarity 30.1%; Pred. No. 3.1e+02;  
RESULT 749  
ID ADH74482 standard; protein; 3859 AA.  
DE Lelystad virus ORFlab protein.  
PN US2003219732-A1.  
PD 27-NOV-2003.  
PA (VRIJ/) VAN RIJN P A.  
PA (MEUL/) MEULENBERG J J M.  
Query Match 15.0%; Score 61.5; DB 8; Length 3859;  
Best Local Similarity 30.1%; Pred. No. 5.3e+02;  
RESULT 750  
ID ABP75625 standard; protein; 72 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 809.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 14.9%; Score 61; DB 6; Length 72;  
Best Local Similarity 35.3%; Pred. No. 6.9;  
RESULT 751  
ID ABB81433 standard; protein; 118 AA.  
DE Human prostate specific protein (PSP) SEQ ID NO:205.  
PN WO200242499-A2.  
PD 30-MAY-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 14.9%; Score 61; DB 5; Length 118;  
Best Local Similarity 34.0%; Pred. No. 12;  
RESULT 752  
ID ADC87275 standard; protein; 306 AA.  
DE Human GPCR protein SEQ ID NO:1728.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 14.9%; Score 61; DB 7; Length 306;  
Best Local Similarity 25.6%; Pred. No. 35;  
RESULT 753

ID ADC01153 standard; protein; 373 AA.  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1197.  
PN JF2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match 14.9%; Score 61; DB 7; Length 373;  
Best Local Similarity 29.4%; Pred. No. 44;  
RESULT 754  
ID ADN23301 standard; protein; 392 AA.  
DE Bacterial polypeptide #5954.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.9%; Score 61; DB 8; Length 392;  
Best Local Similarity 29.3%; Pred. No. 47;  
RESULT 755  
ID ABP41946 standard; protein; 584 AA.  
DE Human ovarian antigen HHEND31. SEQ ID NO:3078.  
PN WO20020677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.9%; Score 61; DB 5; Length 584;  
Best Local Similarity 24.2%; Pred. No. 73;  
RESULT 756  
ID AAU14794 standard; protein; 2298 AA.  
DE Novel bone marrow polypeptide #193.  
PN WO200157187-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.9%; Score 61; DB 4; Length 2298;  
Best Local Similarity 29.1%; Pred. No. 3.4e+02;  
RESULT 757  
ID AAU14720 standard; protein; 2301 AA.  
DE Novel bone marrow polypeptide #119.  
PN WO200157187-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.9%; Score 61; DB 4; Length 2301;  
Best Local Similarity 29.1%; Pred. No. 3.4e+02;  
RESULT 758  
ID ABM73281 standard; protein; 339 AA.  
DE Staphylococcus aureus protein #2521.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 14.8%; Score 60.5; DB 6; Length 339;  
Best Local Similarity 39.0%; Pred. No. 46;  
RESULT 759  
ID ASU32397 standard; protein; 436 AA.  
DE Protein encoded by Prokaryotic essential gene #17924.  
PN WO200271183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.8%; Score 60.5; DB 6; Length 436;  
Best Local Similarity 26.5%; Pred. No. 61;  
RESULT 760  
ID ABO63574 standard; protein; 441 AA.  
DE Klebsiella pneumoniae polypeptide seqid 10091.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 14.8%; Score 60.5; DB 7; Length 441;  
Best Local Similarity 26.5%; Pred. No. 62;  
RESULT 761  
ID ABM67254 standard; protein; 444 AA.  
DE Photorhabdus luminescens protein sequence #351.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 14.8%; Score 60.5; DB 6; Length 444;  
Best Local Similarity 32.6%; Pred. No. 62;  
RESULT 762  
ID ABG96496 standard; protein; 2396 AA.  
DE PRRS virus ORFla protein sequence.  
PN WO200272802-A2.  
PD 19-SEP-2002.  
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
Query Match 14.8%; Score 60.5; DB 5; Length 2396;  
Best Local Similarity 30.1%; Pred. No. 4.2e+02;  
RESULT 763  
ID ADI21643 standard; protein; 137 AA.  
DE Novel human polypeptide #122.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.6%; Score 60; DB 7; Length 137;  
Best Local Similarity 24.4%; Pred. No. 19;  
RESULT 764  
ID ADI95325 standard; protein; 221 AA.  
DE OSPF-related SARS coronavirus matrix protein.  
PN WO2004002415-A2.  
PD 08-JAN-2004.  
PA (DAND) DANA FARMER CANCER INST INC.  
Query Match 14.6%; Score 60; DB 8; Length 221;  
Best Local Similarity 24.0%; Pred. No. 33;  
RESULT 765  
ID ADM20157 standard; protein; 248 AA.  
DE Protein encoded by novel human channel/transporter gene #268 clone 2.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.6%; Score 60; DB 4; Length 248;  
Best Local Similarity 37.9%; Pred. No. 37;  
RESULT 766  
ID ABB83433 standard; protein; 387 AA.  
DE Human repeated protein 42.57.  
PN CN1339463-A.  
PD 13-MAR-2002.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 14.6%; Score 60; DB 5; Length 387;  
Best Local Similarity 24.4%; Pred. No. 62;  
RESULT 767  
ID AAO26227 standard; protein; 387 AA.  
DE MDT related human protein SEQ ID No 5.  
PN WO200296951-A1.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 14.6%; Score 60; DB 6; Length 387;  
Best Local Similarity 24.4%; Pred. No. 62;  
RESULT 768  
ID ADM04402 standard; protein; 387 AA.  
DE Human protein of the invention SEQ ID NO:3087.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 14.6%; Score 60; DB 7; Length 387;  
Best Local Similarity 24.4%; Pred. No. 62;  
RESULT 769  
ID ADO20493 standard; protein; 387 AA.  
DE Human PRO polypeptide #690.  
PN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 14.6%; Score 60; DB 8; Length 387;  
Best Local Similarity 24.4%; Pred. No. 62;  
RESULT 770  
ID ABB66583 standard; protein; 472 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 26541.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.

Query Match 14.6%; Score 60; DB 4; Length 472;  
Best Local Similarity 33.3%; Pred. No. 77;  
RESULT 771  
ID ADG74253 standard; protein; 516 AA.  
DE Human frizzled protein, SEQ ID NO 38.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.6%; Score 60; DB 7; Length 516;  
Best Local Similarity 23.1%; Pred. No. 85;  
RESULT 772  
ID ADQ07984 standard; protein; 526 AA.  
DE Human hypothetical protein FLJ20371-encoding cDNA.  
PN WO2004061123-A2.  
PD 22-JUL-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 14.6%; Score 60; DB 8; Length 526;  
Best Local Similarity 26.4%; Pred. No. 87;  
RESULT 773  
ID ADP25065 standard; protein; 526 AA.  
DE PRO polypeptide SEQ ID NO:2243.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 14.6%; Score 60; DB 8; Length 526;  
Best Local Similarity 26.4%; Pred. No. 87;  
RESULT 774  
ID AAW31271 standard; protein; 585 AA.  
DE Human frizzled-5 protein Mfz5 (Wnt receptor).  
PN WO9739357-A1.  
PD 23-OCT-1997.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (UJJO ) UNIV JOHNS HOPKINS.  
Query Match 14.6%; Score 60; DB 2; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 775  
ID ABEU5900 standard; protein; 585 AA.  
DE Human protein Frizzled-5.  
PN WO20027204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 14.6%; Score 60; DB 6; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 776  
ID AAE34054 standard; protein; 585 AA.  
DE FZD5 protein.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 14.6%; Score 60; DB 6; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 777  
ID ABG75231 standard; protein; 585 AA.  
DE Hair papilla cell growth promoter related human protein SEQ ID NO: 4.  
PN WO2003086334-A1.  
PD 23-OCT-2003.  
PA (TAIS ) TAISHO PHARM CO LTD.  
Query Match 14.6%; Score 60; DB 7; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 778  
ID ADG74266 standard; protein; 585 AA.  
DE Human frizzled protein, SEQ ID NO 51.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.6%; Score 60; DB 7; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 779  
ID ADO29333 standard; protein; 585 AA.  
DE Human GPCR FZD5, SEQ ID NO:434.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.

Query Match 14.6%; Score 60; DB 8; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 780  
ID ADO22260 standard; protein; 585 AA.  
DE Human FZD5 protein (homologue of Drosophila frizzled).  
PN WO2004040208-A2.  
PD 21-MAY-2004.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.6%; Score 60; DB 8; Length 585;  
Best Local Similarity 23.1%; Pred. No. 98;  
RESULT 781  
ID ADI21171 standard; protein; 601 AA.  
DE Novel human protein #146.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.6%; Score 60; DB 7; Length 601;  
Best Local Similarity 24.4%; Pred. No. 1e+02;  
RESULT 782  
ID ABG29043 standard; protein; 728 AA.  
DE Novel human diagnostic protein #29034.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.6%; Score 60; DB 4; Length 728;  
Best Local Similarity 26.9%; Pred. No. 1.3e+02;  
RESULT 783  
ID AAO01208 standard; protein; 124 AA.  
DE Human polypeptide SEQ ID NO 15100.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.5%; Score 59.5; DB 4; Length 124;  
Best Local Similarity 30.2%; Pred. No. 20;  
RESULT 784  
ID ADL04363 standard; protein; 134 AA.  
DE M. catarrhalis protein #129.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 14.5%; Score 59.5; DB 8; Length 134;  
Best Local Similarity 30.8%; Pred. No. 22;  
RESULT 785  
ID AAR60133 standard; protein; 175 AA.  
DE Human G-CSF.  
PN WO9418236-A1.  
PD 18-AUG-1994.  
PA (AMRA-) AMRAD CORP LTD.  
Query Match 14.5%; Score 59.5; DB 2; Length 175;  
Best Local Similarity 29.1%; Pred. No. 29;  
RESULT 786  
ID AAY74779 standard; protein; 214 AA.  
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1032.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 14.5%; Score 59.5; DB 3; Length 214;  
Best Local Similarity 28.3%; Pred. No. 37;  
RESULT 787  
ID AAY74780 standard; protein; 217 AA.  
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1034.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 14.5%; Score 59.5; DB 3; Length 217;  
Best Local Similarity 28.3%; Pred. No. 37;  
RESULT 788  
ID AAY74783 standard; protein; 221 AA.  
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1040.  
PN WO9957280-A2.  
PD 11-NOV-1999.

PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 14.5%; Score 59.5; DB 3; Length 221;  
Best Local Similarity 28.3%; Pred. No. 38;  
RESULT 789  
ID RAY74782 standard; protein; 221 AA.  
DE Neisseria meningitidis ORF 259 protein sequence SEQ ID NO:1038.  
PN WO957280-A2.  
PD 11-NOV-1999.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 14.5%; Score 59.5; DB 3; Length 221;  
Best Local Similarity 28.3%; Pred. No. 38;  
RESULT 790  
ID ABB63281 standard; protein; 351 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16635.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 14.5%; Score 59.5; DB 4; Length 351;  
Best Local Similarity 32.1%; Pred. No. 64;  
RESULT 791  
ID ABB63284 standard; protein; 351 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16644.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 14.5%; Score 59.5; DB 4; Length 351;  
Best Local Similarity 32.1%; Pred. No. 64;  
RESULT 792  
ID AAB01035 standard; protein; 551 AA.  
DE Human death domain-containing receptor (DPCR) protein from HODDX59 clone.  
PN WO200129063-A2.  
PD 26-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.5%; Score 59.5; DB 4; Length 551;  
Best Local Similarity 31.7%; Pred. No. 1.1e+02;  
RESULT 793  
ID AAG75604 standard; protein; 705 AA.  
DE Human colon cancer antigen protein SEQ ID NO:6368.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.5%; Score 59.5; DB 4; Length 705;  
Best Local Similarity 31.7%; Pred. No. 1.4e+02;  
RESULT 794  
ID ADC06850 standard; protein; 1142 AA.  
DE Kidins 220Pc-related protein Pc473.  
PN WO2003064599-A2.  
PD 07-AUG-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 14.5%; Score 59.5; DB 7; Length 1142;  
Best Local Similarity 31.7%; Pred. No. 2.4e+02;  
RESULT 795  
ID ADC06846 standard; protein; 1184 AA.  
DE Human Kidins220Pc protein XM\_045362.  
PN WO2003064599-A2.  
PD 07-AUG-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 14.5%; Score 59.5; DB 7; Length 1184;  
Best Local Similarity 31.7%; Pred. No. 2.5e+02;  
RESULT 796  
ID AAM39025 standard; protein; 1715 AA.  
DE Human polypeptide SEQ ID NO 2170.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.5%; Score 59.5; DB 4; Length 1715;  
Best Local Similarity 31.7%; Pred. No. 3.8e+02;  
RESULT 797  
ID AAM38993 standard; protein; 1715 AA.  
DE Human polypeptide SEQ ID NO 2138.  
PN WO200153312-A1.

PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.5%; Score 59.5; DB 4; Length 1715;  
Best Local Similarity 31.7%; Pred. No. 3.8e+02;  
RESULT 798  
ID RAE25144 standard; protein; 1715 AA.  
DE Human ARMS protein.  
PN WO200250273-A2.  
PD 27-JUN-2002.  
PA (UNY ) UNIV NEW YORK STATE.  
Query Match 14.5%; Score 59.5; DB 5; Length 1715;  
Best Local Similarity 31.7%; Pred. No. 3.8e+02;  
RESULT 799  
ID AAU96840 standard; protein; 1715 AA.  
DE Human kidins220 protein.  
PN WO200220786-A2.  
PD 14-MAR-2002.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 14.5%; Score 59.5; DB 5; Length 1715;  
Best Local Similarity 31.7%; Pred. No. 3.8e+02;  
RESULT 800  
ID RAE32128 standard; protein; 1715 AA.  
DE Human cytoskeleton-associated protein, CSAP-36.  
PN WO200279404-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 14.5%; Score 59.5; DB 6; Length 1715;  
Best Local Similarity 31.7%; Pred. No. 3.8e+02;  
RESULT 801  
ID ADA09888 standard; protein; 1753 AA.  
DE Human receptor and membrane-associated protein REMAP-30, SEQ ID:30.  
PN WO2003070902-A2.  
PD 28-AUG-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 14.5%; Score 59.5; DB 6; Length 1753;  
Best Local Similarity 31.7%; Pred. No. 3.9e+02;  
RESULT 802  
ID ADC06847 standard; protein; 1771 AA.  
DE Human Kidins220Pc protein AB033076.  
PN WO2003064599-A2.  
PD 07-AUG-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 14.5%; Score 59.5; DB 7; Length 1771;  
Best Local Similarity 31.7%; Pred. No. 4e+02;  
RESULT 803  
ID ADB08926 standard; protein; 155 AA.  
DE Alloiococcus otitis antigenic protein SEQ ID NO:2866.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP ) WYETH HOLDINGS CORP.  
Query Match 14.4%; Score 59; DB 6; Length 155;  
Best Local Similarity 31.0%; Pred. No. 29;  
RESULT 804  
ID AAG46085 standard; protein; 174 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57940.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 14.4%; Score 59; DB 3; Length 174;  
Best Local Similarity 35.0%; Pred. No. 34;  
RESULT 805  
ID AAW63009 standard; protein; 244 AA.  
DE Mouse dectin-1.  
PN WO9828332-A2.  
PD 02-JUL-1998.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 14.4%; Score 59; DB 2; Length 244;  
Best Local Similarity 33.3%; Pred. No. 49;  
RESULT 806  
ID ABB82844 standard; protein; 244 AA.  
DE Mouse Dectin-1 polypeptide.  
PN WO200296945-A2.  
PD 05-DEC-2002.  
PA (ISIS-) ISIS INNOVATION LTD.

Query Match 14.4%; Score 59; DB 6; Length 244;  
Best Local Similarity 33.3%; Pred. No. 49;  
RESULT 807  
ID AAE21313 standard; protein; 300 AA.  
DE Mouse MrgA15 (mas-related gene) protein.  
PN WO200183555-A2.  
PD 08-NOV-2001.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 14.4%; Score 59; DB 5; Length 300;  
Best Local Similarity 31.7%; Pred. No. 62;  
RESULT 808  
ID ADH08569 standard; protein; 300 AA.  
DE MrgA15.  
PN WO20040031333-A1.  
PD 08-JAN-2004.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 14.4%; Score 59; DB 8; Length 300;  
Best Local Similarity 31.7%; Pred. No. 62;  
RESULT 809  
ID AAR91225 standard; protein; 328 AA.  
DE Human placenta G-protein coupled receptor protein.  
PN WO9605302-A1.  
PD 22-FEB-1996.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 14.4%; Score 59; DB 2; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 810  
ID AAE04393 standard; protein; 328 AA.  
DE Human P2-purine receptor subtype, P2Y6.  
PN WO200146454-A1.  
PD 28-JUN-2001.  
PA (CORT-) COR THERAPEUTICS INC.  
Query Match 14.4%; Score 59; DB 4; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 811  
ID ABP81869 standard; protein; 328 AA.  
DE Human purine receptor P2Y6 protein SEQ ID NO:1223.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 14.4%; Score 59; DB 6; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 812  
ID ADC37341 standard; protein; 328 AA.  
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 174.  
PN WO2003048202-A2.  
PD 12-JUN-2003.  
PA (ASAH ) ASAH KASEI KK.  
Query Match 14.4%; Score 59; DB 7; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 813  
ID ADD45306 standard; protein; 328 AA.  
DE Human Protein Q15077, SEQ ID NO 10739.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 14.4%; Score 59; DB 7; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 814  
ID ADE38349 standard; protein; 328 AA.  
DE Human protein 2427 amino acid sequence.  
PN WO2003065006-A2.  
PD 07-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.4%; Score 59; DB 7; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 815  
ID ADN39970 standard; protein; 328 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C340.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 14.4%; Score 59; DB 7; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 816  
ID ADO29600 standard; protein; 328 AA.  
DE Human GPCR P2RY6, SEQ ID NO:702.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.4%; Score 59; DB 8; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 817  
ID ADP49195 standard; protein; 328 AA.  
DE Human P2Y6 purinergic receptor protein sequence for odour modulation.  
PN WO2004047749-A2.  
PD 10-JUN-2004.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 14.4%; Score 59; DB 8; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 818  
ID ADR46666 standard; protein; 328 AA.  
DE Cancer-associated protein, SEQ ID 79.  
PN WO2004073657-A2.  
PD 02-SEP-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 14.4%; Score 59; DB 8; Length 328;  
Best Local Similarity 26.9%; Pred. No. 69;  
RESULT 819  
ID ADO29525 standard; protein; 359 AA.  
DE Mouse GPCR IL8RB, SEQ ID NO:627.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.4%; Score 59; DB 8; Length 359;  
Best Local Similarity 23.1%; Pred. No. 76;  
RESULT 820  
ID ABM85488 standard; protein; 369 AA.  
DE Mouse protein sequence MCP2823.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 14.4%; Score 59; DB 7; Length 369;  
Best Local Similarity 23.1%; Pred. No. 78;  
RESULT 821  
ID AAU03816 standard; protein; 376 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #15.  
PN WO200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA ) PHARMACIA & UPJOHN.  
Query Match 14.4%; Score 59; DB 4; Length 376;  
Best Local Similarity 25.7%; Pred. No. 80;  
RESULT 822  
ID ABU50099 standard; protein; 386 AA.  
DE Protein encoded by Prokaryotic essential gene #35626.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.4%; Score 59; DB 6; Length 386;  
Best Local Similarity 37.5%; Pred. No. 82;  
RESULT 823  
ID ADN24200 standard; protein; 399 AA.  
DE Bacterial polypeptide #6853.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.4%; Score 59; DB 8; Length 399;  
Best Local Similarity 25.7%; Pred. No. 86;  
RESULT 824  
ID ABO74175 standard; protein; 473 AA.  
DE Pseudomonas aeruginosa polypeptide #6350.

PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 14.4%; Score 59; DB 7; Length 473;  
Best Local Similarity 23.8%; Pred. No. 1e+02;  
RESULT 825  
ID AAG41250 standard; protein; 612 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51299.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 14.4%; Score 59; DB 3; Length 612;  
Best Local Similarity 35.0%; Pred. No. 1.4e+02;  
RESULT 826  
ID AAG41249 standard; protein; 697 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51298.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 14.4%; Score 59; DB 3; Length 697;  
Best Local Similarity 35.0%; Pred. No. 1.6e+02;  
RESULT 827  
ID AAG41248 standard; protein; 763 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 51297.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 14.4%; Score 59; DB 3; Length 763;  
Best Local Similarity 35.0%; Pred. No. 1.8e+02;  
RESULT 828  
ID AAM83543 standard; protein; 57 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:11136.  
PN W0200157182-A2.  
PD 09-AUG-2001.  
Query Match 14.3%; Score 58.5; DB 4; Length 57;  
Best Local Similarity 35.0%; Pred. No. 11;  
RESULT 829  
ID AAU30233 standard; protein; 246 AA.  
DE Novel human secreted protein #724.  
PN W0200179449-A2.  
PD 25-OCT-2001.  
Query Match 14.3%; Score 58.5; DB 4; Length 246;  
Best Local Similarity 27.1%; Pred. No. 57;  
RESULT 830  
ID ADH09917 standard; protein; 282 AA.  
DE Human host factor protein, SEQ ID No 445.  
PN W02003094847-A2.  
PD 20-NOV-2003.  
Query Match 14.3%; Score 58.5; DB 8; Length 282;  
Best Local Similarity 24.2%; Pred. No. 67;  
RESULT 831  
ID AAY30163 standard; protein; 322 AA.  
DE Human dorsal root receptor 5 hDRR5.  
PN W09932519-A1.  
PD 01-JUL-1999.  
Query Match 14.3%; Score 58.5; DB 2; Length 322;  
Best Local Similarity 30.6%; Pred. No. 78;  
RESULT 832  
ID AEU30868 standard; protein; 358 AA.  
DE Protein encoded by Prokaryotic essential gene #16395.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
Query Match 14.3%; Score 58.5; DB 6; Length 358;  
Best Local Similarity 26.4%; Pred. No. 88;  
RESULT 833  
ID ABR42416 standard; protein; 499 AA.  
DE Human potassium channel Kv1.2.  
PN W02003035690-A2.  
PD 01-MAY-2003.  
Query Match 14.1%; Score 58; DB 5; Length 98;  
Best Local Similarity 41.7%; Pred. No. 23;  
RESULT 842  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Query Match 14.3%; Score 58.5; DB 6; Length 499;  
Best Local Similarity 21.7%; Pred. No. 1.3e+02;  
RESULT 834  
ID AEO85019 standard; protein; 499 AA.  
DE Human cancer-associated protein (CAP) HP07-112.  
PN W02004058146-A2.  
PD 15-JUL-2004.  
Query Match 14.3%; Score 58.5; DB 8; Length 499;  
Best Local Similarity 21.7%; Pred. No. 1.3e+02;  
RESULT 835  
ID ABR43491 standard; protein; 661 AA.  
DE Mouse sweet taste receptor T1R2 protein SEQ ID NO:5.  
PN W02003025137-A2.  
PD 27-MAR-2003.  
Query Match 14.3%; Score 58.5; DB 6; Length 661;  
Best Local Similarity 30.1%; Pred. No. 1.8e+02;  
RESULT 836  
ID AAY77557 standard; protein; 843 AA.  
DE Mouse GPCR-B4 polypeptide.  
PN W0200006593-A1.  
PD 10-FEB-2000.  
Query Match 14.3%; Score 58.5; DB 3; Length 843;  
Best Local Similarity 30.1%; Pred. No. 2.3e+02;  
RESULT 837  
ID ADK90718 standard; protein; 843 AA.  
DE Mouse taste receptor T1R2 protein.  
PN W02003004992-A2.  
PD 16-JAN-2003.  
Query Match 14.3%; Score 58.5; DB 7; Length 843;  
Best Local Similarity 30.1%; Pred. No. 2.3e+02;  
RESULT 838  
ID ADM42817 standard; protein; 843 AA.  
DE Murine taste receptor protein.T1R2 Seqid 61.  
PN W02003100057-A1.  
PD 04-DEC-2003.  
Query Match 14.3%; Score 58.5; DB 8; Length 843;  
Best Local Similarity 30.1%; Pred. No. 2.3e+02;  
RESULT 839  
ID ADP70073 standard; protein; 843 AA.  
DE Mouse T1R2 receptor protein.  
PN JP2004154029-A.  
PD 03-JUN-2004.  
Query Match 14.3%; Score 58.5; DB 8; Length 843;  
Best Local Similarity 30.1%; Pred. No. 2.3e+02;  
RESULT 840  
ID ABP63752 standard; protein; 67 AA.  
DE Human ORF122.  
PN US2002082206-A1.  
PD 27-JUN-2002.  
Query Match 14.3%; Score 58; DB 15;  
Best Local Similarity 28.4%; Pred. No. 15;  
RESULT 841  
ID ADK35554 standard; protein; 98 AA.  
DE Novel human polypeptide SeqID7636.  
PN W0200216439-A2.  
PD 28-FEB-2002.  
Query Match 14.1%; Score 58; DB 5; Length 98;  
Best Local Similarity 41.7%; Pred. No. 23;  
RESULT 842  
PA (HYSE-) HYSEQ INC.

ID AAY74781 standard; protein; 169 AA.  
DE Neisseria gonorrhoeae ORF 259 protein sequence SEQ ID NO:1036.  
PN W09957280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 14.1%; Score 58; DB 3; Length 169;  
Best Local Similarity 26.9%; Pred. No. 43;  
RESULT 843  
ID RAY74778 standard; protein; 216 AA.  
DE Neisseria gonorrhoeae ORF 259 protein sequence SEQ ID NO:1030.  
PN W09957280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 14.1%; Score 58; DB 3; Length 216;  
Best Local Similarity 26.9%; Pred. No. 57;  
RESULT 844  
ID ABP80786 standard; protein; 216 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 8102.  
PN W0200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 14.1%; Score 58; DB 6; Length 216;  
Best Local Similarity 26.9%; Pred. No. 57;  
RESULT 845  
ID RAB96791 standard; protein; 232 AA.  
DE Putative P. abyssi cobalamin-5-phosphate synthase.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Query Match 14.1%; Score 58; DB 4; Length 232;  
Best Local Similarity 46.2%; Pred. No. 62;  
RESULT 846  
ID ADH87199 standard; protein; 234 AA.  
DE Enterococcus faecalis polypeptide #1679.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 14.1%; Score 58; DB 7; Length 234;  
Best Local Similarity 30.8%; Pred. No. 63;  
RESULT 847  
ID ABU39580 standard; protein; 293 AA.  
DE Protein encoded by Prokaryotic essential gene #25107.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.1%; Score 58; DB 6; Length 293;  
Best Local Similarity 35.7%; Pred. No. 81;  
RESULT 848  
ID ABM69224 standard; protein; 294 AA.  
DE Photobacterium luminescens protein sequence #2321.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 14.1%; Score 58; DB 6; Length 294;  
Best Local Similarity 27.9%; Pred. No. 81;  
RESULT 849  
ID ABM67244 standard; protein; 305 AA.  
DE Photobacterium luminescens protein sequence #341.  
PN W0200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 14.1%; Score 58; DB 6; Length 305;  
Best Local Similarity 37.0%; Pred. No. 85;  
RESULT 850  
ID ABU39650 standard; protein; 335 AA.  
DE Protein encoded by Prokaryotic essential gene #25177.  
PN W0200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.1%; Score 58; DB 6; Length 335;  
Best Local Similarity 36.6%; Pred. No. 94;  
RESULT 851  
ID AAU80490 standard; protein; 355 AA.  
DE Rhesus macaque CXCR2 receptor #2.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEDIA INC.  
Query Match 14.1%; Score 58; DB 5; Length 355;  
Best Local Similarity 22.6%; Pred. No. 1e+02;  
RESULT 852  
ID ADD48095 standard; protein; 359 AA.  
DE Rat Protein AAC52961, SEQ ID NO 13793.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 14.1%; Score 58; DB 7; Length 359;  
Best Local Similarity 23.1%; Pred. No. 1e+02;  
RESULT 853  
ID ABB62002 standard; protein; 417 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12798.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 14.1%; Score 58; DB 4; Length 417;  
Best Local Similarity 31.9%; Pred. No. 1.2e+02;  
RESULT 854  
ID ABB66915 standard; protein; 417 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 27537.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 14.1%; Score 58; DB 4; Length 417;  
Best Local Similarity 31.9%; Pred. No. 1.2e+02;  
RESULT 855  
ID RAY42328 standard; protein; 498 AA.  
DE Staphylococcus aureus fntB protein.  
PN W09947662-A1.  
PD 23-SEP-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 14.1%; Score 58; DB 2; Length 498;  
Best Local Similarity 25.4%; Pred. No. 1.5e+02;  
RESULT 856  
ID AAY31821 standard; protein; 498 AA.  
DE Staphylococcus aureus fntB protein.  
PN W09947639-A2.  
PD 23-SEP-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 14.1%; Score 58; DB 2; Length 498;  
Best Local Similarity 25.4%; Pred. No. 1.5e+02;  
RESULT 857  
ID ABM73394 standard; protein; 498 AA.  
DE Staphylococcus aureus protein #2634.  
PN W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 14.1%; Score 58; DB 6; Length 498;  
Best Local Similarity 25.4%; Pred. No. 1.5e+02;  
RESULT 858  
ID ADF43550 standard; protein; 498 AA.  
DE Staphylococcus aureus fntB.  
PN US2003153733-A1.  
PD 14-AUG-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.1%; Score 58; DB 7; Length 498;  
Best Local Similarity 25.4%; Pred. No. 1.5e+02;  
RESULT 859  
ID ADP29710 standard; protein; 537 AA.

DE Human secreted protein SEQ ID #477.  
PN WO2004035732-A2.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 14.1%; Score 58; DB 8; Length 537;  
Best Local Similarity 19.6%; Pred. No. 1.6e+02;  
RESULT 860  
ID ADG74255 standard; protein; 544 AA.  
DE Rat frizzled protein, SEQ ID No 40.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.1%; Score 58; DB 7; Length 544;  
Best Local Similarity 19.6%; Pred. No. 1.6e+02;  
RESULT 861  
ID ABUS5897 standard; protein; 565 AA.  
DE Human protein Frizzled-2.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 14.1%; Score 58; DB 6; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 862  
ID AAE34051 standard; protein; 565 AA.  
DE FZD2 protein.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 14.1%; Score 58; DB 6; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 863  
ID ADP76959 standard; protein; 565 AA.  
DE Novel human secreted and transmembrane protein SeqID 634.  
PN WO2003072035-A2.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 14.1%; Score 58; DB 7; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 865  
ID ADG74261 standard; protein; 565 AA.  
DE Human frizzled protein, SEQ ID No 46.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.1%; Score 58; DB 7; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 866  
ID ADH87897 standard; protein; 565 AA.  
DE Enterococcus faecalis polypeptide #2377.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 14.1%; Score 58; DB 7; Length 565;  
Best Local Similarity 30.0%; Pred. No. 1.7e+02;  
RESULT 867  
ID ADO29327 standard; protein; 565 AA.  
DE Human GPCR FZD2, SEQ ID NO:428.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.1%; Score 58; DB 8; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 868  
ID ADO22254 standard; protein; 565 AA.

DE Human FZD2 protein (homologue of Drosophila frizzled).  
PN WO2004042028-A2.  
PD 21-MAY-2004.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.1%; Score 58; DB 8; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 869  
ID ADO28667 standard; protein; 565 AA.  
DE Human frizzled 2 protein SEQ ID NO:96.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 14.1%; Score 58; DB 8; Length 565;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 870  
ID ADO29328 standard; protein; 570 AA.  
DE Mouse GPCR FZD2, SEQ ID NO:429.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.1%; Score 58; DB 8; Length 570;  
Best Local Similarity 19.6%; Pred. No. 1.7e+02;  
RESULT 871  
ID ABB47273 standard; protein; 572 AA.  
DE Enterococcus faecalis polypeptide Abcll.  
PN WO200179257-A2.  
PD 25-OCT-2001.  
PA (PHYT-) PHYTERA INC.  
Query Match 14.1%; Score 58; DB 4; Length 572;  
Best Local Similarity 30.0%; Pred. No. 1.7e+02;  
RESULT 872  
ID ADO29334 standard; protein; 577 AA.  
DE Mouse GPCR FZD5, SEQ ID NO:435.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.1%; Score 58; DB 8; Length 577;  
Best Local Similarity 21.2%; Pred. No. 1.7e+02;  
RESULT 873  
ID ADG74260 standard; protein; 626 AA.  
DE Mouse frizzled protein, SEQ ID No 45.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.1%; Score 58; DB 7; Length 626;  
Best Local Similarity 19.6%; Pred. No. 1.9e+02;  
RESULT 874  
ID AAB12117 standard; protein; 647 AA.  
DE Hydrophobic domain protein from clone HP02539 isolated from Saos-2 cells.  
PN WO200029448-A2.  
PD 25-MAY-2000.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 14.1%; Score 58; DB 3; Length 647;  
Best Local Similarity 19.6%; Pred. No. 2e+02;  
RESULT 875  
ID ABUS5896 standard; protein; 647 AA.  
DE Human protein Frizzled-1.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 14.1%; Score 58; DB 6; Length 647;  
Best Local Similarity 19.6%; Pred. No. 2e+02;  
RESULT 876  
ID AAE34050 standard; protein; 647 AA.  
DE FZD1 protein.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 14.1%; Score 58; DB 6; Length 647;  
Best Local Similarity 19.6%; Pred. No. 2e+02;  
RESULT 877  
ID ADG74259 standard; protein; 647 AA.

DE Human frizzled protein, SEQ ID NO 44.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.1%; Score 58; DB 7; Length 647;  
Best Local Similarity 19.8%; Pred. No. 2e+02;  
RESULT 878  
ID ADP5222 standard; protein; 647 AA.  
DE Human frizzled 1, frizzled (Drosophila) homologue 1.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 14.1%; Score 58; DB 7; Length 647;  
Best Local Similarity 19.6%; Pred. No. 2e+02;  
RESULT 879  
ID ADO22252 standard; protein; 647 AA.  
DE Human FZD1 protein (homologue of Drosophila frizzled).  
PN WO2004042028-A2.  
PD 21-MAY-2004.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 14.1%; Score 58; DB 8; Length 647;  
Best Local Similarity 19.6%; Pred. No. 2e+02;  
RESULT 880  
ID ADO29693 standard; protein; 648 AA.  
DE Human GPCR FZD1, SEQ ID NO:795.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.1%; Score 58; DB 8; Length 648;  
Best Local Similarity 19.6%; Pred. No. 2e+02;  
RESULT 881  
ID ABU25395 standard; protein; 686 AA.  
DE Protein encoded by Prokaryotic essential gene #10922.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.1%; Score 58; DB 6; Length 686;  
Best Local Similarity 23.3%; Pred. No. 2.1e+02;  
RESULT 882  
ID ABG24263 standard; protein; 1303 AA.  
DE Novel human diagnostic protein #24254.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.1%; Score 58; DB 4; Length 1303;  
Best Local Similarity 22.4%; Pred. No. 4.4e+02;  
RESULT 883  
ID RAW67738 standard; protein; 2476 AA.  
DE Pig p105 zona pellucida-binding protein.  
PN US5851817-A.  
PD 22-DEC-1998.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 14.1%; Score 58; DB 2; Length 2476;  
Best Local Similarity 24.1%; Pred. No. 9e+02;  
RESULT 884  
ID RAM24446 standard; protein; 63 AA.  
DE Human EST encoded protein SEQ ID NO: 1971.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.0%; Score 57.5; DB 4; Length 63;  
Best Local Similarity 36.8%; Pred. No. 17;  
RESULT 885  
ID AAB42727 standard; protein; 73 AA.  
DE Human ORFX ORF2491 polypeptide sequence SEQ ID NO:4982.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.0%; Score 57.5; DB 3; Length 73;  
Best Local Similarity 26.74; Pred. No. 20;  
RESULT 886  
ID ADH88922 standard; protein; 108 AA.  
DE Enterococcus faecalis polypeptide #3402.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 14.0%; Score 57.5; DB 7; Length 108;  
Best Local Similarity 23.3%; Pred. No. 30;  
RESULT 887  
ID ADL92433 standard; protein; 115 AA.  
DE Single domain antibody (dab)-related TAR2h-5 protein.  
PN WO2004003019-A2.  
PD 08-JAN-2004.  
PA (DOMA-) DOMANTIS LTD.  
Query Match 14.0%; Score 57.5; DB 8; Length 115;  
Best Local Similarity 32.7%; Pred. No. 33;  
RESULT 888  
ID ADQ77040 standard; protein; 115 AA.  
DE TAR2h-5 protein sequence.  
PN WO2004058821-A2.  
PD 15-JUL-2004.  
PA (DOMA-) DOMANTIS LTD.  
Query Match 14.0%; Score 57.5; DB 8; Length 115;  
Best Local Similarity 32.7%; Pred. No. 33;  
RESULT 889  
ID ADL92391 standard; protein; 116 AA.  
DE Single domain antibody (dab)-related TAR2-5 protein.  
PN WO2004003019-A2.  
PD 08-JAN-2004.  
PA (DOMA-) DOMANTIS LTD.  
Query Match 14.0%; Score 57.5; DB 8; Length 116;  
Best Local Similarity 32.7%; Pred. No. 33;  
RESULT 890  
ID ADQ76999 standard; protein; 116 AA.  
DE TAR2-5 protein sequence.  
PN WO2004058821-A2.  
PD 15-JUL-2004.  
PA (DOMA-) DOMANTIS LTD.  
Query Match 14.0%; Score 57.5; DB 8; Length 116;  
Best Local Similarity 32.7%; Pred. No. 33;  
RESULT 891  
ID ADB11434 standard; protein; 125 AA.  
DE Alloiococcus otitis antigenic protein SEQ ID NO:5626.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP ) WYETH HOLDINGS CORP.  
Query Match 14.0%; Score 57.5; DB 6; Length 125;  
Best Local Similarity 25.2%; Pred. No. 36;  
RESULT 892  
ID ABB70366 standard; protein; 170 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 37890.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 14.0%; Score 57.5; DB 4; Length 170;  
Best Local Similarity 23.6%; Pred. No. 51;  
RESULT 893  
ID ABB67475 standard; protein; 231 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 29217.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 14.0%; Score 57.5; DB 4; Length 231;  
Best Local Similarity 24.2%; Pred. No. 72;  
RESULT 894  
ID ABB48370 standard; protein; 250 AA.  
DE Listeria monocytogenes protein #1074.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 14.0%; Score 57.5; DB 5; Length 250;  
Best Local Similarity 26.8%; Pred. No. 78;  
RESULT 895  
ID ABE28657 standard; protein; 342 AA.  
DE Novel human diagnostic protein #28648.

PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSQ INC.  
Query Match 14.0%; Score 57.5; DB 4; Length 342;  
Best Local Similarity 25.0%; Pred. No. 1.1e+02;  
RESULT 896  
ID ADI28462 standard; protein; 349 AA.  
DE Mouse GPCR5D polypeptide.  
PN WO2004001060-A2.  
PD 31-DEC-2003.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 14.0%; Score 57.5; DB 8; Length 349;  
Best Local Similarity 33.3%; Pred. No. 1.1e+02;  
RESULT 897  
ID ADO29633 standard; protein; 356 AA.  
DE Mouse GPCR RAI3, SEQ ID NO:735.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 14.0%; Score 57.5; DB 8; Length 356;  
Best Local Similarity 33.3%; Pred. No. 1.2e+02;  
RESULT 898  
ID ABU33917 standard; protein; 408 AA.  
DE Protein encoded by Prokaryotic essential gene #19444.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (SLIT-) ELITRA PHARM INC.  
Query Match 14.0%; Score 57.5; DB 6; Length 408;  
Best Local Similarity 34.6%; Pred. No. 1.4e+02;  
RESULT 899  
ID ADM87323 standard; protein; 436 AA.  
DE Human protein SEQ ID NO:416.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 14.0%; Score 57.5; DB 8; Length 436;  
Best Local Similarity 39.1%; Pred. No. 1.5e+02;  
RESULT 900  
ID ABG28672 standard; protein; 506 AA.  
DE Novel human diagnostic protein #28663.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSQ INC.  
Query Match 14.0%; Score 57.5; DB 4; Length 506;  
Best Local Similarity 25.0%; Pred. No. 1.7e+02;  
RESULT 901  
ID ADA34879 standard; protein; 1062 AA.  
DE Acinetobacter baumannii protein #2040.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 14.0%; Score 57.5; DB 6; Length 1062;  
Best Local Similarity 26.7%; Pred. No. 4e+02;  
RESULT 902  
ID ABU22339 standard; protein; 1077 AA.  
DE Protein encoded by Prokaryotic essential gene #7866.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 14.0%; Score 57.5; DB 6; Length 1077;  
Best Local Similarity 30.0%; Pred. No. 4.1e+02;  
RESULT 903  
ID AAG72380 standard; protein; 145 AA.  
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2061.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
Query Match 13.9%; Score 57; DB 4; Length 145;  
Best Local Similarity 27.0%; Pred. No. 49;  
RESULT 904  
ID AAW58880 standard; protein; 148 AA.  
DE Recombinant MPO protein fragment H11.

PN WO9807848-A1.  
PD 26-FEB-1998.  
PA (TEIK-) TEIKOKU HORMONE MFG CO LTD.  
Query Match 13.9%; Score 57; DB 2; Length 148;  
Best Local Similarity 35.6%; Pred. No. 50;  
RESULT 905  
ID AAU60896 standard; protein; 172 AA.  
DE Propionibacterium acnes immunogenic protein #21792.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.9%; Score 57; DB 4; Length 172;  
Best Local Similarity 33.3%; Pred. No. 60;  
RESULT 906  
ID ARM57415 standard; protein; 172 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #22091.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.9%; Score 57; DB 6; Length 172;  
Best Local Similarity 33.3%; Pred. No. 60;  
RESULT 907  
ID AAW58879 standard; protein; 205 AA.  
DE Recombinant MPO protein fragment H6.  
PN WO9807848-A1.  
PD 26-FEB-1998.  
PA (TEIK-) TEIKOKU HORMONE MFG CO LTD.  
Query Match 13.9%; Score 57; DB 2; Length 205;  
Best Local Similarity 35.6%; Pred. No. 73;  
RESULT 908  
ID AAW58874 standard; protein; 234 AA.  
DE Recombinant MPO protein fragment H3.  
PN WO9807848-A1.  
PD 26-FEB-1998.  
PA (TEIK-) TEIKOKU HORMONE MFG CO LTD.  
Query Match 13.9%; Score 57; DB 2; Length 234;  
Best Local Similarity 35.8%; Pred. No. 84;  
RESULT 909  
ID AAR79060 standard; peptide; 242 AA.  
DE 3 hydroxy-beta-ionone ring methylene to keto group converting peptide.  
PN WO9518220-A1.  
PD 06-JUL-1995.  
PA (KIRI-) KIRIN BEER KK.  
Query Match 13.9%; Score 57; DB 2; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 910  
ID AAW69538 standard; protein; 242 AA.  
DE Amino acid sequence of crtE w1-crt w12.  
PN JP10155497-A.  
PD 16-JUN-1998.  
PA (HOFF-) HOPPMANN LA ROCHE & CO AG F.  
Query Match 13.9%; Score 57; DB 2; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 911  
ID AAW87885 standard; protein; 242 AA.  
DE Protein encoded by the carotenoid biosynthesis gene crtW.  
PN JP10327865-A.  
PD 15-DEC-1998.  
PA (KIRI-) KIRIN BREWERY KK.  
Query Match 13.9%; Score 57; DB 2; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 912  
ID ADO61159 standard; protein; 242 AA.  
DE Alcaligenes sp. ketolase.  
PN DE10238978-A1.  
PD 04-MAR-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match 13.9%; Score 57; DB 8; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 913  
ID ADO61076 standard; protein; 242 AA.

DE Alcaligenes sp. ketolase.  
PN DE10238980-A1.  
PD 04-MAR-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match 13.9%; Score 57; DB 8; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 914  
ID ADQ38245 standard; protein; 242 AA.  
DE Alcaligenes sp. Ketolase.  
PN DE10258971-A1.  
PD 01-JUL-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match 13.9%; Score 57; DB 8; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 915  
ID ADR03860 standard; protein; 242 AA.  
DE Alcaligenes sp ketolase SEQ ID NO: 18.  
PN WO2004063359-A2.  
PD 29-JUL-2004.  
PA (BADI ) BASF AG.  
Query Match 13.9%; Score 57; DB 8; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 916  
ID ADR03940 standard; protein; 242 AA.  
DE Alcaligenes ketolase.  
PN WO2004063358-A1.  
PD 29-JUL-2004.  
PA (BADI ) BASF AG.  
Query Match 13.9%; Score 57; DB 8; Length 242;  
Best Local Similarity 26.0%; Pred. No. 88;  
RESULT 917  
ID ADH09916 standard; protein; 247 AA.  
DE Human host factor protein, SEQ ID No 444.  
PN WO2003094847-A2.  
PD 20-NOV-2003.  
PA (UYEN-) UNIV EMORY.  
Query Match 13.9%; Score 57; DB 8; Length 247;  
Best Local Similarity 26.6%; Pred. No. 90;  
RESULT 918  
ID ADN95988 standard; protein; 299 AA.  
DE Human NOVX polypeptide #21.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON/) ZHONG M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (SPYT/) SPYTEK K A.  
PA (KEKU/) KEKUDA R.  
PA (TAUP/) TAUPIER R. J.  
PA (ANDE/) ANDERSON D W.  
PA (VERN/) VERNET C A M.  
PA (CATT/) CATTERTON E.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (TCHE/) TCHERNEV V T.  
PA (PADI/) PADIGARU M.  
PA (GUSE/) GUSEV Y Y.  
PA (MALY/) MALYANKAR U M.  
PA (BURG/) BURGESS C E.  
PA (GERL/) GERLACH V.  
PA (CASM/) CASMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.  
PA (ROTH/) ROTHENBERG M B.  
PA (LARO/) LAROCHELLE W J.  
PA (SHIM/) SHIMKETS R A.  
PA (CRAB/) CRABTREE J.  
PA (RAST/) RASTELLI L.  
  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (MACD/) MACDOUGALL J R.  
PA (ELLE/) ELLERMAN K.  
PA (CHAP/) CHAPOVAL A.  
Query Match 13.9%; Score 57; DB 8; Length 299;  
Best Local Similarity 26.5%; Pred. No. 1.1e+02;  
RESULT 919  
ID APP25981 standard; protein; 300 AA.  
DE Streptococcus polypeptide SEQ ID NO 1138.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 13.9%; Score 57; DB 5; Length 300;  
Best Local Similarity 38.2%; Pred. No. 1.1e+02;  
RESULT 920  
ID ABB49251 standard; protein; 305 AA.  
DE Listeria monocytogenes protein #1955.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 13.9%; Score 57; DB 5; Length 305;  
Best Local Similarity 24.1%; Pred. No. 1.1e+02;  
RESULT 921  
ID ADI16827 standard; protein; 315 AA.  
DE Murine NOVX protein homologue SeqID 363.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.9%; Score 57; DB 5; Length 315;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 922  
ID ABW02144 standard; protein; 315 AA.  
DE Human GPCR related protein #6.  
PN US2003195335-A1.  
PD 16-OCT-2003.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (CASN/) CASMAN S.  
PA (ALSO/) ALSOBROOK J P.  
PA (BURG/) BURGESS C E.  
PA (PADI/) PADIGARU M.  
PA (TAYL/) TAYLOR S.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (LILL/) LI L.  
PA (SHEN/) SHENOY S.  
PA (KEKU/) KEKUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (STON/) STONE D J.  
PA (SMIT/) SMITHSON G.  
PA (MACD/) MACDOUGALL J R.  
Query Match 13.9%; Score 57; DB 7; Length 315;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 923  
ID ADM42847 standard; protein; 315 AA.  
DE Murine odourant receptor protein Olfr68 SeqID 91.  
PN WO2003100057-A1.  
PD 04-DEC-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Query Match 13.9%; Score 57; DB 8; Length 315;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 924  
ID ADI16828 standard; protein; 316 AA.  
DE Murine NOVX protein homologue SeqID 364.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.9%; Score 57; DB 5; Length 316;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;

RESULT 925  
ID ABO19500 standard; protein; 316 AA.  
DE Mouse GPCR MOR 3' Beta 3.  
PN US2003022237-A1.  
PD 30-JAN-2003.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
PA (HAWK/) HAWKEN D R.  
PA (CACA/) CACACE A.  
PA (BARB/) BARBER L.  
PA (KORN/) KORNACKER M G.  
Query Match 13.9%; Score 57; DB 6; Length 316;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 926  
ID AEW02145 standard; protein; 316 AA.  
DE Human GPCR related protein #7.  
PN US2003195335-A1.  
PD 15-OCT-2003.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (CASM/) CASMAN S.  
PA (ALSO/) ALSOBROOK J P.  
PA (BURG/) BURGESS C E.  
PA (PAD1/) PADIGARU M.  
PA (TAYL/) TAYLOR S.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (LILL/) LI L.  
PA (SHEN/) SHENOY S.  
PA (KEKU/) KEKUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (STON/) STONE D J.  
PA (SMIT/) SMITHSON G.  
PA (MACD/) MACDOUGALL J R.  
Query Match 13.9%; Score 57; DB 7; Length 316;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 927  
ID ADQ98158 standard; protein; 316 AA.  
DE Mouse olfactory receptor 3' beta 3.  
PN US2004121330-A1.  
PD 24-JUN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G A.  
PA (RAMA/) RAMANATHAN C S.  
PA (HAWK/) HAWKEN D R.  
PA (CACA/) CACACE A.  
PA (BARB/) BARBER L E.  
PA (KORN/) KORNACKER M G.  
PA (RYSE/) RYSECK R.  
PA (BENN/) BENNETT K L.  
PA (NELS/) NELSON T C.  
Query Match 13.9%; Score 57; DB 8; Length 316;  
Best Local Similarity 25.0%; Pred. No. 1.2e+02;  
RESULT 928  
ID ADC12684 standard; protein; 317 AA.  
DE Human GPCR protein, SEQ ID No 16.  
PN WO2003000893-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 13.9%; Score 57; DB 7; Length 317;  
Best Local Similarity 27.9%; Pred. No. 1.2e+02;  
RESULT 929  
ID RAO09433 standard; protein; 328 AA.  
DE Human placenta purinergic P-2u receptor, PNR.  
PN WO9638558-A2.  
PD 05-DEC-1996.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 13.9%; Score 57; DB 2; Length 328;  
Best Local Similarity 26.9%; Pred. No. 1.2e+02;  
RESULT 930  
ID AAG72619 standard; protein; 344 AA.  
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2300.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
Query Match 13.9%; Score 57; DB 4; Length 344;  
Best Local Similarity 25.0%; Pred. No. 1.3e+02;  
RESULT 931  
ID AAG72620 standard; protein; 347 AA.  
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2301.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
Query Match 13.9%; Score 57; DB 4; Length 347;  
Best Local Similarity 25.0%; Pred. No. 1.3e+02;  
RESULT 932  
ID AAU80492 standard; protein; 355 AA.  
DE Baboon CXCR2 receptor.  
PN WO200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPETIA INC.  
Query Match 13.9%; Score 57; DB 5; Length 355;  
Best Local Similarity 25.0%; Pred. No. 1.3e+02;  
RESULT 933  
ID ADE08292 standard; protein; 375 AA.  
DE Novel protein (useful for identifying genetic disorders) #447.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.9%; Score 57; DB 7; Length 375;  
Best Local Similarity 22.5%; Pred. No. 1.4e+02;  
RESULT 934  
ID AAW58872 standard; protein; 462 AA.  
DE Recombinant MPO protein fragment NP1.4.  
PN WO9807848-A1.  
PD 26-FEB-1998.  
PA (TEIK-) TEIKOKU HORMONE MFG CO LTD.  
Query Match 13.9%; Score 57; DB 2; Length 462;  
Best Local Similarity 35.6%; Pred. No. 1.8e+02;  
RESULT 935  
ID AAV94518 standard; protein; 500 AA.  
DE Rice diacylglycerol acyltransferase protein #2.  
PN WO200032756-A2.  
PD 08-JUN-2000.  
PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
Query Match 13.9%; Score 57; DB 3; Length 500;  
Best Local Similarity 31.5%; Pred. No. 2e+02;  
RESULT 936  
ID ABB65629 standard; protein; 631 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23679.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 13.9%; Score 57; DB 4; Length 631;  
Best Local Similarity 26.3%; Pred. No. 2.6e+02;  
RESULT 937  
ID ABO70421 standard; protein; 693 AA.  
DE Pseudomonas aeruginosa polypeptide #2596.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.9%; Score 57; DB 7; Length 693;  
Best Local Similarity 23.1%; Pred. No. 2.9e+02;  
RESULT 938  
ID AAW17800 standard; protein; 745 AA.  
DE Myeloperoxidase.  
PN JF09047286-A.  
PD 18-FEB-1997.  
PA (SRLS-) SRL KK.  
Query Match 13.9%; Score 57; DB 2; Length 745;  
Best Local Similarity 35.6%; Pred. No. 3.1e+02;  
RESULT 939  
ID ADJ68744 standard; protein; 745 AA.

DE Human heat mitochondrial protein as a therapeutic target SeqID550.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 13.9%; Score 57; DB 7; Length 745;  
Best Local Similarity 35.6%; Pred. No. 3.1e+02;  
RESULT 940  
ID ADJ68203 standard; protein; 745 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID9.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 13.9%; Score 57; DB 7; Length 745;  
Best Local Similarity 35.6%; Pred. No. 3.1e+02;  
RESULT 941  
ID ADM67178 standard; protein; 745 AA.  
DE Human adipocyte specific myeloperoxidase protein SeqID 531.  
PN WO2004011618-A2.  
PD 05-FEB-2004.  
PA (HMGE-) HMGENE INC.  
Query Match 13.9%; Score 57; DB 8; Length 745;  
Best Local Similarity 35.6%; Pred. No. 3.1e+02;  
RESULT 942  
ID ABM81909 standard; protein; 745 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2839, SEQ:4904.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 13.9%; Score 57; DB 8; Length 745;  
Best Local Similarity 35.6%; Pred. No. 3.1e+02;  
RESULT 943  
ID ADQ39805 standard; protein; 745 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1468.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 13.9%; Score 57; DB 8; Length 777;  
Best Local Similarity 35.6%; Pred. No. 3.3e+02;  
RESULT 944  
ID ADQ39803 standard; protein; 777 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1466.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 13.9%; Score 57; DB 8; Length 777;  
Best Local Similarity 35.6%; Pred. No. 3.3e+02;  
RESULT 945  
ID ADQ39802 standard; protein; 792 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1465.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 13.9%; Score 57; DB 8; Length 792;  
Best Local Similarity 35.8%; Pred. No. 3.3e+02;  
RESULT 946  
ID ABP40237 standard; protein; 118 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5082.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.8%; Score 56.5; DB 5; Length 118;  
Best Local Similarity 23.4%; Pred. No. 45;  
RESULT 947  
ID ABR48486 standard; protein; 170 AA.  
DE Human Benzodiazepine Receptor 2.  
PN WO200294864-A2.  
PD 28-NOV-2002.  
PA (GENT-) GENSET.  
Query Match 13.8%; Score 56.5; DB 6; Length 170;  
Best Local Similarity 34.6%; Pred. No. 68;  
RESULT 948

ID AAR15208 standard; protein; 174 AA.  
DE [Arg11,23,Ser17,27,60,65]huG-CSF.  
PN EP459630-A.  
PD 04-DEC-1991.  
PA (ZENE-) ZENECA LTD.  
Query Match 13.8%; Score 56.5; DB 2; Length 174;  
Best Local Similarity 32.4%; Pred. No. 70;  
RESULT 949  
ID AAR15204 standard; protein; 174 AA.  
DE [Arg11,Ser17,27,60,65]huG-CSF.  
PN EP459630-A.  
PD 04-DEC-1991.  
PA (ICIL-) IMPERIAL CHEM IND PLC.  
Query Match 13.8%; Score 56.5; DB 2; Length 174;  
Best Local Similarity 32.4%; Pred. No. 70;  
RESULT 950  
ID AAR15209 standard; protein; 174 AA.  
DE [Arg11,40,Ser17,27,60,65]huG-CSF.  
PN EP459630-A.  
PD 04-DEC-1991.  
PA (ICIL-) IMPERIAL CHEM IND PLC.  
Query Match 13.8%; Score 56.5; DB 2; Length 174;  
Best Local Similarity 32.4%; Pred. No. 70;  
RESULT 951  
ID ABO59635 standard; protein; 201 AA.  
DE Human genome derived single exon protein #4869.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN-) PENN S G.  
PA (RANK-) RANK D R.  
PA (HANZ-) HANZEL D K.  
Query Match 13.8%; Score 56.5; DB 8; Length 201;  
Best Local Similarity 36.5%; Pred. No. 82;  
RESULT 952  
ID ABU05715 standard; protein; 229 AA.  
DE M. tuberculosis and M. leprae marker protein #366.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP-) INST PASTEUR.  
Query Match 13.8%; Score 56.5; DB 5; Length 229;  
Best Local Similarity 23.7%; Pred. No. 95;  
RESULT 953  
ID ADC94492 standard; protein; 246 AA.  
DE E. faecium protein sequence SEQ ID 4119.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.8%; Score 56.5; DB 7; Length 246;  
Best Local Similarity 25.7%; Pred. No. 1e+02;  
RESULT 954  
ID AAW88334 standard; protein; 339 AA.  
DE Salmonella enterica O antigen whap gene protein product.  
PN WO9850531-A1.  
PD 12-NOV-1998.  
PA (UNSY-) UNIV SYDNEY.  
Query Match 13.8%; Score 56.5; DB 2; Length 339;  
Best Local Similarity 25.0%; Pred. No. 1.5e+02;  
RESULT 955  
ID AAU02946 standard; protein; 452 AA.  
DE Angiotensin converting enzyme (ACEV) splice variant protein #46.  
PN WO200136632-A2.  
PD 25-MAY-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.8%; Score 56.5; DB 4; Length 452;  
Best Local Similarity 22.6%; Pred. No. 2.1e+02;  
RESULT 956  
ID AAU02945 standard; protein; 455 AA.  
DE Angiotensin converting enzyme (ACEV) splice variant protein #45.  
PN WO200136632-A2.  
PD 25-MAY-2001.

PA (COMP-) COMPUGEN LTD. 13.8%; Score 56.5; DB 4; Length 455;  
 Query Match Best Local Similarity 22.6%; Pred. No. 2.1e+02;  
 RESULT 957  
 ID ADM72385 standard; protein; 465 AA.  
 DE Maize CDPK polypeptide.  
 PN W02004029222-A2.  
 PD 08-APR-2004  
 PA (FION-) PIONEER HI-BRED INT INC.  
 Query Match 13.8%; Score 56.5; DB 8; Length 465;  
 Best Local Similarity 31.3%; Pred. No. 2.1e+02;  
 RESULT 958  
 ID ABB82659 standard; protein; 475 AA.  
 DE Arabaena PCC7120 protein.  
 PN W0200281622-A2.  
 PD 17-OCT-2002  
 PA (YISS-) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Query Match 13.8%; Score 56.5; DB 6; Length 475;  
 Best Local Similarity 30.0%; Pred. No. 2.2e+02;  
 RESULT 959  
 ID AUC6455 standard; protein; 475 AA.  
 DE Arabaena sp. all5073 protein.  
 PN US2003192076-A1.  
 PD 09-OCT-2003  
 PA (YISS-) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Query Match 13.8%; Score 56.5; DB 7; Length 475;  
 Best Local Similarity 30.0%; Pred. No. 2.2e+02;  
 RESULT 960  
 ID ADQ07356 standard; protein; 475 AA.  
 DE Arabaena IctB-homologue protein.  
 PN US2004128720-A1.  
 PD 01-JUL-2004  
 PA (KAPL-) KAPLAN A.  
 PA (LIEM-) LIEMAN-HURWITZ J.  
 PA (SCHA-) SCHATZ D.  
 PA (MITT-) MITTLER R.  
 PA (RACH-) RACHMILEVITCH S.  
 Query Match 13.8%; Score 56.5; DB 8; Length 475;  
 Best Local Similarity 30.0%; Pred. No. 2.2e+02;  
 RESULT 961  
 ID AAY44568 standard; protein; 506 AA.  
 DE Mouse Voltage-gated Potassium channel monomer, Kv6.2 variant #3.  
 PN W0200001811-A1.  
 PD 13-JAN-2000  
 PA (ICAG-) ICAGEN INC.  
 Query Match 13.8%; Score 56.5; DB 3; Length 506;  
 Best Local Similarity 25.9%; Pred. No. 2.3e+02;  
 RESULT 962  
 ID AAY4566 standard; protein; 506 AA.  
 DE Mouse Voltage-gated Potassium channel monomer, Kv6.2 variant #1.  
 PN W0200001811-A1.  
 PD 13-JAN-2000  
 PA (ICAG-) ICAGEN INC.  
 Query Match 13.8%; Score 56.5; DB 3; Length 506;  
 Best Local Similarity 25.9%; Pred. No. 2.3e+02;  
 RESULT 963  
 ID AAY44564 standard; protein; 506 AA.  
 DE Mouse Voltage-gated Potassium channel monomer, Kv6.2 polypeptide.  
 PN W0200001811-A1.  
 PD 13-JAN-2000  
 PA (ICAG-) ICAGEN INC.  
 Query Match 13.8%; Score 56.5; DB 3; Length 506;  
 Best Local Similarity 25.9%; Pred. No. 2.3e+02;  
 RESULT 964  
 ID AAY4567 standard; protein; 506 AA.  
 DE Mouse Voltage-gated Potassium channel monomer, Kv6.2 variant #2.  
 PN W0200001811-A1.  
 PD 13-JAN-2000  
 PA (ICAG-) ICAGEN INC.  
 Query Match 13.8%; Score 56.5; DB 3; Length 506;  
 Best Local Similarity 25.9%; Pred. No. 2.3e+02;  
 RESULT 965  
 ID ABM83196 standard; protein; 517 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3445.  
 PN W02004023973-A2.  
 PD 25-MAR-2004  
 PA (INCY-) INCYTE CORP.  
 Query Match 13.8%; Score 56.5; DB 8; Length 517;  
 Best Local Similarity 22.6%; Pred. No. 2.4e+02;  
 RESULT 966  
 ID ABB63658 standard; protein; 519 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 17766.  
 PN W0200171042-A2.  
 PD 27-SEP-2001  
 PA (PEKE-) PE CORP NY.  
 Query Match 13.8%; Score 56.5; DB 4; Length 519;  
 Best Local Similarity 20.7%; Pred. No. 2.4e+02;  
 RESULT 967  
 ID ABB80692 standard; protein; 541 AA.  
 DE Human GLUT 10 glucose transporter protein.  
 PN W0200218621-A2.  
 PD 07-MAR-2002  
 PA (UYWA-) UNIV WAKE FOREST.  
 Query Match 13.8%; Score 56.5; DB 5; Length 541;  
 Best Local Similarity 36.5%; Pred. No. 2.5e+02;  
 RESULT 968  
 ID ABB08251 standard; protein; 541 AA.  
 DE Human glucose transporting protein.  
 PN W0200202586-A1.  
 PD 10-JAN-2002  
 PA (UYDU-) UNIV DUKE.  
 Query Match 13.8%; Score 56.5; DB 5; Length 541;  
 Best Local Similarity 36.5%; Pred. No. 2.5e+02;  
 RESULT 969  
 ID ABP97191 standard; protein; 541 AA.  
 DE Tumour-associated antigenic target protein TAT198 SEQ ID NO:73.  
 PN W02003024392-A2.  
 PD 27-MAR-2003  
 PA (GETH-) GENENTECH INC.  
 Query Match 13.8%; Score 56.5; DB 6; Length 541;  
 Best Local Similarity 36.5%; Pred. No. 2.5e+02;  
 RESULT 970  
 ID ADD22916 standard; protein; 562 AA.  
 DE Human sugar transporter, 8105, protein.  
 PN US2003113841-A1.  
 PD 19-JUN-2003  
 PA (CURT-) CURTIS R A J.  
 PA (GUWW-) GU W.  
 Query Match 13.8%; Score 56.5; DB 7; Length 562;  
 Best Local Similarity 36.5%; Pred. No. 2.6e+02;  
 RESULT 971  
 ID AQ081765 standard; protein; 565 AA.  
 DE A deliciosa multifunctional germacrene-D synthase.  
 PN W02004058814-A1.  
 PD 15-JUL-2004  
 PA (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.  
 Query Match 13.8%; Score 56.5; DB 8; Length 565;  
 Best Local Similarity 32.4%; Pred. No. 2.6e+02;  
 RESULT 972  
 ID AAO14209 standard; protein; 614 AA.  
 DE Human transporter and ion channel TRICH-26.  
 PN W0200204520-A2.  
 PD 17-JAN-2002  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 13.8%; Score 56.5; DB 5; Length 614;  
 Best Local Similarity 36.5%; Pred. No. 2.9e+02;  
 RESULT 973  
 ID ASG26622 standard; protein; 639 AA.  
 DE Novel human diagnostic protein #26613.  
 PN W0200175067-A2.  
 PD 11-OCT-2001  
 PA (HYSE-) HYSEQ INC.  
 Query Match 13.8%; Score 56.5; DB 4; Length 639;  
 Best Local Similarity 36.5%; Pred. No. 3e+02;  
 RESULT 974  
 ID ABR42418 standard; protein; 653 AA.

DE Human potassium channel Kv1.4.  
PN WO2003035690-A2.  
PD 01-MAY-2003.  
PA (TMCO-) IMPERIAL COLLEGE INNOVATIONS LTD. Length 653;  
Query Match 13.8%; Score 56.5; DB 6; Length 653;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 975  
ID ADA83742 standard; protein; 653 AA.  
DE Human KCNA4 protein.  
PN WO2002103028-A2.  
PD 27-DEC-2002.  
PA (BIOM-) BIOMEDICAL CENT.  
Query Match 13.8%; Score 56.5; DB 6; Length 653;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 976  
ID ADE57786 standard; protein; 653 AA.  
DE Human Protein P22459, SEQ ID NO 3651.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.8%; Score 56.5; DB 7; Length 653;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 977  
ID ADE63497 standard; protein; 653 AA.  
DE Human Protein P22459, SEQ ID NO 9441.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.8%; Score 56.5; DB 7; Length 653;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 978  
ID ABO59441 standard; protein; 653 AA.  
DE Human genome derived single exon protein #5675.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 13.8%; Score 56.5; DB 8; Length 653;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 979  
ID ADE63495 standard; protein; 655 AA.  
DE Rat Protein CAA34133, SEQ ID NO 9439.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.8%; Score 56.5; DB 7; Length 655;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 980  
ID ADE57784 standard; protein; 655 AA.  
DE Rat Protein P15385, SEQ ID NO 3649.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.8%; Score 56.5; DB 7; Length 655;  
Best Local Similarity 22.0%; Pred. No. 3.1e+02;  
RESULT 981  
ID ADN22745 standard; protein; 658 AA.  
DE Bacterial polypeptide #5398.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.8%; Score 56.5; DB 8; Length 658;  
Best Local Similarity 26.7%; Pred. No. 3.1e+02;  
RESULT 982

ID ABP80763 standard; protein; 717 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 8056.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 13.8%; Score 56.5; DB 6; Length 717;  
Best Local Similarity 27.8%; Pred. No. 3.5e+02;  
RESULT 983  
ID ABU40365 standard; protein; 971 AA.  
DE Protein encoded by Prokaryotic essential gene #25892.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.8%; Score 56.5; DB 6; Length 971;  
Best Local Similarity 33.3%; Pred. No. 4.9e+02;  
RESULT 984  
ID AAY21815 standard; protein; 1308 AA.  
DE A. nidulans atrC polypeptide.  
PN WO932505-A1.  
PD 01-JUL-1999.  
PA (ELIL) LILLY & CO ELI.  
PA (UTWA-) UNIV WAGENINGEN AGRIC.  
Query Match 13.8%; Score 56.5; DB 2; Length 1308;  
Best Local Similarity 20.0%; Pred. No. 6.8e+02;  
RESULT 985  
ID AAM37179 standard; protein; 60 AA.  
DE Peptide #11216 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 13.7%; Score 56; DB 4; Length 60;  
Best Local Similarity 28.6%; Pred. No. 24;  
RESULT 986  
ID ABG28619 standard; protein; 117 AA.  
DE Novel human diagnostic protein #28610.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.7%; Score 56; DB 4; Length 117;  
Best Local Similarity 32.1%; Pred. No. 52;  
RESULT 987  
ID AAG27278 standard; protein; 144 AA.  
DE Zea mays protein fragment SEQ ID NO: 32051.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 13.7%; Score 56; DB 3; Length 144;  
Best Local Similarity 30.2%; Pred. No. 65;  
RESULT 988  
ID AAG27277 standard; protein; 145 AA.  
DE Zea mays protein fragment SEQ ID NO: 32050.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 13.7%; Score 56; DB 3; Length 145;  
Best Local Similarity 30.2%; Pred. No. 66;  
RESULT 989  
ID ABU44223 standard; protein; 198 AA.  
DE Protein encoded by Prokaryotic essential gene #29750.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.7%; Score 56; DB 6; Length 198;  
Best Local Similarity 35.5%; Pred. No. 94;  
RESULT 990  
ID ABB89782 standard; protein; 228 AA.  
DE Human polypeptide SEQ ID NO 2158.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.7%; Score 56; DB 5; Length 228;  
Best Local Similarity 28.8%; Pred. No. 1.1e+02;  
RESULT 991  
ID ABP70453 standard; peptide; 242 AA.  
DE Partial amino acid sequence of fish taste receptor T1RA.

PN WO2003001876-A2.  
PD 09-JAN-2003.  
PA (SENSO-) SENOMYX INC.  
Query Match 13.7%; Score 56; DB 6; Length 242;  
Best Local Similarity 34.1%; Pred. No. 1.2e+02;  
RESULT 992  
ID AGU73587 standard; protein; 242 AA.  
DE Puffer fish TIRA #2.  
PN US200323407-A1.  
PD 18-DEC-2003.  
PA (SENSO-) SENOMYX INC.  
Query Match 13.7%; Score 56; DB 8; Length 242;  
Best Local Similarity 34.1%; Pred. No. 1.2e+02;  
RESULT 993  
ID ADR29266 standard; protein; 242 AA.  
DE Taste receptor modulation-related tetraodon TIRA part protein SeqID205.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENSO-) SENOMYX INC.  
Query Match 13.7%; Score 56; DB 8; Length 242;  
Best Local Similarity 34.1%; Pred. No. 1.2e+02;  
RESULT 994  
ID ABP25982 standard; protein; 300 AA.  
DE Streptococcus polypeptide SEQ ID NO 1140.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (SENSO-) INST GENOMIC RES.  
Query Match 13.7%; Score 56; DB 5; Length 300;  
Best Local Similarity 35.3%; Pred. No. 1.5e+02;  
RESULT 995  
ID AAB87760 standard; protein; 319 AA.  
DE Human T2R30 amino acid sequence SEQ ID NO:51.  
PN WO200118050-A2.  
PD 15-MAR-2001.  
PA (REGC) UNIV CALIFORNIA.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 13.7%; Score 56; DB 4; Length 319;  
Best Local Similarity 24.7%; Pred. No. 1.6e+02;  
RESULT 996  
ID ADR29112 standard; protein; 319 AA.  
DE Taste receptor modulation-related human T2R30 protein sequence SeqID51.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENSO-) SENOMYX INC.  
Query Match 13.7%; Score 56; DB 8; Length 319;  
Best Local Similarity 24.7%; Pred. No. 1.6e+02;  
RESULT 997  
ID AAU80489 standard; protein; 355 AA.  
DE Rhesus macaque CXCR2 receptor #1.  
PN WO200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.7%; Score 56; DB 5; Length 355;  
Best Local Similarity 25.0%; Pred. No. 1.8e+02;  
RESULT 998  
ID AAU80491 standard; protein; 355 AA.  
DE Vervet monkey CXCR2 receptor #1.  
PN WO200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.7%; Score 56; DB 5; Length 355;  
Best Local Similarity 25.0%; Pred. No. 1.8e+02;  
RESULT 999  
ID AB081142 standard; protein; 356 AA.  
DE Pseudomonas aeruginosa polypeptide #13317.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (SENSO-) GENOME THERAPEUTICS CORP.  
Query Match 13.7%; Score 56; DB 7; Length 356;  
Best Local Similarity 26.0%; Pred. No. 1.8e+02;  
RESULT 1000  
ID AAW98234 standard; protein; 389 AA.

DE H. pylori GHPO 558 protein.  
PN WO9843478-A1.  
PD 08-OCT-1998.  
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.7%; Score 56; DB 2; Length 389;  
Best Local Similarity 36.5%; Pred. No. 2e+02;  
RESULT 1001  
ID ABU49219 standard; protein; 393 AA.  
DE Protein encoded by Prokaryotic essential gene #34746.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.7%; Score 56; DB 6; Length 393;  
Best Local Similarity 26.5%; Pred. No. 2e+02;  
RESULT 1002  
ID ADS23341 standard; protein; 417 AA.  
DE Bacterial polypeptide #12374.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.7%; Score 56; DB 8; Length 417;  
Best Local Similarity 28.1%; Pred. No. 2.2e+02;  
RESULT 1003  
ID ABU30937 standard; protein; 429 AA.  
DE Protein encoded by Prokaryotic essential gene #16464.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.7%; Score 56; DB 6; Length 429;  
Best Local Similarity 36.5%; Pred. No. 2.2e+02;  
RESULT 1004  
ID ADN22966 standard; protein; 645 AA.  
DE Bacterial polypeptide #5619.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.7%; Score 56; DB 8; Length 645;  
Best Local Similarity 28.8%; Pred. No. 3.6e+02;  
RESULT 1005  
ID AAW94919 standard; protein; 667 AA.  
DE Rat pheromone receptor Go-VN3.  
PN WO9900422-A1.  
PD 07-JAN-1999.  
PA (HARD) HARVARD COLLEGE.  
Query Match 13.7%; Score 56; DB 2; Length 667;  
Best Local Similarity 26.3%; Pred. No. 3.7e+02;  
RESULT 1006  
ID ABB71797 standard; protein; 694 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42183.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 13.7%; Score 56; DB 4; Length 694;  
Best Local Similarity 21.2%; Pred. No. 3.9e+02;  
RESULT 1007  
ID ABG26663 standard; protein; 789 AA.  
DE Novel human diagnostic protein #26654.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.7%; Score 56; DB 4; Length 789;  
Best Local Similarity 24.7%; Pred. No. 4.5e+02;  
RESULT 1008  
ID ABB66062 standard; protein; 1035 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 24978.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.7%; Score 56; DB 4; Length 1035;  
Best Local Similarity 38.5%; Pred. No. 6.1e+02;  
RESULT 1009  
ID ADR10240 standard; protein; 1300 AA.  
DE Human protein useful for treating neurological disease Seq 3746.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.7%; Score 56; DB 8; Length 1300;  
Best Local Similarity 26.9%; Pred. No. 7.8e+02;  
RESULT 1010  
ID AAU19518 standard; protein; 1603 AA.  
DE Human diagnostic and therapeutic polypeptide (DITHP) #104.  
PN WO200162927-A2.  
PD 30-AUG-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.7%; Score 56; DB 4; Length 1603;  
Best Local Similarity 27.0%; Pred. No. 9.9e+02;  
RESULT 1011  
ID ADE60401 standard; protein; 1682 AA.  
DE Human Protein Q01118, SEQ ID NO: 6310.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 13.7%; Score 56; DB 7; Length 1682;  
Best Local Similarity 23.4%; Pred. No. 1e+03;  
RESULT 1012  
ID AAB82242 standard; protein; 2015 AA.  
DE Human SCNSA mutant delF1617.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2015;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1013  
ID ADF56441 standard; protein; 2015 AA.  
DE Human Nav1.5 sodium channel alpha subunit SCNSA hH1b.  
PN US2003157600-A1.  
PD 21-AUG-2003.  
PA (MAKI/) MAKIELSKI J C.  
PA (YEBE/) YE B.  
Query Match 13.7%; Score 56; DB 7; Length 2015;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1014  
ID ADM34001 standard; protein; 2015 AA.  
DE Human SCNSA variant 4 protein SEQ ID NO:8.  
PN WO2004012668-A2.  
PD 12-FEB-2004.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Query Match 13.7%; Score 56; DB 8; Length 2015;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1015  
ID ADM33999 standard; protein; 2015 AA.  
DE Human SCNSA variant 3 protein SEQ ID NO:6.  
PN WO2004012668-A2.  
PD 12-FEB-2004.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Query Match 13.7%; Score 56; DB 8; Length 2015;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1016  
ID AAW23994 standard; protein; 2016 AA.  
DE Human hH1 sodium channel protein.  
PN WO9802040-A1.  
PD 22-JAN-1998.  
PA (MEDT ) MEDTRONIC INC.  
Query Match 13.7%; Score 56; DB 2; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1017  
ID AAB82239 standard; protein; 2016 AA.  
DE Human SCNSA protein.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1018  
ID AAB82240 standard; protein; 2016 AA.  
DE Human SCNSA mutant D1114N.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1019  
ID AAB82245 standard; protein; 2016 AA.  
DE Human SCNSA mutant S1787N.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1020  
ID AAB82243 standard; protein; 2016 AA.  
DE Human SCNSA mutant R1623L.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1021  
ID AAB82244 standard; protein; 2016 AA.  
DE Human SCNSA mutant E1784K.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1022  
ID AAB82241 standard; protein; 2016 AA.  
DE Human SCNSA mutant L1501V.  
PN WO200124681-A2.  
PD 12-APR-2001.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.7%; Score 56; DB 4; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1023  
ID ADD44756 standard; protein; 2016 AA.  
DE Human Protein Q14524, SEQ ID NO 10185.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 13.7%; Score 56; DB 7; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1024  
ID ADE55106 standard; protein; 2016 AA.  
DE Human Protein NP\_000326, SEQ ID NO 911.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 13.7%; Score 56; DB 7; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1025  
ID ADM33997 standard; protein; 2016 AA.  
DE Human SCNSA variant 2 protein SEQ ID NO:4.  
PN WO2004012668-A2.  
PD 12-FEB-2004.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Query Match 13.7%; Score 56; DB 8; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;

RESULT 1026  
ID ADM3395 standard; protein; 2016 AA.  
DE Human SCNSA variant 1 protein SEQ ID NO:2.  
PN WO2004012668-A2.  
PD 12-FEB-2004.  
PA (WISC) WISCONSIN ALUMNI RES FOUND.  
Query Match 13.7%; Score 56; DB 8; Length 2016;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1027  
ID AAR67913 standard; protein; 2019 AA.  
DE Cardiac sodium channel protein.  
PN US5380836-A.  
PD 10-JAN-1995.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 13.7%; Score 56; DB 2; Length 2019;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1028  
ID AAR06584 standard; protein; 2020 AA.  
DE Cardiac sodium channel.  
PN WO9009391-A.  
PD 23-AUG-1990.  
PA (ARCH-) ARCH DEV CORP.  
Query Match 13.7%; Score 56; DB 2; Length 2020;  
Best Local Similarity 27.0%; Pred. No. 1.3e+03;  
RESULT 1029  
ID ABP00874 standard; protein; 54 AA.  
DE Human ORFX protein sequence SEQ ID NO:1730.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.5%; Score 55.5; DB 5; Length 54;  
Best Local Similarity 36.6%; Pred. No. 25;  
RESULT 1030  
ID ABB50756 standard; protein; 86 AA.  
DE Human secreted protein encoded by gene 62 SEQ ID NO:708.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.5%; Score 55.5; DB 4; Length 86;  
Best Local Similarity 25.0%; Pred. No. 42;  
RESULT 1031  
ID ABO45013 standard; protein; 86 AA.  
DE Novel human secreted protein #62 fragment #1.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.5%; Score 55.5; DB 6; Length 86;  
Best Local Similarity 25.0%; Pred. No. 42;  
RESULT 1032  
ID ABO26493 standard; protein; 86 AA.  
DE Protein associated with novel secreted protein gene 62 #1.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.5%; Score 55.5; DB 7; Length 86;  
Best Local Similarity 25.0%; Pred. No. 42;  
RESULT 1033  
ID AAO00339 standard; protein; 103 AA.  
DE Human polypeptide SEQ ID NO 14231.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.5%; Score 55.5; DB 4; Length 103;  
Best Local Similarity 26.6%; Pred. No. 52;  
RESULT 1034  
ID ABO63309 standard; protein; 122 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9826.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.5%; Score 55.5; DB 7; Length 122;  
Best Local Similarity 20.2%; Pred. No. 63;  
RESULT 1035  
ID AAY41225 standard; protein; 168 AA.  
DE M. polymorpha YM16-MARPO protein.  
PN WO951753-A1.  
PD 14-OCT-1999.  
PA (UVAL-) UNIV ALBERTA.  
Query Match 13.5%; Score 55.5; DB 2; Length 168;  
Best Local Similarity 29.1%; Pred. No. 90;  
RESULT 1036  
ID AAR15206 standard; protein; 174 AA.  
DE [Arg11, Glu15, Ser17, 27, 60, 65, Ala26, 28, Lys30] huG-CSF.  
PN EP459630-A.  
PD 04-DEC-1991.  
PA (ICIL) IMPERIAL CHEM IND PLC.  
PA (ZENE) ZENECA LTD.  
Query Match 13.5%; Score 55.5; DB 2; Length 174;  
Best Local Similarity 32.4%; Pred. No. 94;  
RESULT 1037  
ID AAB65780 standard; protein; 174 AA.  
DE Cysteine protease #21.  
PN WO200075331-A1.  
PD 14-DEC-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 13.5%; Score 55.5; DB 4; Length 174;  
Best Local Similarity 40.0%; Pred. No. 94;  
RESULT 1038  
ID ABG74380 standard; protein; 174 AA.  
DE Partial human granulocyte colony stimulating factor T38A mutant.  
PN US2002151488-A1.  
PD 17-OCT-2002.  
PA (SARK/) SARKAR C A.  
PA (LAUF/) LAUFFENBURGER D A.  
Query Match 13.5%; Score 55.5; DB 6; Length 174;  
Best Local Similarity 31.0%; Pred. No. 94;  
RESULT 1039  
ID ADE94799 standard; protein; 174 AA.  
DE Programmed cell death pathway cysteine protease #21.  
PN US2003082724-A1.  
PD 01-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 13.5%; Score 55.5; DB 7; Length 174;  
Best Local Similarity 40.0%; Pred. No. 94;  
RESULT 1040  
ID AAU97123 standard; protein; 175 AA.  
DE Human G-CSF mutant, Thr38Ala.  
PN WO200220767-A2.  
PD 14-MAR-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 13.5%; Score 55.5; DB 5; Length 175;  
Best Local Similarity 31.0%; Pred. No. 94;  
RESULT 1041  
ID ABB15590 standard; protein; 177 AA.  
DE Human nervous system related polypeptide SEQ ID NO 4247.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.5%; Score 55.5; DB 4; Length 177;  
Best Local Similarity 34.0%; Pred. No. 96;  
RESULT 1042  
ID ABP30450 standard; protein; 266 AA.  
DE Streptococcus polypeptide SEQ ID NO 10076.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 13.5%; Score 55.5; DB 5; Length 266;  
Best Local Similarity 30.2%; Pred. No. 1.5e+02;  
RESULT 1043  
ID ADC87335 standard; protein; 286 AA.  
DE Human GPCR protein SEQ ID NO:1788.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 13.5%; Score 55.5; DB 7; Length 286;  
Best Local Similarity 27.5%; Pred. No. 1.6e+02;  
RESULT 1044  
ID AAB68530 standard; protein; 292 AA.  
DE Human GTP-binding associated protein #30.  
PN WO200105970-A2.  
PD 25-JAN-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.5%; Score 55.5; DB 4; Length 292;  
Best Local Similarity 34.0%; Pred. No. 1.7e+02;  
RESULT 1045  
ID AAU79300 standard; protein; 292 AA.  
DE Accessory factor TIP30-32.12 polypeptide.  
PN CN131116-A.  
PD 16-JAN-2002.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 13.5%; Score 55.5; DB 5; Length 292;  
Best Local Similarity 34.0%; Pred. No. 1.7e+02;  
RESULT 1046  
ID ADC79326 standard; protein; 292 AA.  
DE Human G protein coupled receptor X (GPCRX) cDNA seq id 12.  
PN US2003083463-A1.  
PD 01-MAY-2003.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (COLM/) COLMAN S D.  
PA (SPYT/) SPYTEK K A.  
PA (BALL/) BALLINGER R A.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (SHEN/) SHENOY S G.  
PA (CASH/) CASHMAN S J.  
PA (GUSE/) GUSEV V Y.  
Query Match 13.5%; Score 55.5; DB 7; Length 292;  
Best Local Similarity 24.2%; Pred. No. 1.7e+02;  
RESULT 1047  
ID ABP29833 standard; protein; 310 AA.  
DE Streptococcus polypeptide SEQ ID NO 8842.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 13.5%; Score 55.5; DB 5; Length 310;  
Best Local Similarity 30.2%; Pred. No. 1.8e+02;  
RESULT 1048  
ID ABP27806 standard; protein; 310 AA.  
DE Streptococcus polypeptide SEQ ID NO 4788.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 13.5%; Score 55.5; DB 5; Length 310;  
Best Local Similarity 30.2%; Pred. No. 1.8e+02;  
RESULT 1049  
ID AAG71553 standard; protein; 313 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1234.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA) YEDA RES & DEV CO LTD.  
Query Match 13.5%; Score 55.5; DB 4; Length 313;  
Best Local Similarity 24.2%; Pred. No. 1.8e+02;  
RESULT 1050  
ID ABP61134 standard; protein; 313 AA.  
DE Human GPCR protein #6.  
PN WO200255557-A2.  
PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.5%; Score 55.5; DB 5; Length 313;  
Best Local Similarity 24.2%; Pred. No. 1.8e+02;  
RESULT 1051  
ID ADC86365 standard; protein; 313 AA.

DE Human GPCR protein SEQ ID NO:818.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 13.5%; Score 55.5; DB 7; Length 313;  
Best Local Similarity 24.2%; Pred. No. 1.8e+02;  
RESULT 1052  
ID RAU36197 standard; protein; 322 AA.  
DE Pseudomonas aeruginosa cellular proliferation protein #187.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.5%; Score 55.5; DB 4; Length 322;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
RESULT 1053  
ID ABU38266 standard; protein; 322 AA.  
DE Protein encoded by Prokaryotic essential gene #23793.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.5%; Score 55.5; DB 6; Length 322;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
RESULT 1054  
ID ADF06388 standard; protein; 326 AA.  
DE Bacterial polypeptide #2501.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.5%; Score 55.5; DB 7; Length 326;  
Best Local Similarity 27.7%; Pred. No. 1.9e+02;  
RESULT 1055  
ID ABP69626 standard; protein; 328 AA.  
DE Human polypeptide SEQ ID NO 1673.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.5%; Score 55.5; DB 5; Length 328;  
Best Local Similarity 34.0%; Pred. No. 1.9e+02;  
RESULT 1056  
ID AAG90308 standard; protein; 345 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4062.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match 13.5%; Score 55.5; DB 4; Length 345;  
Best Local Similarity 41.9%; Pred. No. 2e+02;  
RESULT 1057  
ID ABU41969 standard; protein; 349 AA.  
DE Protein encoded by Prokaryotic essential gene #27496.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.5%; Score 55.5; DB 6; Length 349;  
Best Local Similarity 24.4%; Pred. No. 2.1e+02;  
RESULT 1058  
ID AAU80487 standard; protein; 355 AA.  
DE Orangutan CXCR2 receptor #1.  
PN WO200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEDIA INC.  
Query Match 13.5%; Score 55.5; DB 5; Length 355;  
Best Local Similarity 19.0%; Pred. No. 2.1e+02;  
RESULT 1059  
ID AAB34521 standard; protein; 360 AA.  
DE Human secreted protein BLAST search protein SEQ ID NO: 139.  
PN WO200056767-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.5%; Score 55.5; DB 3; Length 360;  
Best Local Similarity 37.0%; Pred. No. 2.1e+02;  
RESULT 1060  
ID ADD44831 standard; protein; 360 AA.

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DE Rat Protein CAA68971, SEQ ID NO 10262.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.5%; Score 55.5; DB 7; Length 360;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1061
ID ADD44835 standard; protein; 360 AA.
DE Rat Protein CAA68971, SEQ ID NO 10266.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.5%; Score 55.5; DB 7; Length 360;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1062
ID ADD44839 standard; protein; 360 AA.
DE Rat Protein CAA68971, SEQ ID NO 10270.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.5%; Score 55.5; DB 7; Length 360;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1063
ID ADD46478 standard; protein; 360 AA.
DE Rat Protein CAA68971, SEQ ID NO 12159.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.5%; Score 55.5; DB 7; Length 360;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1064
ID ADD4843 standard; protein; 360 AA.
DE Rat Protein CAA68971, SEQ ID NO 10274.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 13.5%; Score 55.5; DB 7; Length 360;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1065
ID ADJ76258 standard; protein; 362 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1510.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.5%; Score 55.5; DB 8; Length 362;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1066
ID ADJ76153 standard; protein; 362 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1405.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 13.5%; Score 55.5; DB 8; Length 362;
Best Local Similarity 37.0%; Pred. No. 2.1e+02;
RESULT 1067
ID ABP95656 standard; protein; 365 AA.
DE Human GPCR polypeptide SEQ ID NO 122.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 13.5%; Score 55.5; DB 5; Length 365;
Best Local Similarity 24.2%; Pred. No. 2.2e+02;
RESULT 1068
ID AAU95698 standard; protein; 365 AA.
DE Human olfactory and pheromone G protein-coupled receptor #185.
PN WO200224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
Query Match 13.5%; Score 55.5; DB 4; Length 498;

Query Match 13.5%; Score 55.5; DB 5; Length 365;
Best Local Similarity 24.2%; Pred. No. 2.2e+02;
RESULT 1069
ID ADC95364 standard; protein; 370 AA.
DE E. faecium protein sequence SEQ ID 4991.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.5%; Score 55.5; DB 7; Length 370;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 1070
ID ABO71130 standard; protein; 373 AA.
DE Pseudomonas aeruginosa polypeptide #3305.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.5%; Score 55.5; DB 7; Length 373;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
RESULT 1071
ID ABO61721 standard; protein; 374 AA.
DE Klebsiella pneumoniae polypeptide seqid 8238.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 13.5%; Score 55.5; DB 7; Length 374;
Best Local Similarity 35.1%; Pred. No. 2.2e+02;
RESULT 1072
ID AAU24559 standard; protein; 384 AA.
DE Human olfactory receptor AOLF46.
PN WO200168805-A2.
PD 20-SEP-2001.
PA (SENSO-) SENOMYX INC.
Query Match 13.5%; Score 55.5; DB 4; Length 384;
Best Local Similarity 24.2%; Pred. No. 2.3e+02;
RESULT 1073
ID AAU85179 standard; protein; 384 AA.
DE G-coupled olfactory receptor #40.
PN WO200198526-A2.
PD 27-DEC-2001.
PA (SENSO-) SENOMYX INC.
Query Match 13.5%; Score 55.5; DB 5; Length 384;
Best Local Similarity 24.2%; Pred. No. 2.3e+02;
RESULT 1074
ID ABB67596 standard; protein; 423 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29580.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 13.5%; Score 55.5; DB 4; Length 423;
Best Local Similarity 26.2%; Pred. No. 2.6e+02;
RESULT 1075
ID ABP74050 standard; protein; 453 AA.
DE Candida albicans essential protein SEQ ID NO 7887.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 13.5%; Score 55.5; DB 5; Length 453;
Best Local Similarity 22.9%; Pred. No. 2.8e+02;
RESULT 1076
ID AA88350 standard; protein; 476 AA.
DE Salmonella enterica O antigen pathway galactosyl transferase.
PN WO9850531-A1.
PD 12-NOV-1998.
PA (UNSY ) UNIV SYDNEY.
Query Match 13.5%; Score 55.5; DB 2; Length 476;
Best Local Similarity 25.0%; Pred. No. 2.9e+02;
RESULT 1077
ID ABG21153 standard; protein; 498 AA.
DE Novel human diagnostic protein #21144.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.5%; Score 55.5; DB 4; Length 498;

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Best Local Similarity 25.8%; Pred. No. 3.1e+02;  
RESULT 1078  
ID ABO61660 standard; protein; 506 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8177.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.5%; Score 55.5; DB 7; Length 506;  
Best Local Similarity 25.8%; Pred. No. 3.1e+02;  
RESULT 1079  
ID ADN26658 standard; protein; 702 AA.  
DE Bacterial polypeptide #9311.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.5%; Score 55.5; DB 8; Length 702;  
Best Local Similarity 28.2%; Pred. No. 4.5e+02;  
RESULT 1080  
ID ADS28704 standard; protein; 720 AA.  
DE Bacterial polypeptide #17737.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.5%; Score 55.5; DB 8; Length 720;  
Best Local Similarity 28.2%; Pred. No. 4.7e+02;  
RESULT 1081  
ID AAY77556 standard; protein; 843 AA.  
DE Rat GPCR-B4 polypeptide.  
PN WO200006593-A1.  
PD 10-FEB-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 13.5%; Score 55.5; DB 3; Length 843;  
Best Local Similarity 26.8%; Pred. No. 5.6e+02;  
RESULT 1082  
ID ABR43494 standard; protein; 843 AA.  
DE Rat sweet taste receptor T1R2 protein SEQ ID NO:6.  
PN WO2003025137-A2.  
PD 27-MAR-2003.  
PA (IRMI-) IRM LLC.  
PA (SCRI ) SCRIPPS RES INST.  
Query Match 13.5%; Score 55.5; DB 6; Length 843;  
Best Local Similarity 26.8%; Pred. No. 5.6e+02;  
RESULT 1083  
ID ADK90717 standard; protein; 843 AA.  
DE Rat taste receptor T1R2 protein.  
PN WO2003004992-A2.  
PD 16-JAN-2003.  
PA (REGC ) UNIV CALIFORNIA.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 13.5%; Score 55.5; DB 7; Length 843;  
Best Local Similarity 26.8%; Pred. No. 5.6e+02;  
RESULT 1084  
ID ADI41010 standard; protein; 843 AA.  
DE Rat taste receptor TR2 #2.  
PN US2004018976-A1.  
PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 13.5%; Score 55.5; DB 8; Length 843;  
Best Local Similarity 26.8%; Pred. No. 5.6e+02;  
RESULT 1085  
ID ADI40978 standard; protein; 843 AA.  
DE Rat taste receptor TR2.  
PN US2004018976-A1.

PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 13.5%; Score 55.5; DB 8; Length 843;  
Best Local Similarity 26.8%; Pred. No. 5.6e+02;  
RESULT 1086  
ID ADP06662 standard; protein; 883 AA.  
DE Bacterial polypeptide #2775.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.5%; Score 55.5; DB 7; Length 883;  
Best Local Similarity 31.7%; Pred. No. 5.9e+02;  
RESULT 1087  
ID ABU41831 standard; protein; 930 AA.  
DE Protein encoded by Prokaryotic essential gene #27358.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.5%; Score 55.5; DB 6; Length 930;  
Best Local Similarity 31.2%; Pred. No. 6.2e+02;  
RESULT 1088  
ID ABG25961 standard; protein; 1212 AA.  
DE Novel human diagnostic protein #25952.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.5%; Score 55.5; DB 4; Length 1212;  
Best Local Similarity 20.8%; Pred. No. 8.4e+02;  
RESULT 1089  
ID ABP07353 standard; protein; 51 AA.  
DE Human ORFX protein sequence SEQ ID NO:14688.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.4%; Score 55; DB 5; Length 51;  
Best Local Similarity 48.1%; Pred. No. 27;  
RESULT 1090  
ID ADF59396 standard; protein; 58 AA.  
DE Human polypeptide sequence SEQ ID NO:1804.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.4%; Score 55; DB 7; Length 58;  
Best Local Similarity 33.3%; Pred. No. 31;  
RESULT 1091  
ID ABB11090 standard; peptide; 116 AA.  
DE Human hydrophobic domain protein homologue, SEQ ID NO:1460.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.4%; Score 55; DB 4; Length 116;  
Best Local Similarity 25.0%; Pred. No. 69;  
RESULT 1092  
ID ABP70452 standard; peptide; 137 AA.  
DE Partial amino acid sequence of fish taste receptor T1RA.  
PN WO200301876-A2.  
PD 09-JAN-2003.  
PA (SENSO-) SENOMYX INC.  
Query Match 13.4%; Score 55; DB 6; Length 137;  
Best Local Similarity 34.1%; Pred. No. 83;  
RESULT 1093  
ID ADG73586 standard; protein; 137 AA.  
DE Puffer fish T1RA #1.  
PN US2003232407-A1.  
PD 18-DEC-2003.  
PA (SENSO-) SENOMYX INC.  
Query Match 13.4%; Score 55; DB 8; Length 137;  
Best Local Similarity 34.1%; Pred. No. 83;  
RESULT 1094  
ID ADR29265 standard; protein; 137 AA.  
DE Taste receptor modulation-related fugu T1RA partial protein SeqID204.

PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENSO-) SENOMYX INC.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 137;  
RESULT 1095  
ID AM06762 standard; protein; 155 AA.  
DE Human foetal protein, SEQ ID NO: 970.  
PN WO200155339-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 4; Length 155;  
RESULT 1096  
ID AAW29673 standard; protein; 189 AA.  
DE Homo sapiens clone CO851\_1 secreted protein.  
PN WO9832853-A2.  
PD 30-JUL-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 2; Length 189;  
RESULT 1097  
ID ADS93517 standard; protein; 224 AA.  
DE Apple tree alpha-farnesene synthase partial protein SeqID 7.  
PD 29-APR-2004.  
PA (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 224;  
RESULT 1098  
ID AAW2260 standard; protein; 242 AA.  
DE C. utilis crtw protein.  
PN JP10248575-A.  
PD 22-SEP-1998.  
PA (KIRI) KIRIN BREWERY KK.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 2; Length 242;  
RESULT 1099  
ID AD061157 standard; protein; 242 AA.  
DE A. aurantiacum ketolase.  
PN DE10238978-A1.  
PD 04-MAR-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 242;  
RESULT 1100  
ID AD061074 standard; protein; 242 AA.  
DE A. aurantiacum ketolase.  
PN DE10258971-A1.  
PD 04-MAR-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 242;  
RESULT 1101  
ID ADQ38243 standard; protein; 242 AA.  
DE Agrobacterium aurantiacum ketolase.  
PN DE10258971-A1.  
PD 01-JUL-2004.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 242;  
RESULT 1102  
ID ADR03858 standard; protein; 242 AA.  
DE Agrobacterium aurantiacum ketolase SEQ ID NO: 16.  
PN WO2004063359-A2.  
PD 29-JUL-2004.  
PA (BADI) BASF AG.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 242;  
RESULT 1103  
ID ADR03938 standard; protein; 242 AA.  
DE A. aurantiacum ketolase.  
PN WO2004063358-A1.

PD 29-JUL-2004.  
PA (BADI) BASF AG.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 242;  
RESULT 1104  
ID ABU29533 standard; protein; 249 AA.  
DE Protein encoded by Prokaryotic essential gene #15060.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 6; Length 249;  
RESULT 1105  
ID ADS29715 standard; protein; 249 AA.  
DE Bacterial polypeptide #18748.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 249;  
RESULT 1106  
ID ABP38072 standard; protein; 289 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:2917.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 5; Length 289;  
RESULT 1107  
ID ADS07459 standard; protein; 289 AA.  
DE Staphylococcus epidermis polypeptide seqid 6754.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC) DOUCETTE-STAMM L.  
PA (BUSH) BUSH D.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 289;  
RESULT 1108  
ID ABG71364 standard; protein; 294 AA.  
DE Potato starch degrading enzyme CSD23.  
PN WO200286112-A2.  
PD 31-OCT-2002.  
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 6; Length 294;  
RESULT 1109  
ID ADC94895 standard; protein; 327 AA.  
DE E. faecium protein sequence SEQ ID 4522.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 7; Length 327;  
RESULT 1110  
ID ADO29264 standard; protein; 347 AA.  
DE Mouse GPCR CNR2, SEQ ID NO:365.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 8; Length 347;  
RESULT 1111  
ID ABB57956 standard; protein; 351 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 660.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 13.4%; Score 55; DB 4; Length 351;  
RESULT 1112  
ID ADR03938 standard; protein; 242 AA.  
DE A. aurantiacum ketolase.  
PN WO2004063358-A1.

RESULT 1112  
ID AAR53932 standard; protein; 354 AA.  
DE Interleukin 8 (IL-8) receptor.  
PN JF06100595-A.  
PD 12-APR-1994.  
PA (UYBO-) UNIV BOSTON.  
Query Match 13.4%; Score 55; DB 2; Length 354;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1113  
ID ADH61817 standard; protein; 354 AA.  
DE Human interleukin-8 receptor beta protein sequence.  
PN US2003224426-A1.  
PD 04-DEC-2003.  
PA (LIYY/) LI Y.  
Query Match 13.4%; Score 55; DB 8; Length 354;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1114  
ID AAR28272 standard; protein; 355 AA.  
DE Sequence in a high affinity recombinant rabbit interleukin-8 (IL-8)  
receptor polypeptide in F3R.  
PN W09218641-A1.  
PD 29-OCT-1992.  
PA (UYBO-) UNIV BOSTON.  
PA (REPK ) REPLIGEN CORP.  
Query Match 13.4%; Score 55; DB 2; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1115  
ID AAR33420 standard; protein; 355 AA.  
DE Human IL-8 receptor from clone p2.  
PN W09306229-A1.  
PD 01-APR-1993.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
Query Match 13.4%; Score 55; DB 2; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1116  
ID AAR80950 standard; protein; 355 AA.  
DE Recombinant high affinity interleukin-8 receptor subtype A.  
PN W09525126-A1.  
PD 21-SEP-1995.  
PA (REPK ) REPLIGEN CORP.  
PA (UYBO-) UNIV BOSTON.  
Query Match 13.4%; Score 55; DB 2; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1117  
ID AAB09990 standard; protein; 355 AA.  
DE Human IL-8 receptor protein hIL8RB.  
PN JF08103276-A.  
PD 23-APR-1996.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 13.4%; Score 55; DB 2; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1118  
ID AAR0483 standard; protein; 355 AA.  
DE Chimpanzee CXCR2 receptor #1.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.4%; Score 55; DB 5; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1119  
ID AAU80485 standard; protein; 355 AA.  
DE Gorilla CXCR2 receptor #1.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.4%; Score 55; DB 5; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1120  
ID AAU80488 standard; protein; 355 AA.  
DE Orangutan CXCR2 receptor #2.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.4%; Score 55; DB 4; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1121  
ID AAU80482 standard; protein; 355 AA.  
DE Human CXCR2 receptor #1.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.4%; Score 55; DB 5; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1122  
ID AAU80484 standard; protein; 355 AA.  
DE Chimpanzee CXCR2 receptor #2.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.4%; Score 55; DB 5; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1123  
ID AAU80486 standard; protein; 355 AA.  
DE Gorilla CXCR2 receptor #2.  
PN W0200190134-A1.  
PD 29-NOV-2001.  
PA (PHAR-) PHARMACOPEIA INC.  
Query Match 13.4%; Score 55; DB 5; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1124  
ID ABU79168 standard; protein; 355 AA.  
DE Rabbit interleukin 8A (IL8A) receptor.  
PN US2002197706-A1.  
PD 26-DEC-2002.  
PA (CADU-) CADUS PHARM CORP.  
Query Match 13.4%; Score 55; DB 6; Length 355;  
Best Local Similarity 20.8%; Pred. No. 2.4e+02;  
RESULT 1125  
ID AAR28273 standard; protein; 360 AA.  
DE Sequence in a low affinity recombinant human interleukin-8 (IL-8)  
receptor polypeptide in 4AB.  
PN W09218641-A1.  
PD 29-OCT-1992.  
PA (UYBO-) UNIV BOSTON.  
PA (REPK ) REPLIGEN CORP.  
Query Match 13.4%; Score 55; DB 2; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1126  
ID AAR0953 standard; protein; 360 AA.  
DE Recombinant high affinity interleukin-8 receptor subtype B.  
PN W09525126-A1.  
PD 21-SEP-1995.  
PA (REPK ) REPLIGEN CORP.  
PA (UYBO-) UNIV BOSTON.  
Query Match 13.4%; Score 55; DB 2; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1127  
ID AAR80758 standard; protein; 360 AA.  
DE Interleukin 8 receptor B.  
PN US5440021-A.  
PD 08-AUG-1995.  
PA (HEBE/) HEBERT C.  
PA (CHUN/) CHUNTHARAPAI A.  
PA (KIMK/) KIM K J.  
PA (LEEJ/) LEE J.  
Query Match 13.4%; Score 55; DB 2; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1128  
ID AAG80121 standard; protein; 360 AA.  
DE Human CXCR2 protein.  
PN W0200172830-A2.  
PD 04-OCT-2001.  
PA (IPFP-) IPF PHARM GMBH.  
PA (FORS/) FORSSMANN U.  
Query Match 13.4%; Score 55; DB 4; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1129  
ID AAV10557 standard; protein; 360 AA.  
DE Human interleukin 8 receptor beta (IL8RB) polypeptide.  
PN WO200179221-A2.  
PD 25-OCT-2001.  
PA (GENA-) GENAISANCE PHARM INC.  
Query Match 13.4%; Score 55; DB 5; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1130  
ID ABP54802 standard; protein; 360 AA.  
DE Human CORP-related immunoglobulin-derived protein.  
PN WO200272788-A2.  
PD 19-SEP-2002.  
PA (CENZ) CENTOCOR INC.  
Query Match 13.4%; Score 55; DB 5; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1131  
ID ASP81950 standard; protein; 360 AA.  
DE Human interleukin-8 receptor B protein SEQ ID NO:386.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 13.4%; Score 55; DB 6; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1132  
ID ADD48097 standard; protein; 360 AA.  
DE Human Protein NP 001548, SEQ ID NO 13795.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.4%; Score 55; DB 7; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1133  
ID ABM85489 standard; protein; 360 AA.  
DE Human protein sequence hCP35582.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 13.4%; Score 55; DB 7; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1134  
ID ADN04275 standard; protein; 360 AA.  
DE Antipeptidic protein sequence #332.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.4%; Score 55; DB 8; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1135  
ID ADO29524 standard; protein; 360 AA.  
DE Human GPCR IL8RB, SEQ ID NO:626.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 13.4%; Score 55; DB 8; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1136  
ID ADO19582 standard; protein; 360 AA.  
DE Human PRO polypeptide #256.  
PN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.4%; Score 55; DB 8; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;  
RESULT 1137  
ID ADP24006 standard; protein; 360 AA.  
DE PRO polypeptide SEQ ID NO:1184.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.4%; Score 55; DB 8; Length 360;  
Best Local Similarity 20.8%; Pred. No. 2.5e+02;

RESULT 1138  
ID ABG72361 standard; protein; 363 AA.  
DE Rabbit orphan G-protein coupled receptor HM74A.  
PN WO200284298-A2.  
PD 24-OCT-2002.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 13.4%; Score 55; DB 6; Length 363;  
Best Local Similarity 26.8%; Pred. No. 2.5e+02;  
RESULT 1139  
ID ADQ97953 standard; protein; 363 AA.  
DE Mouse cancer associated sequence MP11-028, SEQ ID 930.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 13.4%; Score 55; DB 8; Length 363;  
Best Local Similarity 27.8%; Pred. No. 2.5e+02;  
RESULT 1140  
ID AAB96070 standard; protein; 375 AA.  
DE Putative glutathione-dependent Na/H antiporter transmembrane domain #1.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Query Match 13.4%; Score 55; DB 4; Length 375;  
Best Local Similarity 29.3%; Pred. No. 2.6e+02;  
RESULT 1141  
ID ABB12024 standard; peptide; 399 AA.  
DE Human IL-8R B homologue, SEQ ID NO:2394.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.4%; Score 55; DB 4; Length 399;  
Best Local Similarity 20.8%; Pred. No. 2.8e+02;  
RESULT 1142  
ID AEG13609 standard; protein; 399 AA.  
DE Novel human diagnostic protein #13600.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.4%; Score 55; DB 4; Length 399;  
Best Local Similarity 20.8%; Pred. No. 2.8e+02;  
RESULT 1143  
ID ADK40900 standard; protein; 399 AA.  
DE Novel human kinase protein #7.  
PN WO2003057841-A2.  
PD 17-JUL-2003.  
PA (GRIG/) GRIGORIEV I V.  
PA (SUDA/) SUDARSANAM S.  
Query Match 13.4%; Score 55; DB 7; Length 399;  
Best Local Similarity 20.8%; Pred. No. 2.8e+02;  
RESULT 1144  
ID ADR15624 standard; protein; 399 AA.  
DE Kinase 35582 HCT7327, SEQ ID 17.  
PN WO2004069154-A2.  
PD 19-AUG-2004.  
PA (GRIG/) GRIGORIEV I V.  
PA (SUDA/) SUDARSANAM S.  
Query Match 13.4%; Score 55; DB 8; Length 399;  
Best Local Similarity 20.8%; Pred. No. 2.8e+02;  
RESULT 1145  
ID AAG07601 standard; protein; 428 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4817.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 13.4%; Score 55; DB 3; Length 428;  
Best Local Similarity 24.5%; Pred. No. 3e+02;  
RESULT 1146  
ID AAU34470 standard; protein; 439 AA.  
DE E. coli cellular proliferation protein #51.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.4%; Score 55; DB 4; Length 439;

Best Local Similarity 24.6%; Pred. No. 3.1e+02;  
RESULT 1147  
ID ABU28522 standard; protein; 439 AA.  
DE Protein encoded by Prokaryotic essential gene #14049.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.4%; Score 55; DB 6; Length 439;  
Best Local Similarity 24.6%; Pred. No. 3.1e+02;  
RESULT 1148  
ID ABU28316 standard; protein; 443 AA.  
DE Protein encoded by Prokaryotic essential gene #13843.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.4%; Score 55; DB 6; Length 443;  
Best Local Similarity 35.8%; Pred. No. 3.1e+02;  
RESULT 1149  
ID AAG07600 standard; protein; 467 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4816.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 13.4%; Score 55; DB 3; Length 467;  
Best Local Similarity 24.5%; Pred. No. 3.3e+02;  
RESULT 1150  
ID ABB67349 standard; protein; 526 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28839.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.4%; Score 55; DB 4; Length 526;  
Best Local Similarity 34.9%; Pred. No. 3.8e+02;  
RESULT 1151  
ID ADG74258 standard; protein; 570 AA.  
DE Fruit fly frizzled protein, SEQ ID No 43.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 13.4%; Score 55; DB 7; Length 570;  
Best Local Similarity 21.2%; Pred. No. 4.1e+02;  
RESULT 1152  
ID ABB68074 standard; protein; 581 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 31014.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.4%; Score 55; DB 4; Length 581;  
Best Local Similarity 34.9%; Pred. No. 4.2e+02;  
RESULT 1153  
ID AAW31267 standard; protein; 694 AA.  
DE Drosophila frizzled-2 protein (Wnt receptor).  
PN WO9739357-A1.  
PD 23-OCT-1997.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Query Match 13.4%; Score 55; DB 2; Length 694;  
Best Local Similarity 21.2%; Pred. No. 5.2e+02;  
RESULT 1154  
ID ABB58605 standard; protein; 995 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2607.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.4%; Score 55; DB 4; Length 995;  
Best Local Similarity 24.6%; Pred. No. 7.8e+02;  
RESULT 1155  
ID AAR70124 standard; protein; 1064 AA.  
DE IL8-R type 2-GFP 130 fusion protein.  
PN WO956737-A1.  
PD 09-MAR-1995.  
PA (PREN/) PRENDERGAST K F.  
Query Match 13.4%; Score 55; DB 2; Length 1064;  
Best Local Similarity 20.8%; Pred. No. 8.4e+02;  
RESULT 1156  
ID ABU50193 standard; protein; 1139 AA.  
DE Protein encoded by Prokaryotic essential gene #35720.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.4%; Score 55; DB 6; Length 1139;  
Best Local Similarity 23.7%; Pred. No. 9.1e+02;  
RESULT 1157  
ID ADF59164 standard; protein; 58 AA.  
DE Human polypeptide sequence SEQ ID NO:1572.  
PN WO2003080795-A2.  
PD 02-OCT-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 58;  
Best Local Similarity 30.4%; Pred. No. 36;  
RESULT 1158  
ID ABJ03718 standard; protein; 84 AA.  
DE Human ovary specific protein SEQ ID NO: 160.  
PN WO200240720-A2.  
PD 23-MAY-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 13.3%; Score 54.5; DB 5; Length 84;  
Best Local Similarity 27.4%; Pred. No. 55;  
RESULT 1159  
ID ADF04506 standard; protein; 100 AA.  
DE Bacterial polypeptide #619.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.3%; Score 54.5; DB 7; Length 100;  
Best Local Similarity 28.2%; Pred. No. 67;  
RESULT 1160  
ID ABO67299 standard; protein; 109 AA.  
DE Klebsiella pneumoniae polypeptide seqid 13816.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.3%; Score 54.5; DB 7; Length 109;  
Best Local Similarity 35.5%; Pred. No. 74;  
RESULT 1161  
ID ADS88808 standard; protein; 152 AA.  
DE Amino acid sequence of a truncated GPR54 receptor.  
PN EP1464652-A1.  
PD 06-OCT-2004.  
PA (INEM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYPA-) UNIV PARIS SUD.  
PA (UYPA-) UNIV PARIS DESCARTES.  
Query Match 13.3%; Score 54.5; DB 8; Length 152;  
Best Local Similarity 27.3%; Pred. No. 1.1e+02;  
RESULT 1162  
ID AAB14852 standard; protein; 175 AA.  
DE Granulopoietic activity protein bndry4\_2.  
PN WO200040728-A1.  
PD 13-JUL-2000.  
PA (XENG-) XENCOR INC.  
Query Match 13.3%; Score 54.5; DB 3; Length 175;  
Best Local Similarity 26.7%; Pred. No. 1.3e+02;  
RESULT 1163  
ID ADM47962 standard; protein; 244 AA.  
DE Polypeptide sequence #12 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match 13.3%; Score 54.5; DB 8; Length 244;  
Best Local Similarity 28.8%; Pred. No. 1.8e+02;  
RESULT 1164  
ID AAW61620 standard; protein; 245 AA.  
DE Clone HSBP02 of TM4SF superfamily.  
PN WO9831799-A2.  
PD 23-JUL-1998.

[illegible]

PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1182  
ID ABO33459 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1183  
ID ADA06847 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1184  
ID ADA08335 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1185  
ID ADB99628 standard; protein; 245 AA.  
DE Human PRO polypeptide SEQ ID 4.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1186  
ID ADB86911 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1187  
ID ADB66066 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1188  
ID ADB99744 standard; protein; 245 AA.  
DE Human PRO polypeptide SEQ ID 4.  
PN US2003073192-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1189  
ID ADB99399 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1190  
ID ADB65950 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003082732-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1191  
ID ADC17873 standard; protein; 245 AA.  
DE Human PRO polypeptide #1.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1192  
ID ADC23348 standard; protein; 245 AA.  
DE Human transmembrane PRO polypeptide (SeqID 4).  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1193  
ID ADC26041 standard; protein; 245 AA.  
DE Human PRO1560 protein.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1194  
ID ABW01502 standard; protein; 245 AA.  
DE Human receptor protein from clone HSBF02.  
PN US2003129696-A1.  
PD 10-JUL-2003.  
PA (NIJJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (GENTZ/) GENTZ R.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1195  
ID ADD70519 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1196  
ID ADD39596 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1197  
ID ADD70042 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1198  
ID ADD38163 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1199  
ID ADD39119 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.

PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1200  
ID ADD38642 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1201  
ID ADD40073 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1202  
ID ADE04868 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1203  
ID ADE50294 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1204  
ID ADE11174 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1205  
ID ADE19906 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1206  
ID ADD88105 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1207  
ID ADD95400 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1208  
ID ADE06330 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003073195-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1209  
ID ADE38105 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1210  
ID ADE49817 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1211  
ID ADE21375 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1212  
ID ADD88221 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1213  
ID ADD89032 standard; protein; 245 AA.  
DE TAT273.  
PN WO2003057160-A2.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1214  
ID ADD90802 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1215  
ID ADF29800 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1216  
ID ADF55693 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1217  
ID ADF99357 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003078401-A1.  
PD 24-APR-2003.

Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1227				
ID ADE37984 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003104566-A1.				
PD 05-JUN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1228				
ID ADE76073 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003124665-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1229				
ID ADE39396 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003119117-A1.				
PD 26-JUN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1230				
ID ADE04200 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003096364-A1.				
PD 22-MAY-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1231				
ID ADE39797 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003138896-A1.				
PD 24-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1232				
ID ADE19662 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003138903-A1.				
PD 24-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1233				
ID ADE77240 standard; protein; 245 AA.				
DE Human secreted/transmembrane polypeptide PRO1560.				
PN US2003124666-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1234				
ID ADE65348 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003119116-A1.				
PD 26-JUN-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1235				
ID ADE75957 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003124663-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1236				
ID ADE75957 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003124663-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1237				
ID ADE75957 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003124663-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1238				
ID ADE75957 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003124663-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;	DB 8;	Length 245;
Best Local Similarity	25.3%;	Pred. No. 1.8e+02;		
RESULT 1239				
ID ADE75957 standard; protein; 245 AA.				
DE Human PRO polypeptide #2.				
PN US2003124663-A1.				
PD 03-JUL-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	13.3%;	Score 54.5;		

Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1236  
ID ADE37868 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1237  
ID ADE64478 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1238  
ID ADE38813 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1239  
ID ADE51887 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1240  
ID ADD90918 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1241  
ID ADE38697 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1242  
ID ADE37397 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1243  
ID ADE06214 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1244  
ID ADD90073 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1245  
ID ADE38581 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1246  
ID ADE39512 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1247  
ID ADD89117 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1248  
ID ADD8884 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1249  
ID ADE19778 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1250  
ID ADE77356 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1251  
ID ADE65232 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1252  
ID ADE39280 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1253  
ID ADE38465 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1254

ID ADE96377 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1255  
ID ADF25688 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1256  
ID ADF24587 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1257  
ID ADF29323 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1258  
ID ADE96854 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1259  
ID ADG11018 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1260  
ID ADG10902 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1261  
ID ADH31430 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1262  
ID ADH38678 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1263  
ID ADH02892 standard; protein; 245 AA.

DE Human secreted/transmembrane protein PRO1560.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1264  
ID ADH03846 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1265  
ID ADH03369 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1266  
ID ADH29313 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1267  
ID ADH23616 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1268  
ID ADH26946 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1269  
ID ADH38214 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1270  
ID ADH26830 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1271  
ID ADH38098 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1272  
ID ADH38794 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.

PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1273  
ID ADH23732 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1274  
ID ADH40108 standard; protein; 245 AA.  
DE Human PRO1560 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1275  
ID ADH39992 standard; protein; 245 AA.  
DE Human PRO1560 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1276  
ID ADH31314 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1277  
ID ADH29192 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1278  
ID ADH49407 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1279  
ID ADH51871 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1280  
ID ADH49726 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1281  
ID ADH52327 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119130-A1.

PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1282  
ID ADH52443 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1283  
ID ADH58440 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1284  
ID ADH51755 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1285  
ID ADH59316 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1286  
ID ADH04323 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1287  
ID ADI13513 standard; protein; 245 AA.  
DE Novel human secreted and transmembrane protein PRO1560.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1288  
ID ADH61324 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1289  
ID ADK00769 standard; protein; 245 AA.  
DE Human PRO polypeptide #2.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1290  
ID ADL08510 standard; protein; 245 AA.  
DE Human secreted/transmembrane polypeptide PRO1560.  
PN US2003186372-A1.  
PD 02-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1291  
ID ADL31184 standard; protein; 245 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3217.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1292  
ID ADL94523 standard; protein; 245 AA.  
DE Human secreted/transmembrane protein PRO1560.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 245;  
Best Local Similarity 25.3%; Pred. No. 1.8e+02;  
RESULT 1293  
ID ADC79358 standard; protein; 272 AA.  
DE Human G protein coupled receptor X (GPCRX) cDNA seq id 44.  
PN US2003083463-A1.  
PD 01-MAY-2003.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (COLM/) COLMAN S. D.  
PA (SPYT/) SPYTEK K. A.  
PA (BALL/) BALLINGER R. A.  
PA (VERN/) VERNET C. A. M.  
PA (LILL/) LI L.  
PA (SHEN/) SHENOY S. G.  
PA (CASM/) CASHMAN S. J.  
PA (GUSE/) GUSEV V. Y.  
Query Match 13.3%; Score 54.5; DB 7; Length 272;  
Best Local Similarity 25.3%; Pred. No. 2.1e+02;  
RESULT 1294  
ID ADC87479 standard; protein; 279 AA.  
DE Human GPCR protein SEQ ID NO:1932.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 13.3%; Score 54.5; DB 7; Length 279;  
Best Local Similarity 22.2%; Pred. No. 2.1e+02;  
RESULT 1295  
ID AAG75531 standard; protein; 284 AA.  
DE Human colon cancer antigen protein SEQ ID NO:6295.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 284;  
Best Local Similarity 25.3%; Pred. No. 2.2e+02;  
RESULT 1296  
ID ABB47532 standard; protein; 287 AA.  
DE Listeria monocytogenes protein #236.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 13.3%; Score 54.5; DB 5; Length 287;  
Best Local Similarity 26.2%; Pred. No. 2.2e+02;  
RESULT 1297  
ID ABB32938 standard; protein; 287 AA.  
DE Protein encoded by Prokaryotic essential gene #18465.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 287;  
Best Local Similarity 26.2%; Pred. No. 2.2e+02;  
RESULT 1298  
ID ABP61150 standard; protein; 293 AA.  
DE Human GPCR protein #22.  
PN WO200255557-A2.

PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.3%; Score 54.5; DB 5; Length 293;  
Best Local Similarity 25.3%; Pred. No. 2.3e+02;  
RESULT 1299  
ID ADC12690 standard; protein; 316 AA.  
DE Human GPCR protein, SEQ ID NO 22.  
PN WO2003000893-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS BHP.  
Query Match 13.3%; Score 54.5; DB 7; Length 316;  
Best Local Similarity 34.8%; Pred. No. 2.5e+02;  
RESULT 1300  
ID AAG71540 standard; protein; 318 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1221.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 13.3%; Score 54.5; DB 4; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1301  
ID AAG72395 standard; protein; 318 AA.  
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2076.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 13.3%; Score 54.5; DB 4; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1302  
ID ABP95657 standard; protein; 318 AA.  
DE Human GPCR polypeptide SEQ ID NO 124.  
PN WO200216548-A2.  
PD 28-FEB-2002.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 13.3%; Score 54.5; DB 5; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1303  
ID AAU95699 standard; protein; 318 AA.  
DE Human olfactory and pheromone G protein-coupled receptor #186.  
PN WO200224726-A2.  
PD 28-MAR-2002.  
PA (CHEM-) CHENCOM SA.  
Query Match 13.3%; Score 54.5; DB 5; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1304  
ID AAB71168 standard; protein; 318 AA.  
DE Human GPCR protein SEQ ID 12.  
PN WO200250275-A2.  
PD 27-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.3%; Score 54.5; DB 5; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1305  
ID ABU11220 standard; protein; 318 AA.  
DE Human G-protein coupled receptor GCRC-73.  
PN WO200279448-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1306  
ID ADC86371 standard; protein; 318 AA.  
DE Human GPCR protein SEQ ID NO:824.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 13.3%; Score 54.5; DB 7; Length 318;  
Best Local Similarity 22.4%; Pred. No. 2.5e+02;  
RESULT 1307  
ID ADD12737 standard; protein; 318 AA.

DE Novel human olfactory receptor (OR) seq id 7.  
PN US2003109692-A1.  
PD 12-JUN-2003.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (LILL/) LI L.  
PA (BALL/) BALLINGER R A.  
PA (CASM/) CASMAN S J.  
PA (SPYT/) SPYTEK K A.  
PA (BAUM/) BAUMGARTNER J C.  
PA (BURG/) BURGESS C E.  
Query Match 13.3%; Score 54.5; DB 7; Length 318;  
Best Local Similarity 23.4%; Pred. No. 2.5e+02;  
RESULT 1308  
ID ADC12678 standard; protein; 323 AA.  
DE Human GPCR protein, SEQ ID NO 10.  
PN WO2003000893-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS EHP.  
Query Match 13.3%; Score 54.5; DB 7; Length 323;  
Best Local Similarity 27.3%; Pred. No. 2.5e+02;  
RESULT 1309  
ID ABU48609 standard; protein; 362 AA.  
DE Protein encoded by Prokaryotic essential gene #34136.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 362;  
Best Local Similarity 33.3%; Pred. No. 2.9e+02;  
RESULT 1310  
ID ABU19559 standard; protein; 368 AA.  
DE Protein encoded by Prokaryotic essential gene #5086.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 368;  
Best Local Similarity 23.7%; Pred. No. 2.9e+02;  
RESULT 1311  
ID AAB75200 standard; protein; 374 AA.  
DE Drosophila gustatory receptor GR23A.1b protein sequence.  
PN WO200077208-A2.  
PD 21-DEC-2000.  
PA (UYVA) UNIV YALE.  
Query Match 13.3%; Score 54.5; DB 4; Length 374;  
Best Local Similarity 35.4%; Pred. No. 3e+02;  
RESULT 1312  
ID AAB30507 standard; protein; 374 AA.  
DE Fruit fly gustatory receptor protein, Gr23A1b.  
PN WO200268593-A2.  
PD 06-SEP-2002.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match 13.3%; Score 54.5; DB 5; Length 374;  
Best Local Similarity 35.4%; Pred. No. 3e+02;  
RESULT 1313  
ID AAB03545 standard; protein; 397 AA.  
DE Human G-protein coupled receptor, AXOR12 related protein.  
PN WO200142486-A1.  
PD 14-JUN-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 13.3%; Score 54.5; DB 4; Length 397;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1314  
ID ADC87413 standard; protein; 397 AA.  
DE Human GPCR protein SEQ ID NO:1866.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 13.3%; Score 54.5; DB 7; Length 397;  
Best Local Similarity 28.6%; Pred. No. 3.2e+02;  
RESULT 1315  
ID AAY91094 standard; protein; 398 AA.  
DE Human G protein-coupled receptor protein hOT7T175.  
PN WO200024890-A1.  
PD 04-MAY-2000.  
PA (TAXE) TAKEDA CHEM IND LTD.  
Query Match 13.3%; Score 54.5; DB 3; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1316  
ID AAB08540 standard; protein; 398 AA.  
DE A human G protein-coupled receptor designated GPR54.  
PN WO200050563-A2.  
PD 31-AUG-2000.  
PA (MERI) MERCK & CO INC.  
PA (MERI) MERCK FROSST CANADA & CO.  
PA (UTOR) UNIV TORONTO.  
Query Match 13.3%; Score 54.5; DB 3; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1317  
ID AAU08997 standard; protein; 398 AA.  
DE Human G protein-coupled receptor, GPCR, 52872.  
PN WO200164882-A2.  
PD 07-SEP-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1318  
ID AAB03544 standard; protein; 398 AA.  
DE Human G-protein coupled receptor, AXOR12.  
PN WO200142486-A1.  
PD 14-JUN-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 13.3%; Score 54.5; DB 4; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1319  
ID AAG64300 standard; protein; 398 AA.  
DE Human GTP-binding protein-coupled receptor GPRV78.  
PN WO200148189-A1.  
PD 05-JUL-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 13.3%; Score 54.5; DB 4; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1320  
ID AAM51415 standard; protein; 398 AA.  
DE Human OT7T175 SEQ ID NO 7.  
PN WO200175104-A1.  
PD 11-OCT-2001.  
PA (TAXE) TAKEDA CHEM IND LTD.  
Query Match 13.3%; Score 54.5; DB 4; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1321  
ID AAE04550 standard; protein; 398 AA.  
DE Human G-protein coupled receptor-6 (GCREC-6) protein.  
PN WO200142288-A2.  
PD 14-JUN-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1322  
ID ABB79864 standard; protein; 398 AA.  
DE Human G-protein coupled receptor GPR54.  
PN WO200259344-A2.  
PD 01-AUG-2002.  
PA (MERI) MERCK & CO INC.  
Query Match 13.3%; Score 54.5; DB 5; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1323  
ID ABP97222 standard; protein; 398 AA.  
DE Tumour-associated antigenic target protein TAT184 SEQ ID NO:104.  
PN WO2003024392-A2.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;

RESULT 1324  
ID ABU09340 standard; protein; 398 AA.  
DE Human SNORF11 receptor.  
PN US2003022839-A1.  
PD 30-JAN-2003.  
PA (BORO/) BOROWSKY B E.  
PA (QUAN/) QUAN Y.  
PA (SMIT/) SMITH K E.  
Query Match 13.3%; Score 54.5; DB 6; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1325  
ID ABP81995 standard; protein; 398 AA.  
DE Human G protein-coupled receptor GPR54 protein SEQ ID NO:477.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1326  
ID ABU61629 standard; protein; 398 AA.  
DE Human G protein-coupled receptor SNORF11.  
PN US2002077469-A1.  
PD 20-JUN-2002.  
PA (BORO/) BOROWSKY B E.  
PA (QUAN/) QUAN Y.  
PA (SMIT/) SMITH K E.  
Query Match 13.3%; Score 54.5; DB 7; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1327  
ID ADN39505 standard; protein; 398 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A105.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1328  
ID ADN39430 standard; protein; 398 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A30.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 13.3%; Score 54.5; DB 7; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1329  
ID ADG19755 standard; protein; 398 AA.  
DE Human G protein coupled receptor (GPCR) 52872.  
PN US2003215860-A1.  
PD 20-NOV-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1330  
ID ADL91585 standard; protein; 398 AA.  
DE Human immune-related polypeptide PRO47351, SEQ ID NO:100.  
PN WO2004024072-A2.  
PD 25-MAR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1331  
ID ADO29412 standard; protein; 398 AA.  
DE Human GPCR GPR54, SEQ ID NO:514.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1332  
ID ADQ89080 standard; protein; 398 AA.  
DE Human urological disorder related protein 52872 SEQ:32.  
PN WO2004065576-A2.  
PD 05-AUG-2004.

PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1333  
ID ADR21325 standard; protein; 398 AA.  
DE Human metastatin-related protein OT7T175, SEQ ID 9.  
PN WO2004063221-A1.  
PD 29-JUL-2004.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1334  
ID ADS88809 standard; protein; 398 AA.  
DE Amino acid sequence of a mutant GPR54 receptor.  
PN EP1464652-A1.  
PD 06-OCT-2004.  
PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYPA-) UNIV PARIS SUD.  
PA (UYPA-) UNIV PARIS DESCARTES.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1335  
ID ADS88807 standard; protein; 398 AA.  
DE Amino acid sequence of GPR54 receptor.  
PN EP1464652-A1.  
PD 06-OCT-2004.  
PA (INRM-) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYPA-) UNIV PARIS SUD.  
PA (UYPA-) UNIV PARIS DESCARTES.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1336  
ID ADT05941 standard; protein; 398 AA.  
DE Human OT7T175 polypeptide.  
PN WO2004080479-A1.  
PD 23-SEP-2004.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 13.3%; Score 54.5; DB 8; Length 398;  
Best Local Similarity 27.3%; Pred. No. 3.2e+02;  
RESULT 1337  
ID AAY32141 standard; protein; 403 AA.  
DE Human G-protein coupled receptor AXOR3.  
PN WO9552944-A1.  
PD 21-OCT-1999.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 13.3%; Score 54.5; DB 2; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1338  
ID RAY57287 standard; protein; 403 AA.  
DE Human GPCR protein (HGRP) sequence (clone ID 2705201).  
PN WO200015793-A2.  
PD 23-MAR-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 13.3%; Score 54.5; DB 3; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1339  
ID RAB43085 standard; protein; 403 AA.  
DE Human ORPX ORF2849 polypeptide sequence SEQ ID NO:5698.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.3%; Score 54.5; DB 3; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1340  
ID AAW93548 standard; protein; 403 AA.  
DE Human polypeptide, SEQ ID NO: 3306.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 13.3%; Score 54.5; DB 4; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1341  
ID AAM78615 standard; protein; 403 AA.

DE Human protein SEQ ID NO 1277.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1342  
ID ABG96333 standard; protein; 403 AA.  
DE Human ovarian cancer marker M446.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.3%; Score 54.5; DB 5; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1343  
ID ASU54869 standard; protein; 403 AA.  
DE Human G-protein coupled receptor #5, Incyte clone 2705201CD1.  
PN US2002106655-A1.  
PD 08-AUG-2002.  
PA (BAND/) BANDMAN O.  
PA (LALP/) LAL P G.  
PA (TANG/) TANG Y T.  
PA (BAUG/) BAUGHN M R.  
Query Match 13.3%; Score 54.5; DB 5; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1344  
ID ABB81627 standard; protein; 403 AA.  
DE Human GPCR5B-like protein SEQ ID NO:2.  
PN WO200252931-A2.  
PD 11-JUL-2002.  
PA (DELT-) DELTAGEN INC.  
Query Match 13.3%; Score 54.5; DB 5; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1345  
ID ABB81712 standard; protein; 403 AA.  
DE Human G-protein-coupled receptor GPCR5B protein SEQ ID NO:599.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1346  
ID ADN95281 standard; protein; 403 AA.  
DE Human BEC/LEC-related protein sequence SeqID203.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDM-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD.  
Query Match 13.3%; Score 54.5; DB 7; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1347  
ID ADJ31962 standard; protein; 403 AA.  
DE Human orphan GPCR5B protein.  
PN US2003235912-A1.  
PD 25-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1348  
ID ADI28533 standard; protein; 403 AA.  
DE Mouse GPCR5B polypeptide.  
PN WO2004001060-A2.  
PD 31-DEC-2003.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 13.3%; Score 54.5; DB 8; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1349  
ID ADI31273 standard; protein; 403 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3306.  
PN EPI396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.3%; Score 54.5; DB 8; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1350  
ID ADO29462 standard; protein; 403 AA.  
DE Human GPCR5B, SEQ ID NO:564.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 403;  
Best Local Similarity 26.4%; Pred. No. 3.2e+02;  
RESULT 1351  
ID AAW98252 standard; protein; 413 AA.  
DE H. pylori GHPD 1312 protein.  
PN WO9843478-A1.  
PD 08-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.3%; Score 54.5; DB 2; Length 413;  
Best Local Similarity 25.0%; Pred. No. 3.3e+02;  
RESULT 1352  
ID ABU30707 standard; protein; 413 AA.  
DE Protein encoded by Prokaryotic essential gene #16234.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 413;  
Best Local Similarity 25.0%; Pred. No. 3.3e+02;  
RESULT 1353  
ID AAY32142 standard; protein; 427 AA.  
DE Human G-protein coupled receptor AXOR3-related polypeptide.  
PN WO9952944-A1.  
PD 21-OCT-1999.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 13.3%; Score 54.5; DB 2; Length 427;  
Best Local Similarity 26.4%; Pred. No. 3.5e+02;  
RESULT 1354  
ID ABU15404 standard; protein; 438 AA.  
DE Protein encoded by Prokaryotic essential gene #931.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 438;  
Best Local Similarity 25.7%; Pred. No. 3.6e+02;  
RESULT 1355  
ID ADK62370 standard; protein; 442 AA.  
DE Disease treating protein complex-derived protein #311.  
PN EPI338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 13.3%; Score 54.5; DB 7; Length 442;  
Best Local Similarity 30.0%; Pred. No. 3.6e+02;  
RESULT 1356  
ID ADO08029 standard; protein; 481 AA.  
DE Mouse polypeptide #36.  
PN US2004071700-A1.  
PD 15-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Query Match 13.3%; Score 54.5; DB 8; Length 481;  
Best Local Similarity 27.7%; Pred. No. 4e+02;  
RESULT 1357  
ID AAW49911 standard; protein; 482 AA.  
DE Mouse CLK serine/threonine kinase mCLKI.  
PN WO9748723-A2.  
PD 24-DEC-1997.  
PA (PLAC-) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
Query Match 13.3%; Score 54.5; DB 2; Length 482;  
Best Local Similarity 28.3%; Pred. No. 4e+02;  
RESULT 1358  
ID ADO08030 standard; protein; 483 AA.  
DE Mouse polypeptide #37.  
PN US2004071700-A1.  
PD 15-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Query Match 13.3%; Score 54.5; DB 8; Length 483;

Best Local Similarity 28.3%; Pred. No. 4e+02;  
RESULT 1359  
ID ABO5018 standard; protein; 499 AA.  
DE Murine cancer-associated protein (CAP) MP07-112.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 499;  
Best Local Similarity 20.7%; Pred. No. 4.1e+02;  
RESULT 1360  
ID ADA34498 standard; protein; 509 AA.  
DE Acinetobacter baumannii protein #1659.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.3%; Score 54.5; DB 6; Length 509;  
Best Local Similarity 32.4%; Pred. No. 4.2e+02;  
RESULT 1361  
ID AAU10966 standard; protein; 510 AA.  
DE Xylella fastidiosa protein XFGUWJ.  
PN WO200185905-A2.  
PD 15-NOV-2001.  
PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.  
Query Match 13.3%; Score 54.5; DB 5; Length 510;  
Best Local Similarity 34.0%; Pred. No. 4.2e+02;  
RESULT 1362  
ID AAU49463 standard; protein; 518 AA.  
DE Propionibacterium acnes immunogenic protein #10359.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.3%; Score 54.5; DB 4; Length 518;  
Best Local Similarity 18.5%; Pred. No. 4.3e+02;  
RESULT 1363  
ID AEM45982 standard; protein; 518 AA.  
DE Propionibacterium acnes membrane-related polypeptide #10658.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.3%; Score 54.5; DB 6; Length 518;  
Best Local Similarity 18.5%; Pred. No. 4.3e+02;  
RESULT 1364  
ID ABB58577 standard; protein; 560 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2523.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.3%; Score 54.5; DB 4; Length 560;  
Best Local Similarity 26.3%; Pred. No. 4.7e+02;  
RESULT 1365  
ID ABB67283 standard; protein; 576 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 28641.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.3%; Score 54.5; DB 4; Length 576;  
Best Local Similarity 26.3%; Pred. No. 4.9e+02;  
RESULT 1366  
ID ABR53821 standard; protein; 616 AA.  
DE Protein sequence #SEQ ID 2507.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 13.3%; Score 54.5; DB 6; Length 616;  
Best Local Similarity 32.8%; Pred. No. 5.2e+02;  
RESULT 1367  
ID ADK65000 standard; protein; 616 AA.  
DE Disease treating protein complex-derived protein #1516.  
PN EP1338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 13.3%; Score 54.5; DB 7; Length 616;  
Best Local Similarity 32.8%; Pred. No. 5.2e+02;  
RESULT 1368  
ID ADF70413 standard; protein; 641 AA.  
DE Orphan receptor ligand-related human protein SeqID36.  
PN WO2003071272-A1.  
PD 28-AUG-2003.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match 13.3%; Score 54.5; DB 7; Length 641;  
Best Local Similarity 26.4%; Pred. No. 5.5e+02;  
RESULT 1369  
ID ABB63136 standard; protein; 747 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16200.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 13.3%; Score 54.5; DB 4; Length 747;  
Best Local Similarity 32.0%; Pred. No. 6.5e+02;  
RESULT 1370  
ID ADI41001 standard; protein; 931 AA.  
DE Mouse EMR1 hormone receptor.  
PN US2004018976-A1.  
PD 29-JAN-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
Query Match 13.3%; Score 54.5; DB 8; Length 931;  
Best Local Similarity 34.1%; Pred. No. 8.4e+02;  
RESULT 1371  
ID ADO29306 standard; protein; 931 AA.  
DE Mouse GPCR EMR1, SEQ ID NO:407.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIN-) PRIMAL INC.  
Query Match 13.3%; Score 54.5; DB 8; Length 931;  
Best Local Similarity 34.1%; Pred. No. 8.4e+02;  
RESULT 1372  
ID ABR41799 standard; protein; 1653 AA.  
DE Human DITHP growth/development-associated protein.  
PN WO200297031-A2.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 1653;  
Best Local Similarity 27.3%; Pred. No. 1.6e+03;  
RESULT 1373  
ID ABU11522 standard; protein; 1653 AA.  
DE Human MDTT polypeptide SEQ ID 469.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.3%; Score 54.5; DB 6; Length 1653;  
Best Local Similarity 27.3%; Pred. No. 1.6e+03;  
RESULT 1374  
ID ABG13667 standard; protein; 1682 AA.  
DE Novel human diagnostic protein #13658.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 1682;  
Best Local Similarity 27.3%; Pred. No. 1.6e+03;  
RESULT 1375  
ID ABG07239 standard; protein; 1682 AA.  
DE Novel human diagnostic protein #7230.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 1682;  
Best Local Similarity 27.3%; Pred. No. 1.6e+03;  
RESULT 1376  
ID AAW10344 standard; protein; 2763 AA.  
DE Maize dwarf mosaic virus polypeptide.  
PN WO9702352-A1.  
PD 23-JAN-1997.  
PA (CIBA ) CIBA GEIGY AG.  
Query Match 13.3%; Score 54.5; DB 2; Length 2763;

Best Local Similarity 30.4%; Pred. No. 2.9e+03;  
RESULT 1377  
ID AAR22268 standard; protein; 2818 AA.  
DE NF1 gene product.  
PN WO9200387-A.  
PD 09-JAN-1992.  
PA (UNMI ) UNIV MICHIGAN.  
Query Match 13.3%; Score 54.5; DB 2; Length 2818;  
Best Local Similarity 27.3%; Pred. No. 2.9e+03;  
RESULT 1378  
ID AAW13280 standard; protein; 2818 AA.  
DE Human neurofibromin.  
PN US5605799-A.  
PD 25-FEB-1997.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 13.3%; Score 54.5; DB 2; Length 2818;  
Best Local Similarity 27.3%; Pred. No. 2.9e+03;  
RESULT 1379  
ID AAE03486 standard; protein; 2818 AA.  
DE Human neurofibromatosis type 1 (NF1) protein.  
PN US6261761-B1.  
PD 17-JUL-2001.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 13.3%; Score 54.5; DB 4; Length 2818;  
Best Local Similarity 27.3%; Pred. No. 2.9e+03;  
RESULT 1380  
ID ABB08078 standard; protein; 2818 AA.  
DE Human neurofibromatosis 1 (NF1) protein.  
PN US6365126-B1.  
PD 02-APR-2002.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 13.3%; Score 54.5; DB 5; Length 2818;  
Best Local Similarity 27.3%; Pred. No. 2.9e+03;  
RESULT 1381  
ID ABG13665 standard; protein; 2871 AA.  
DE Novel human diagnostic protein #13656.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 2871;  
Best Local Similarity 27.3%; Pred. No. 3e+03;  
RESULT 1382  
ID ABG13555 standard; protein; 2871 AA.  
DE Novel human diagnostic protein #13546.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 2871;  
Best Local Similarity 27.3%; Pred. No. 3e+03;  
RESULT 1383  
ID ABG07243 standard; protein; 2871 AA.  
DE Novel human diagnostic protein #7234.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 2871;  
Best Local Similarity 27.3%; Pred. No. 3e+03;  
RESULT 1384  
ID ABG13666 standard; protein; 2891 AA.  
DE Novel human diagnostic protein #13657.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 2891;  
Best Local Similarity 27.3%; Pred. No. 3e+03;  
RESULT 1385  
ID ABG07240 standard; protein; 2891 AA.  
DE Novel human diagnostic protein #7231.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 2891;  
Best Local Similarity 27.3%; Pred. No. 3e+03;  
RESULT 1386  
ID AEG13556 standard; protein; 2891 AA.  
DE Novel human diagnostic protein #13547.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 54.5; DB 4; Length 2891;  
Best Local Similarity 27.3%; Pred. No. 3e+03;  
RESULT 1387  
ID AAM91185 standard; protein; 77 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:18778.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.2%; Score 54; DB 4; Length 77;  
Best Local Similarity 31.0%; Pred. No. 58;  
RESULT 1388  
ID AAO23284 standard; protein; 81 AA.  
DE Glyceraldehyde-3-phosphate protein 8\_91.  
PN CN1386850-A.  
PD 25-DEC-2002.  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
Query Match 13.2%; Score 54; DB 6; Length 81;  
Best Local Similarity 34.3%; Pred. No. 61;  
RESULT 1389  
ID AAM24134 standard; protein; 89 AA.  
DE Human EST encoded protein SEQ ID NO: 1659.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.2%; Score 54; DB 4; Length 89;  
Best Local Similarity 24.0%; Pred. No. 68;  
RESULT 1390  
ID ADL05626 standard; protein; 98 AA.  
DE M. catarrhalis protein #1392.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.2%; Score 54; DB 8; Length 98;  
Best Local Similarity 30.4%; Pred. No. 76;  
RESULT 1391  
ID AAO08448 standard; protein; 133 AA.  
DE Human polypeptide SEQ ID NO 20340.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.2%; Score 54; DB 4; Length 133;  
Best Local Similarity 36.4%; Pred. No. 1.1e+02;  
RESULT 1392  
ID ADC94829 standard; protein; 182 AA.  
DE E. faecium protein sequence SEQ ID 4456.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.2%; Score 54; DB 7; Length 182;  
Best Local Similarity 26.5%; Pred. No. 1.5e+02;  
RESULT 1393  
ID ADA55585 standard; protein; 188 AA.  
DE Human protein, SEQ ID 3153.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
Query Match 13.2%; Score 54; DB 6; Length 188;  
Best Local Similarity 22.6%; Pred. No. 1.6e+02;  
RESULT 1394  
ID AAW69535 standard; protein; 242 AA.  
DE ctw2396 gene product beta-carotene beta-oxygenase.  
PN JP10155497-A.  
PD 16-JUN-1998.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 13.2%; Score 54; DB 2; Length 242;  
Best Local Similarity 25.5%; Pred. No. 2.1e+02;

RESULT 1395  
 ID ABU97244 standard; protein; 242 AA.  
 DE Enzyme polypeptide #10.  
 PN WO20029905-A2.  
 PD 12-DEC-2002.  
 PA (HOFF ) ROCHE VITAMINS AG.  
 Query Match 13.2%; Score 54; DB 6; Length 242;  
 Best Local Similarity 25.5%; Pred. No. 2.1e+02;  
 RESULT 1396  
 ID ADO61161 standard; protein; 242 AA.  
 DE P. marcusii ketolase.  
 PN DE10238978-A1.  
 PD 04-MAR-2004.  
 PA (SUNG-) SUNGENE GMBH & CO KGAA.  
 Query Match 13.2%; Score 54; DB 8; Length 242;  
 Best Local Similarity 25.5%; Pred. No. 2.1e+02;  
 RESULT 1397  
 ID ADO61078 standard; protein; 242 AA.  
 DE P. marcusii ketolase.  
 PN DE10238980-A1.  
 PD 04-MAR-2004.  
 PA (SUNG-) SUNGENE GMBH & CO KGAA.  
 Query Match 13.2%; Score 54; DB 8; Length 242;  
 Best Local Similarity 25.5%; Pred. No. 2.1e+02;  
 RESULT 1398  
 ID ADO38247 standard; protein; 242 AA.  
 DE Paracoccus marcusii ketolase.  
 PN DE10258971-A1.  
 PD 01-JUL-2004.  
 PA (SUNG-) SUNGENE GMBH & CO KGAA.  
 Query Match 13.2%; Score 54; DB 8; Length 242;  
 Best Local Similarity 25.5%; Pred. No. 2.1e+02;  
 RESULT 1399  
 ID ADO3862 standard; protein; 242 AA.  
 DE Paracoccus marcusii ketolase SEQ ID NO: 20.  
 PN WO2004063359-A2.  
 PD 29-JUL-2004.  
 PA (BADI ) BASF AG.  
 Query Match 13.2%; Score 54; DB 8; Length 242;  
 Best Local Similarity 25.5%; Pred. No. 2.1e+02;  
 RESULT 1400  
 ID ADO3942 standard; protein; 242 AA.  
 DE P. marcusii ketolase.  
 PN WO2004063358-A1.  
 PD 29-JUL-2004.  
 PA (BADI ) BASF AG.  
 Query Match 13.2%; Score 54; DB 8; Length 242;  
 Best Local Similarity 25.5%; Pred. No. 2.1e+02;  
 RESULT 1401  
 ID ABM8551 standard; protein; 294 AA.  
 DE Human protein sequence HCF34831.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 13.2%; Score 54; DB 7; Length 294;  
 Best Local Similarity 19.6%; Pred. No. 2.6e+02;  
 RESULT 1402  
 ID ADG76719 standard; protein; 331 AA.  
 DE Phospholipase amino acid sequence SEQ ID NO:102.  
 PN WO2003089620-A2.  
 PD 30-OCT-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 13.2%; Score 54; DB 8; Length 331;  
 Best Local Similarity 57.1%; Pred. No. 3e+02;  
 RESULT 1403  
 ID ABU38629 standard; protein; 347 AA.  
 DE Protein encoded by Prokaryotic essential gene #24156.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 13.2%; Score 54; DB 6; Length 347;  
 Best Local Similarity 40.5%; Pred. No. 3.2e+02;  
 RESULT 1404

ID AAR80952 standard; protein; 358 AA.  
 DE Recombinant high affinity interleukin-8 receptor subtype B.  
 PN WO9525126-A1.  
 PD 21-SEP-1995.  
 PA (REPK ) REPLIGEN CORP.  
 PA (UYBO-) UNIV BOSTON.  
 Query Match 13.2%; Score 54; DB 2; Length 358;  
 Best Local Similarity 24.5%; Pred. No. 3.3e+02;  
 RESULT 1405  
 ID AAW97788 standard; protein; 360 AA.  
 DE Pig-tailed macaque HIV/SIV receptor protein Bob.  
 PN WO903888-A1.  
 PD 28-JAN-1999.  
 PA (UYNY ) UNIV NEW YORK STATE.  
 Query Match 13.2%; Score 54; DB 2; Length 360;  
 Best Local Similarity 26.4%; Pred. No. 3.3e+02;  
 RESULT 1406  
 ID AAU04037 standard; protein; 360 AA.  
 DE Pigtailed macaque SIV translocation agent, BOB.  
 PN US6251582-B1.  
 PD 26-JUN-2001.  
 PA (UYNY ) UNIV NEW YORK STATE.  
 Query Match 13.2%; Score 54; DB 4; Length 360;  
 Best Local Similarity 26.4%; Pred. No. 3.3e+02;  
 RESULT 1407  
 ID ABB79748 standard; protein; 360 AA.  
 DE Pig-tailed macaque G-protein coupled receptor BOB.  
 PN US2002076694-A1.  
 PD 20-JUN-2002.  
 PA (LITT/) LITTMAN D R.  
 PA (DENG/) DENG H.  
 PA (UNUT/) UNUTMAZ D.  
 PA (KEWA/) KEWALRAMANI V N.  
 Query Match 13.2%; Score 54; DB 5; Length 360;  
 Best Local Similarity 26.4%; Pred. No. 3.3e+02;  
 RESULT 1408  
 ID ABU41907 standard; protein; 378 AA.  
 DE Protein encoded by Prokaryotic essential gene #27434.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 13.2%; Score 54; DB 6; Length 378;  
 Best Local Similarity 34.2%; Pred. No. 3.5e+02;  
 RESULT 1409  
 ID ABO78765 standard; protein; 384 AA.  
 DE Pseudomonas aeruginosa polypeptide #10940.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 13.2%; Score 54; DB 7; Length 384;  
 Best Local Similarity 34.5%; Pred. No. 3.6e+02;  
 RESULT 1410  
 ID ABO74075 standard; protein; 400 AA.  
 DE Pseudomonas aeruginosa polypeptide #6250.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 13.2%; Score 54; DB 7; Length 400;  
 Best Local Similarity 40.5%; Pred. No. 3.7e+02;  
 RESULT 1411  
 ID ADC87419 standard; protein; 412 AA.  
 DE Human GPCR protein SEQ ID NO:1872.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Query Match 13.2%; Score 54; DB 7; Length 412;  
 Best Local Similarity 28.6%; Pred. No. 3.9e+02;  
 RESULT 1412  
 ID ADF08669 standard; protein; 434 AA.  
 DE Bacterial polypeptide #2982.  
 PN US6605709-B1.  
 PD 12-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 13.2%; Score 54; DB 7; Length 434;  
 Best Local Similarity 41.4%; Pred. No. 4.1e+02;  
 RESULT 1413  
 ID ABU18049 standard; protein; 483 AA.  
 DE Protein encoded by Prokaryotic essential gene #3576.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (SLIT-) ELITRA PHARM INC.  
 Query Match 13.2%; Score 54; DB 6; Length 483;  
 Best Local Similarity 31.5%; Pred. No. 4.6e+02;  
 RESULT 1414  
 ID ABB66372 standard; protein; 504 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 25908.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 13.2%; Score 54; DB 4; Length 504;  
 Best Local Similarity 29.2%; Pred. No. 4.8e+02;  
 RESULT 1415  
 ID ADG74270 standard; protein; 512 AA.  
 DE Mouse frizzled protein, SEQ ID NO 55.  
 PN W0200292635-A2.  
 PD 21-NOV-2002.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 13.2%; Score 54; DB 7; Length 512;  
 Best Local Similarity 19.6%; Pred. No. 4.9e+02;  
 RESULT 1416  
 ID ABB68395 standard; protein; 527 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 31977.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 13.2%; Score 54; DB 4; Length 527;  
 Best Local Similarity 34.0%; Pred. No. 5.1e+02;  
 RESULT 1417  
 ID ADG74256 standard; protein; 529 AA.  
 DE Rat frizzled protein, SEQ ID NO 41.  
 PN W0200292635-A2.  
 PD 21-NOV-2002.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 13.2%; Score 54; DB 7; Length 529;  
 Best Local Similarity 19.6%; Pred. No. 5.1e+02;  
 RESULT 1418  
 ID ABB65176 standard; protein; 540 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 22320.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 13.2%; Score 54; DB 4; Length 540;  
 Best Local Similarity 40.0%; Pred. No. 5.2e+02;  
 RESULT 1419  
 ID AAU38962 standard; protein; 540 AA.  
 DE Drosophila G-protein coupled receptor, GCPR #40.  
 PN W0200170980-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 13.2%; Score 54; DB 4; Length 540;  
 Best Local Similarity 40.0%; Pred. No. 5.2e+02;  
 RESULT 1420  
 ID AAB86952 standard; protein; 540 AA.  
 DE D. melanogaster peptide receptor SEQ ID 2.  
 PN DB10013618-A1.  
 PD 20-SEP-2001.  
 PA (FARB ) BAYER AG.  
 Query Match 13.2%; Score 54; DB 4; Length 540;  
 Best Local Similarity 40.0%; Pred. No. 5.2e+02;  
 RESULT 1421  
 ID ADC35868 standard; protein; 540 AA.  
 DE Drosophila G protein coupled receptor seq id 42.  
 PN US2003092124-A1.  
 PD 15-MAY-2003.  
 PA (APPL-) APPLERA CORP.

Query Match 13.2%; Score 54; DB 7; Length 540;  
 Best Local Similarity 40.0%; Pred. No. 5.2e+02;  
 RESULT 1422  
 ID AAU03213 standard; protein; 542 AA.  
 DE Fruit fly G protein coupled receptor, DmGPCR7.  
 PN W0200131005-A2.  
 PD 03-MAY-2001.  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 Query Match 13.2%; Score 54; DB 4; Length 542;  
 Best Local Similarity 40.0%; Pred. No. 5.3e+02;  
 RESULT 1423  
 ID AAE38178 standard; protein; 542 AA.  
 DE Fruit fly G protein-coupled receptor (GPCR) protein #27.  
 PN W02003052078-A2.  
 PD 26-JUN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 13.2%; Score 54; DB 7; Length 542;  
 Best Local Similarity 40.0%; Pred. No. 5.3e+02;  
 RESULT 1424  
 ID ADL83388 standard; protein; 542 AA.  
 DE Drosophila G protein coupled receptor 7 (DmGPCR7).  
 PN US2003162223-A1.  
 PD 28-AUG-2003.  
 PA (LOWE/) LOWERY D E.  
 PA (SMIT/) SMITH V G.  
 PA (KUBI/) KUBIAK T M.  
 PA (LARS/) LARSEN M J.  
 Query Match 13.2%; Score 54; DB 7; Length 542;  
 Best Local Similarity 40.0%; Pred. No. 5.3e+02;  
 RESULT 1425  
 ID ADR03108 standard; protein; 542 AA.  
 DE Drosophila G-protein coupled receptor DmGPCR7.  
 PN US2004121956-A1.  
 PD 24-JUN-2004.  
 PA (LOWE/) LOWERY D E.  
 PA (SMIT/) SMITH V G.  
 PA (KUBI/) KUBIAK T M.  
 PA (LARS/) LARSEN M J.  
 Query Match 13.2%; Score 54; DB 8; Length 542;  
 Best Local Similarity 40.0%; Pred. No. 5.3e+02;  
 RESULT 1426  
 ID ABB75749 standard; protein; 543 AA.  
 DE Mentha spicata limonene synthase.  
 PN W0200220815-A2.  
 PD 14-MAR-2002.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Query Match 13.2%; Score 54; DB 5; Length 543;  
 Best Local Similarity 26.3%; Pred. No. 5.3e+02;  
 RESULT 1427  
 ID ABG75232 standard; protein; 570 AA.  
 DE Hair papilla cell growth promoter related rat protein SEQ ID NO: 6.  
 PN W02003086334-A1.  
 PD 23-OCT-2003.  
 PA (TAIS ) TAIISHO PHARM CO LTD.  
 Query Match 13.2%; Score 54; DB 7; Length 570;  
 Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
 RESULT 1428  
 ID AAW31273 standard; protein; 572 AA.  
 DE Mouse frizzled-7 protein Mfz7 (Wnt receptor).  
 PN W09739357-A1.  
 PD 23-OCT-1997.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 Query Match 13.2%; Score 54; DB 2; Length 572;  
 Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
 RESULT 1429  
 ID ADO29338 standard; protein; 572 AA.  
 DE Mouse GPCR FZD7, SEQ ID NO:439.  
 PN W02004040000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMAL INC.  
 Query Match 13.2%; Score 54; DB 8; Length 572;  
 Best Local Similarity 19.6%; Pred. No. 5.6e+02;

RESULT 1430  
ID ABUS5902 standard; protein; 574 AA.  
DE Human protein Frizzled-7.  
PN WO20027204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 13.2%; Score 54; DB 6; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1431  
ID AAE34056 standard; protein; 574 AA.  
DE FZD7 protein.  
PN WO20029092-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 13.2%; Score 54; DB 6; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1432  
ID ADG74269 standard; protein; 574 AA.  
DE Human frizzled protein, SEQ ID No 54.  
PN WO200292635-A2.  
PD 21-NOV-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 13.2%; Score 54; DB 7; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1433  
ID ADN03982 standard; protein; 574 AA.  
DE Antipsoriatic protein sequence #186.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.2%; Score 54; DB 8; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1434  
ID ADO29337 standard; protein; 574 AA.  
DE Human GPCR FZD7, SEQ ID NO:438.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIN-) PRIMAL INC.  
Query Match 13.2%; Score 54; DB 8; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1435  
ID ADO22264 standard; protein; 574 AA.  
DE Human FZD7 protein (homologue of Drosophila frizzled).  
PN WO2004042028-A2.  
PD 21-MAY-2004.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 13.2%; Score 54; DB 8; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1436  
ID ADQ18261 standard; protein; 574 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1079.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 13.2%; Score 54; DB 8; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1437  
ID ADS92964 standard; protein; 574 AA.  
DE Frizzled homologue 7.  
PN WO2004037990-A2.  
PD 06-MAY-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 13.2%; Score 54; DB 8; Length 574;  
Best Local Similarity 19.6%; Pred. No. 5.6e+02;  
RESULT 1438  
ID AAR74291 standard; protein; 599 AA.  
DE Spearmint limonene synthase.  
PN WO9511913-A1.  
PD 04-MAY-1995.  
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.  
Query Match 13.2%; Score 54; DB 2; Length 599;  
Best Local Similarity 26.3%; Pred. No. 5.9e+02;  
RESULT 1439

ID AAY90838 standard; protein; 599 AA.  
DE Spearmint limonene synthase protein sequence SEQ ID NO:22.  
PN WO200017327-A2.  
PD 30-MAR-2000.  
PA (KENT) UNIV KENTUCKY RES DEPT.  
PA (SALK) SALK INST BIOLOGICAL STUDIES.  
Query Match 13.2%; Score 54; DB 3; Length 599;  
Best Local Similarity 26.3%; Pred. No. 5.9e+02;  
RESULT 1440  
ID AAB29400 standard; protein; 599 AA.  
DE Spearmint limonene synthase.  
PN JP2000245482-A.  
PD 12-SEP-2000.  
PA (SOZO-) SOZOTEKI SEIBUTSU KOGAKU KENKYUSHO KK.  
Query Match 13.2%; Score 54; DB 3; Length 599;  
Best Local Similarity 26.3%; Pred. No. 5.9e+02;  
RESULT 1441  
ID AAY70716 standard; protein; 599 AA.  
DE Mint 4S-limonene synthase.  
PN WO200022150-A2.  
PD 20-APR-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 13.2%; Score 54; DB 3; Length 599;  
Best Local Similarity 26.3%; Pred. No. 5.9e+02;  
RESULT 1442  
ID AAE29781 standard; protein; 599 AA.  
DE M. spicata limonene synthase.  
PN WO200276189-A1.  
PD 03-OCT-2002.  
PA (SCEN-) SCENTGENE POLLINATION LTD.  
Query Match 13.2%; Score 54; DB 6; Length 599;  
Best Local Similarity 26.3%; Pred. No. 5.9e+02;  
RESULT 1443  
ID ABP77333 standard; protein; 626 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 1196.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 13.2%; Score 54; DB 6; Length 626;  
Best Local Similarity 23.3%; Pred. No. 6.2e+02;  
RESULT 1444  
ID AAG30550 standard; protein; 646 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36543.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 13.2%; Score 54; DB 3; Length 646;  
Best Local Similarity 28.3%; Pred. No. 6.4e+02;  
RESULT 1445  
ID ADQ96834 standard; protein; 648 AA.  
DE CrtWcrty amino acid sequence.  
PN CN1380415-A.  
PD 20-NOV-2002.  
PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.  
Query Match 13.2%; Score 54; DB 7; Length 648;  
Best Local Similarity 25.5%; Pred. No. 6.4e+02;  
RESULT 1446  
ID ABB91533 standard; protein; 651 AA.  
DE Herbicidally active polypeptide SEQ ID NO 744.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 13.2%; Score 54; DB 5; Length 651;  
Best Local Similarity 25.0%; Pred. No. 6.5e+02;  
RESULT 1447  
ID ADS28528 standard; protein; 662 AA.  
DE Bacterial polypeptide #17561.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.

Query Match 13.2%; Score 54; DB 8; Length 662;  
Best Local Similarity 30.9%; Pred. No. 6.6e+02;  
RESULT 1448  
ID AAG30549 standard; protein; 666 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36542.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 13.2%; Score 54; DB 3; Length 666;  
Best Local Similarity 28.3%; Pred. No. 6.6e+02;  
RESULT 1449  
ID AAG30548 standard; protein; 690 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36541.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 13.2%; Score 54; DB 3; Length 690;  
Best Local Similarity 28.3%; Pred. No. 6.9e+02;  
RESULT 1450  
ID ABB91874 standard; protein; 690 AA.  
DE Herbicidically active polypeptide SEQ ID NO 1085.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 13.2%; Score 54; DB 5; Length 690;  
Best Local Similarity 28.3%; Pred. No. 6.9e+02;  
RESULT 1451  
ID ABM8550 standard; protein; 693 AA.  
DE Mouse protein sequence MCP20781.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 13.2%; Score 54; DB 7; Length 693;  
Best Local Similarity 19.6%; Pred. No. 6.9e+02;  
RESULT 1452  
ID ASG06948 standard; protein; 726 AA.  
DE Klebsiella pneumoniae polypeptide seqid 7465.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.2%; Score 54; DB 7; Length 726;  
Best Local Similarity 37.0%; Pred. No. 7.3e+02;  
RESULT 1453  
ID ABU08035 standard; protein; 1040 AA.  
DE Protein encoded by Prokaryotic essential gene #6362.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.2%; Score 54; DB 6; Length 1040;  
Best Local Similarity 26.1%; Pred. No. 1.1e+03;  
RESULT 1454  
ID AAY19585 standard; protein; 42 AA.  
DE Amino acid sequence of a human secreted protein.  
PN WO9922243-A1.  
PD 06-MAY-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.0%; Score 53.5; DB 2; Length 42;  
Best Local Similarity 41.7%; Pred. No. 34;  
RESULT 1455  
ID AAU67019 standard; protein; 75 AA.  
DE Propionibacterium acnes immunogenic protein #27915.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.0%; Score 53.5; DB 4; Length 75;  
Best Local Similarity 35.9%; Pred. No. 65;  
RESULT 1456  
ID ABM63538 standard; protein; 75 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28214.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.0%; Score 53.5; DB 6; Length 75;  
Best Local Similarity 35.9%; Pred. No. 65;  
RESULT 1457

ID ABG16129 standard; protein; 81 AA.  
DE Novel human diagnostic protein #16120.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSB-) HYSRQ INC.  
Query Match 13.0%; Score 53.5; DB 4; Length 81;  
Best Local Similarity 35.7%; Pred. No. 71;  
RESULT 1458  
ID AAU65184 standard; protein; 86 AA.  
DE Propionibacterium acnes immunogenic protein #26080.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 13.0%; Score 53.5; DB 4; Length 86;  
Best Local Similarity 35.9%; Pred. No. 76;  
RESULT 1459  
ID ABM61703 standard; protein; 86 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #26379.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 13.0%; Score 53.5; DB 6; Length 86;  
Best Local Similarity 35.9%; Pred. No. 76;  
RESULT 1460  
ID AAM85927 standard; protein; 90 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:13520.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.0%; Score 53.5; DB 4; Length 90;  
Best Local Similarity 25.0%; Pred. No. 80;  
RESULT 1461  
ID ABP52882 standard; protein; 91 AA.  
DE Human lung specific protein sequence SEQ ID NO:125.  
PN WO200264788-A2.  
PD 22-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 13.0%; Score 53.5; DB 5; Length 91;  
Best Local Similarity 33.3%; Pred. No. 81;  
RESULT 1462  
ID AAO17175 standard; protein; 92 AA.  
DE Human secreted protein SEQ ID NO: 74.  
PN WO200228877-A1.  
PD 11-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.0%; Score 53.5; DB 5; Length 92;  
Best Local Similarity 31.7%; Pred. No. 82;  
RESULT 1463  
ID ABG64769 standard; protein; 92 AA.  
DE Human albumin fusion protein #1444.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.0%; Score 53.5; DB 5; Length 92;  
Best Local Similarity 31.7%; Pred. No. 82;  
RESULT 1464  
ID ADL78036 standard; protein; 92 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1518.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 13.0%; Score 53.5; DB 8; Length 92;  
Best Local Similarity 31.7%; Pred. No. 82;  
RESULT 1465  
ID AAB25032 standard; peptide; 98 AA.  
DE Plant SDF encoded polypeptide sequence SEQ List 2 NO:71.  
PN WO200040695-A2.  
PD 13-JUL-2000.  
PA (CERE-) CERES INC.  
Query Match 13.0%; Score 53.5; DB 3; Length 98;  
Best Local Similarity 34.8%; Pred. No. 88;  
RESULT 1466

ID AAB25031 standard; peptide; 99 AA.  
DE Plant SDF encoded polypeptide sequence SEQ List 2 NO:70.  
PN WO200040695-A2.  
PD 13-JUL-2000.  
PA (CERE-) CERES INC.  
Query Match 13.0%; Score 53.5; DB 3; Length 99;  
Best Local Similarity 34.8%; Pred. No. 89;  
RESULT 1467  
ID AAB25030 standard; peptide; 112 AA.  
DE Plant SDF encoded polypeptide sequence SEQ List 2 NO:69.  
PN WO200040695-A2.  
PD 13-JUL-2000.  
PA (CERE-) CERES INC.  
Query Match 13.0%; Score 53.5; DB 3; Length 112;  
Best Local Similarity 34.8%; Pred. No. 1e+02;  
RESULT 1468  
ID AAB95044 standard; protein; 127 AA.  
DE Human protein sequence SEQ ID NO:16813.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 13.0%; Score 53.5; DB 4; Length 127;  
Best Local Similarity 25.3%; Pred. No. 1.2e+02;  
RESULT 1469  
ID ADQ67536 standard; protein; 132 AA.  
DE Novel human protein sequence #2202.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIO TECHNOLOGY.  
Query Match 13.0%; Score 53.5; DB 8; Length 132;  
Best Local Similarity 22.1%; Pred. No. 1.2e+02;  
RESULT 1470  
ID ABO67211 standard; protein; 147 AA.  
DE Klebsiella pneumoniae polypeptide seqid 13728.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 13.0%; Score 53.5; DB 7; Length 147;  
Best Local Similarity 27.4%; Pred. No. 1.4e+02;  
RESULT 1471  
ID AAU31413 standard; protein; 152 AA.  
DE Novel human secreted protein #1904.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.0%; Score 53.5; DB 4; Length 152;  
Best Local Similarity 25.9%; Pred. No. 1.4e+02;  
RESULT 1472  
ID AAE14696 standard; protein; 174 AA.  
DE Human G-CSF analog (Asp112His).  
PN WO200220766-A2.  
PD 14-MAR-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 13.0%; Score 53.5; DB 5; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1473  
ID AAE14697 standard; protein; 174 AA.  
DE Human G-CSF analog (Gln119His).  
PN WO200220766-A2.  
PD 14-MAR-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 13.0%; Score 53.5; DB 5; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1474  
ID AAE30729 standard; protein; 174 AA.  
DE Human granulocyte colony-stimulating factor (G-CSF) mutant, 'G51X'.  
PN WO200277034-A2.  
PD 03-OCT-2002.  
PA (MERE-) MERCK PATENT GMBH.  
Query Match 13.0%; Score 53.5; DB 6; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1475  
ID AAE30669 standard; protein; 174 AA.

DE Human granulocyte colony-stimulating factor (G-CSF) mutant, L69X #1.  
PN WO200277034-A2.  
PD 03-OCT-2002.  
PA (MERE-) MERCK PATENT GMBH.  
Query Match 13.0%; Score 53.5; DB 6; Length 174;  
Best Local Similarity 26.8%; Pred. No. 1.7e+02;  
RESULT 1476  
ID ABG74382 standard; protein; 174 AA.  
DE Partial human granulocyte colony stimulating factor E46A mutant.  
PN US2002151488-A1.  
PD 17-OCT-2002.  
PA (SARK/) SARKAR C A.  
Query Match 13.0%; Score 53.5; DB 6; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1477  
ID ABG74376 standard; protein; 174 AA.  
DE Partial human granulocyte colony stimulating factor E33A mutant.  
PN US2002151488-A1.  
PD 17-OCT-2002.  
PA (SARK/) SARKAR C A.  
Query Match 13.0%; Score 53.5; DB 6; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1478  
ID ADL90164 standard; protein; 174 AA.  
DE Human G-CSF mutant Asp112His protein.  
PN US2003166527-A1.  
PD 04-SEP-2003.  
PA (SARK/) SARKAR C A.  
Query Match 13.0%; Score 53.5; DB 7; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1479  
ID ADL90166 standard; protein; 174 AA.  
DE Human G-CSF mutant Gln119His protein.  
PN US2003166527-A1.  
PD 04-SEP-2003.  
PA (SARK/) SARKAR C A.  
Query Match 13.0%; Score 53.5; DB 7; Length 174;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1480  
ID AAR14731 standard; protein; 175 AA.  
DE G-CSF mutant G52X.  
PN EP456200-A.  
PD 13-NOV-1991.  
PA (BOEF-) BOEHRINGER MANNHEIM GMBH.  
Query Match 13.0%; Score 53.5; DB 2; Length 175;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1481  
ID AAR56571 standard; protein; 175 AA.  
DE G-CSF analogue, E47A.  
PN WO9417185-A1.  
PD 04-AUG-1994.  
PA (AMGE-) AMGEN INC.  
Query Match 13.0%; Score 53.5; DB 2; Length 175;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1482  
ID AAU97119 standard; protein; 175 AA.  
DE Human G-CSF mutant, Glu33Ala.  
PN WO200220767-A2.  
PD 14-MAR-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 13.0%; Score 53.5; DB 5; Length 175;  
Best Local Similarity 29.6%; Pred. No. 1.7e+02;  
RESULT 1483  
ID AAU97125 standard; protein; 175 AA.  
DE Human G-CSF mutant, Glu46Ala.  
PN WO200220767-A2.  
PD 14-MAR-2002.

PA (AMGE-) AMGEN INC. 13.0%; Score 53.5; DB 5; Length 175;  
 Query Match 29.6%; Pred. No. 1.7e+02;  
 Best Local Similarity  
 RESULT 1484  
 ID AAO00732 standard; protein; 184 AA.  
 DE Human polypeptide SEQ ID NO 14624.  
 PN W0200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC. 13.0%; Score 53.5; DB 4; Length 184;  
 Query Match 25.7%; Pred. No. 1.8e+02;  
 Best Local Similarity  
 RESULT 1485  
 ID ADJ48371 standard; protein; 214 AA.  
 DE Maize oil-associated gene protein #30.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C. 13.0%; Score 53.5; DB 8; Length 214;  
 PA (RAVA/) RAVANELLO M. 26.7%; Pred. No. 2.1e+02;  
 PA (SAVA/) SAVAGE T. 13.0%; Score 53.5; DB 5; DB 8; Length 219;  
 PA (LEDE/) LEDEUX J R. 27.3%; Pred. No. 2.2e+02;  
 PA (ROGE/) ROGERS J A.  
 Query Match  
 Best Local Similarity  
 RESULT 1486  
 ID AP66123 standard; protein; 219 AA.  
 DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:867.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST ) SOC PROD NESTLE SA. 13.0%; Score 53.5; DB 5; Length 219;  
 Query Match 27.3%; Pred. No. 2.2e+02;  
 Best Local Similarity  
 RESULT 1487  
 ID AAU31713 standard; protein; 225 AA.  
 DE Novel human secreted protein #2204.  
 PN W0200179449-A2.  
 PD 25-OCT-2001.  
 PA (HYSE-) HYSEQ INC. 13.0%; Score 53.5; DB 4; Length 225;  
 Query Match 26.9%; Pred. No. 2.3e+02;  
 Best Local Similarity  
 RESULT 1488  
 ID ADS12132 standard; protein; 225 AA.  
 DE Human therapeutic contig protein - SEQ ID 2369.  
 PN W02004080148-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC. 13.0%; Score 53.5; DB 8; Length 225;  
 Query Match 26.9%; Pred. No. 2.3e+02;  
 Best Local Similarity  
 RESULT 1489  
 ID ABG06665 standard; protein; 246 AA.  
 DE Novel human diagnostic protein #6656.  
 PN W0200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC. 13.0%; Score 53.5; DB 4; Length 246;  
 Query Match 24.1%; Pred. No. 2.5e+02;  
 Best Local Similarity  
 RESULT 1490  
 ID AAE21321 standard; protein; 273 AA.  
 DE Mouse MrgB8 (mas-related gene) protein.  
 PN W0200183555-A2.  
 PD 08-NOV-2001.  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY. 13.0%; Score 53.5; DB 5; Length 273;  
 Query Match 35.9%; Pred. No. 2.8e+02;  
 Best Local Similarity  
 RESULT 1491  
 ID ADH08585 standard; protein; 273 AA.  
 DE MrgB8.  
 PN W02004003133-A1.  
 PD 08-JAN-2004.  
 PA (CALY ) CALIFORNIA INST OF TECHNOLOGY. 13.0%; Score 53.5; DB 8; Length 273;  
 Query Match 35.9%; Pred. No. 2.8e+02;  
 Best Local Similarity  
 RESULT 1492  
 ID ABP56664 standard; protein; 301 AA.

DE Chimpanzee C68 adenovirus E4 ORF6 33 kDa protein SEQ ID NO:29.  
 PN W02003000851-A2.  
 PD 03-JAN-2003.  
 PA (UYPE-) UNIV PENNSYLVANIA. 13.0%; Score 53.5; DB 6; Length 301;  
 Query Match 26.9%; Pred. No. 3.1e+02;  
 Best Local Similarity  
 RESULT 1493  
 ID AAW62687 standard; protein; 302 AA.  
 DE Streptococcus pneumoniae polypeptide.  
 PN W09823631-A1.  
 PD 04-JUN-1998.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP. 13.0%; Score 53.5; DB 2; Length 302;  
 PA (SMIK ) SMITHKLINE BEECHAM PLC. 27.8%; Pred. No. 3.1e+02;  
 Query Match  
 Best Local Similarity  
 RESULT 1494  
 ID ABU01717 standard; protein; 302 AA.  
 DE S. pneumoniae type 4 strain protein from coding region #1293.  
 PN W0200277021-A2.  
 PD 03-OCT-2002.  
 PA (CHIR-) CHIRON SPA. 13.0%; Score 53.5; DB 6; Length 302;  
 PA (GENO-) INST GENOMIC RES. 27.8%; Pred. No. 3.1e+02;  
 Query Match  
 Best Local Similarity  
 RESULT 1495  
 ID AAG72999 standard; protein; 313 AA.  
 DE Olfactory receptor-like polypeptide, SEQ ID NO: 2681.  
 PN W0200127158-A2.  
 PD 19-APR-2001.  
 PA (DIGI-) DIGISCENTS. 13.0%; Score 53.5; DB 4; Length 313;  
 PA (YEDA ) YEDA RES & DEV CO LTD. 28.4%; Pred. No. 3.3e+02;  
 Query Match  
 Best Local Similarity  
 RESULT 1496  
 ID AAG71568 standard; protein; 319 AA.  
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1249.  
 PN W0200127158-A2.  
 PD 19-APR-2001.  
 PA (DIGI-) DIGISCENTS. 13.0%; Score 53.5; DB 4; Length 319;  
 PA (YEDA ) YEDA RES & DEV CO LTD. 24.4%; Pred. No. 3.3e+02;  
 Query Match  
 Best Local Similarity  
 RESULT 1497  
 ID ABP38603 standard; protein; 340 AA.  
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3448.  
 PN US6380370-B1.  
 PD 30-APR-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP. 13.0%; Score 53.5; DB 5; Length 340;  
 Query Match 23.1%; Pred. No. 3.6e+02;  
 Best Local Similarity  
 RESULT 1498  
 ID ADS06383 standard; protein; 340 AA.  
 DE Staphylococcus epidermis polypeptide seqid 5678.  
 PN US2004147734-A1.  
 PD 23-JUL-2004.  
 PA (DOUC/) DOUCETTE-STAMM L. 13.0%; Score 53.5; DB 8; Length 340;  
 PA (BUSH/) BUSH D. 23.1%; Pred. No. 3.6e+02;  
 Query Match  
 Best Local Similarity  
 RESULT 1499  
 ID ABP29664 standard; protein; 419 AA.  
 DE Streptococcus polypeptide SEQ ID NO 8504.  
 PN W0200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA. 13.0%; Score 53.5; DB 5; Length 419;  
 PA (GENO-) INST GENOMIC RES. 33.3%; Pred. No. 4.5e+02;  
 Query Match  
 Best Local Similarity  
 RESULT 1500  
 ID ABU21535 standard; protein; 420 AA.  
 DE Protein encoded by Prokaryotic essential gene #7062.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
Query Match 13.0%; Score 53.5; DB 6; Length 420;  
Best Local Similarity 29.6%; Pred. No. 4.6e+02;